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*Publication Title:*

*NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS*

*Abstract:*

*The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.*

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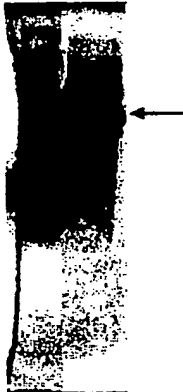
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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<p>(21) International Application Number: PCT/US99/09346</p> <p>(22) International Filing Date: 30 April 1999 (30.04.99)</p> <p>(30) Priority Data:</p> <table style="width: 100%; border: none;"> <tr> <td style="width: 30%;">60/083,758</td> <td style="width: 40%;">1 May 1998 (01.05.98)</td> <td style="width: 30%;">US</td> </tr> <tr> <td>60/094,869</td> <td>31 July 1998 (31.07.98)</td> <td>US</td> </tr> <tr> <td>60/098,994</td> <td>2 September 1998 (02.09.98)</td> <td>US</td> </tr> <tr> <td>60/099,062</td> <td>2 September 1998 (02.09.98)</td> <td>US</td> </tr> <tr> <td>60/103,749</td> <td>9 October 1998 (09.10.98)</td> <td>US</td> </tr> <tr> <td>60/103,794</td> <td>9 October 1998 (09.10.98)</td> <td>US</td> </tr> <tr> <td>60/103,796</td> <td>9 October 1998 (09.10.98)</td> <td>US</td> </tr> <tr> <td>60/121,528</td> <td>25 February 1999 (25.02.99)</td> <td>US</td> </tr> </table> <p>(71) Applicants (for all designated States except US): CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US). THE INSTITUTE FOR GENOMIC RESEARCH [US/US]; 9212 Medical Center Drive, Rockville, MD 20850 (US).</p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; Rockville, MD (US). GALEOTTI, Cesira [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). GRANDI, Guido [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). HICKEY, Erin [US/US]; Gaithersburg, MD</p>			60/083,758	1 May 1998 (01.05.98)	US	60/094,869	31 July 1998 (31.07.98)	US	60/098,994	2 September 1998 (02.09.98)	US	60/099,062	2 September 1998 (02.09.98)	US	60/103,749	9 October 1998 (09.10.98)	US	60/103,794	9 October 1998 (09.10.98)	US	60/103,796	9 October 1998 (09.10.98)	US	60/121,528	25 February 1999 (25.02.99)	US
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<p><b>919 (46 kDa)</b></p> <p><b>A) PURIFICATION</b></p> <div style="text-align: center;"> <p>M1 919</p>  </div>																										



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## NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

### BACKGROUND

*Neisseria meningitidis* is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

*N. meningitidis* causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

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United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of  $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

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Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (eg. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

## BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

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Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

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Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

## THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

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homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least *n* consecutive amino acids from the sequences and, depending on the particular sequence, *n* is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (*ie.* substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins)

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least *n* consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, *n* is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

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organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (I) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

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Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

#### Methodology - Summary of standard procedures and techniques.

##### General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

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All publications, patents, and patent applications cited herein are incorporated in full by reference.

### Expression systems

The *Neisseria* menB nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

#### i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

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regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Bimstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

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Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

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## ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Rept.* 11(2):165-185.

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Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

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The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

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These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

### iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

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those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

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Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human ( $\alpha$ -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

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Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15  $\mu$ m in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

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The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

#### iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

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initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

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(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

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signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

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vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with  $\text{CaCl}_2$  or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

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electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412.

#### v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

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Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

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superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

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sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

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Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guilliermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

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*Bacteriol.* 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; Pichia]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

#### Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisserial* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisserial* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisserial* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

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An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

#### Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria menB* proteins.

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Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

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are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly  $^{32}\text{P}$  and  $^{125}\text{I}$ ), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example,  $^{125}\text{I}$  may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with  $^{125}\text{I}$ , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

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or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

#### Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

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organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

#### Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

#### Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

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liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi<sup>TM</sup> adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox<sup>TM</sup>); (3) saponin adjuvants, such as Stimulon<sup>TM</sup> (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

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The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

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### Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

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Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

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described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

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immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

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Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP- 0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

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A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

### **Delivery Methods**

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

### **Polynucleotide and polypeptide pharmaceutical compositions**

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

#### **A. Polypeptides**

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

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granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

#### B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

#### C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

#### D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

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DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, eg. Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See eg. Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

#### E. Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (supra); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

#### F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

#### Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin<sup>®</sup>, and lipofectAMINE<sup>®</sup> are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

#### Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are



assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

### **Nucleic Acid Hybridisation**

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated  $T_m$  of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to  $10^{-9}$  to  $10^{-8}$  g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

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yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of  $10^8$  cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than  $10^8$  cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature ( $T_m$ ) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4\%[(G + C)] - 0.6(\% \text{formamide}) - 600/n - 1.5(\% \text{mismatch}).$$

where  $C_i$  is the salt concentration (monovalent ions) and  $n$  is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with 95% to 100% homology to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

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washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

### **Nucleic Acid Probe Assays**

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

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Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

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containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

## EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

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alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

#### **Chromosomal DNA Preparation**

*N.meningitidis* strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl<sub>3</sub>/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

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The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

### Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	( <i>Bam</i> HI- <i>Nde</i> I )
	<u>CGCGGATCCGCTAGC</u>	( <i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	( <i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	( <i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	( <i>Xho</i> I)
	<u>CCCGCTCGAG</u>	( <i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) AAAG <u>AA</u> TTT	( <i>Eco</i> RI )
	(AAA) AAAGGTACC	( <i>Kpn</i> I)
3'-end primer tail:	(AAA) AAACTGCAG	( <i>Pst</i> I)
	(AAA) AAATCTAGA	( <i>Xba</i> I)

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

## Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40μM of each oligonucleotide primer, 400-800μM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl<sub>2</sub>), 2.5 units *TaqI* DNA polymerase (using



Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H<sub>2</sub>O or 10mM Tris, pH 8.5.

#### **Digestion of PCR fragments**

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H<sub>2</sub>O or 10mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

#### **Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)**

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD<sub>260</sub> of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD<sub>260nm</sub> and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

#### **Cloning**

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

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ratio of 3:1 fragment/vector was ligated using 0.5  $\mu$ l of NEB T4 DNA ligase (400 units/ $\mu$ l), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100  $\mu$ l *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800  $\mu$ l LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200  $\mu$ l of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml ).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100  $\mu$ g/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30  $\mu$ l. 5  $\mu$ l of each individual miniprep (approximately 1g ) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20 $\mu$ l, that included 0.5 $\mu$ l T4 DNA ligase (400 units/ $\mu$ l, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100 $\mu$ l of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800 $\mu$ l LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200 $\mu$ l of the supernatant and plated onto LB ampicillin (100mg/ml ) agar.

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Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

### Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD<sub>600</sub> ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

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resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

#### **GST-fusion proteins large-scale purification.**

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD<sub>550</sub> 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD<sub>280</sub> of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M'') (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD<sub>550nm</sub> reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

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The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD<sub>280nm</sub> of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

#### **His-fusion soluble proteins large-scale purification.**

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD<sub>550</sub> 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni<sup>2+</sup>-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

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resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

#### **His-fusion insoluble proteins large-scale purification.**

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D<sub>550</sub> 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni<sup>2+</sup>-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD<sub>280</sub> of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

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**Purification of His-fusion proteins.**

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD<sub>550nm</sub> reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni<sup>2+</sup>-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

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collected until the  $OD_{280nm}$  indicated all the recombinant protein was obtained. 20 $\mu$ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

### **His-fusion proteins renaturation**

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 $\mu$ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 $\mu$ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

### **Purification of proteins**

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 $\mu$ l buffer M1 (PBS pH 7.2). 25 $\mu$ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH<sub>2</sub> PO<sub>4</sub>] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH<sub>2</sub>PO<sub>4</sub>] overnight at 4°C. The

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supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

### **Mice immunisations**

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)<sub>3</sub> as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

### **ELISA assay (sera analysis)**

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN<sub>3</sub> in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H<sub>2</sub>O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H<sub>2</sub>SO<sub>4</sub> was added to each well and OD<sub>490</sub> was followed. The ELISA was considered positive when OD<sub>490</sub> was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN<sub>3</sub> in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

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phenildiamine and 10 $\mu$ l of H<sub>2</sub>O<sub>2</sub>) were added to each well and the plates were left at room temperature for 20 minutes. 100 $\mu$ l of 12.5% H<sub>2</sub>SO<sub>4</sub> was added to each well and OD<sub>490</sub> was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD<sub>490</sub> value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD<sub>490</sub> of 0.4 was higher than 1:400.

#### **FACScan bacteria Binding Assay procedure.**

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN<sub>3</sub>) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD<sub>620</sub> of 0.07. 100 $\mu$ l bacterial cells were added to each well of a Costar 96 well plate. 100 $\mu$ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 $\mu$ l/well of blocking buffer in each well. 100 $\mu$ l of R-Phicoerytrin conjugated F(ab)<sub>2</sub> goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 $\mu$ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 $\mu$ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

#### **OMV preparations**

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice ( 50% duty cycle, 50% output ). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

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fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

#### **Whole Extracts preparation**

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

#### **Western blotting**

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

#### **Bactericidal assay**

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD<sub>620</sub> was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD<sub>620</sub> of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

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50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

### Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° ( in according to Tm of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

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- 919.1 (forward) AAAATGCCTCTCCACGGCTG or  
CTGCGCCCTGTGTTAAAATCCCCT
- 919.2 (forward) ATCCTTCCGCCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or  
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCCC
- 919.10 (reverse) TCGTTCCGGCGGGGTCGGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

### EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

**Table 1: Oligonucleotides used for PCR for Examples 2-10**

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCAGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTACTTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
206	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA <SEQ ID 3032>	XhoI
	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
287	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
406	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC <SEQ ID 3036>	XhoI
	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

### Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the



designated sequences being compared, the designated sequence controls and is the actual sequence being compared.

ORF:      contig:

279 gnm4.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3039>:  
m279.seq

1	ATAACGCGGA	TTTGCGGCTG	CTTGATTTC	ACGTTTTTCA	GGCTTCGGC
51	AAGTTTGTCT	GCGGCGGGTT	TCATCAGGCT	GCAATGGGAA	GGTACGGACA
101	CGGGCAGCGG	CAGGGCGCGT	TTGGCACCGG	CTTCTTTGTC	GGCAGCCATG
151	GCGCGTCCGA	CGCGGGCGCT	CTTGCTTCGA	ATCACGATTT	GTCCGGGTGA
201	GTTGAAGTTG	AGGGCTTCGA	GGATTCCTGT	TTGGCGGGCT	TCGGACAAAA
251	TGGCTTTAAC	CTGCTCATCT	TCCAAGCCGA	GAATCCGCGC	CATTGCGCCC
301	ACGCCTTGCG	GTAACGCGGA	CTGCATCAGT	TCGGCGCGCA	GGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	TCAATGCGCC	GGCGGCAACG	AGTGCGGTGT
401	ATTCCCGCG	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCTAAATAG				

This corresponds to the amino acid sequence <SEQ ID 3040; ORF 279>:  
m279.pep

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1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTSLWAA SAQMALTCS SKPRIAATAP
101 TPCGTADCIS SARRRSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

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The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3041>:  
g279.seq

1	atgacgcgga	tttgcggtg	cttgatttca	acggttttga	gtgtttcggc
51	aagtttgtcg	gcggcggggt	tcatcaggct	gcaatgggaa	ggaacggata
101	cgggcagcgg	cagggcgcgt	ttggcccg	cttctttggc	ggcagccatg
151	gtgcgtccga	cggcgcgccg	cttgctctga	atcacgactt	gtccgggcga
201	gttgaaattg	acggcttcga	ccattctgcc	ctgtgcggat	tcgggacaaa
251	tctgcctgac	ctgttcatct	tccaaaccca	aaatggccgc	caatgcgcct
301	acgccttgcg	gtacggcgga	ctgcattcagt	tcggcgcgca	ggcggacgag
351	tttgacggga	tcggcaaaat	ccaatgcttc	ggcggcgaca	agcgcggtgt
401	attcgccgag	gctgtgtccg	gcaacggcgg	caggcgtttt	gccgccact
451	tccaataaq				

This corresponds to the amino acid sequence <SEQ ID 3042; ORF 279.ng>:  
q279.pep

1 MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM  
51 VRPTAAALPA ITTCPGELKL TASITSPCAD SAQICLTCS SKPKMAAIAP  
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPTT  
151 SK\*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

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      10          20          30          40          50          60
m279.pep  ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA
           :|||:|||::|: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g279       MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA
           10          20          30          40          50          60

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a279.seq

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1 ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNN A GGGCTTCGGC
51 GAGTTTGTCT GCGGCGGGTT TCATGAGGCT GCAATGGGA GGTACNGACA
101 CNGGCAGCGG CAGGCGCGCT TTGGCGCCGG CTTCCTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGT ATTGCCTGCA ATCAGCACTT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACCTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTTCATCT TCCAAGCCGA GAATCGCGCG CATTCGCGCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GGCGGCAACN AGTGCGGTGT
401 ATCCGCCGAN GCTGTGTCCG GCAACGCGCG CAGGCGTTTT GCCGCCCGCT
451 TCCGAATAG
```

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	ARSTAAALPA	ITTCPELKL	TASTTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRTSLTA	SAKSNAPAA	SAVYSPXCLP	ATAAGVLPPA
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA					
	:					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAOALTCCSSSKPRIAAAIAPTPCGTADCISSARRRTSLTA					
			:			
a279	ITTCPGELKLTASTTSSCADSAQICFTCCSSSKPRIAAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279	SAKSNAPAATSAVYSPXLCFATAAGVLPPASEX					
	130	140	150			

```
m519.seq (partial)
1 ..TCCGTATCG GCGCATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTt9GG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAG ACTTGGTTCC GCCGCAAGAA
151 ATGCTTCGCT CAATGCAGGC GCAAATTACT GCCGCAACGC AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
```

```

251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCC3CATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTGTG CGAAGCCAAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLLSAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
1 atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggtttcaa
51 atcctttgtc gtcatccccc agcaggaagt ccacgttgctc gaaagcctcg
101 ggcgtttcca tcgcgccttg acggccggtt tgaatatattt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta ttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cggtatcggtg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgcgga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcggtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgcog agaaaatcgc ccgcatcaac cgcgccaag
701 gcgaagcgga atccctgctc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag ccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaataa
951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
1 MEFFIILLAA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFQV TDPKCLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLYRIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAN
251 RQIAAALQTO SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFP S EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519

m519.pep                               10      20      30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
g519      YFQVTDPKCLASYGSSNYIMAITQLAQTTLRVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100      110      120      130      140

m519.pep          40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGGQREAE

```

```

a519.seq
1  ATGGAATTTT  TCATTATCTT  GCTGGCAGCC  GTCGTTGTTT  TCGGCTTCAA
51  ATGCGTTTGT  GTCATCCGAC  AGCAGGAAGT  CCACGTTGTG  GAAAGGCTCG
101 GGCCTTTCCA  TCGCGCCCTG  ACGCGCGGTT  TGAATATTTC  GATTCCCTTT
151 ATCGACCCGC  TCGCCTACCG  CCATTGCTG  AAAGAAATCC  GTTTAGACTT
201 ACCCAGCCAG  GTCTGCATCA  CGCGCGACAA  TACGCAGGTG  ACTGTTGACG
251 STATCATCTA  TTTCCAAGTA  ACCGACCCCA  AACTCGCCTC  ATACGGTTTC
301 AGCAACTACA  TTAGGCGGAT  TACCCAGCTT  GCCCAAACGA  CGCTGCGTTG
351 CGTTATCGGG  CGTATGGAAT  TGGACAAAAC  GTTTGAAGAA  CGCGACGAAA
401 TCAACAGCAC  CGTCGTCTCC  GCCTCGATG  AAGCCGCGCG  AGCTTTGGGT
451 GTGAAGGTTT  TGCCTTATGA  GATTAAGAC  TTGGTTCCGC  CGCAAGAAAT
501 CCTTCGCTCA  ATCGAGCGCG  AAATTACTGC  TGAACGCGAA  AAGCGCGCCC
551 GTATCGCCGA  ATCCGAAGGT  CGTAAATCG  AACAAATCAA  CCTTGCCAGT
601 GGTCAGCGCG  AAGCCGAAT  CCAACAATCC  GAAGCGCAGG  CTCAGGCTGC
651 GGTCAATGCG  TCAAATGCCG  AGAAATCGC  CGGCATCAAC  CGCGCCAAAG
701 GTGAAGCGGA  ATCCTTGCGC  CTTGTTGCCG  AACCCAATGC  CGAAGCCATC
751 CGTCAAATTG  CCGCCGCCCT  TCAAACCCAA  GGCGGTGCGG  ATGCGGTCAA
801 TCTGAGATT  GCGGAACAAT  ACGTCGCCGC  GTTCAACACAT  CTGCCCAAAG
851 AAAGCAATAC  GGTGATTATG  CCGCGCAATG  TTGCCGCACAT  CGGCAGCCTG
901 ATTTCTGCCG  GTATGAAAAAT  TATCGACAGC  AGCAAAACCG  CCAAAATAA

```

a519.pep

1	MEFFIILLAA	VVVFGEKSFV	VIPQEEVHV	ERLGRFHRAL	TAGLNILIPF
51	IDRVAYRHSL	KEIPLDVPQS	VCITDRNTQL	TVDGIIYFQV	TDPKLASYGS
101	SNYIMAITQL	AQTLRSVIG	RMELDKTFEE	REINSTVVS	ALDEAAGAWG
151	VKVLRYEIKD	LVPPEILRS	MQAQITAERE	KRARIAESEG	RKIEQINLAS
201	GQREAEIQQS	EGEAQAAVNA	SNAEKIARIN	RAKGEAESLR	LVAEANAIAI
251	QRIAAALQDS	GGADAVNLKI	AEQYVAEFNN	LAKESNTLIM	PANVADIGSL
301	ISAGMKIOTS	SKTAK*			

m519.pep				10	20	30
				SVIGRMELDKT	FEERDEINSTV	VVAALDEAA
a519	YFQV	DPKL	ASYG	SSNY	IMAIT	QLAQ
	90	100	110	120	130	140
				TLRSVIGRMELDKT	FEERDEINSTV	VVSALDEAA
m519.pep		40	50	60	70	80
		GAWGV	KVLR	YEIK	DLVP	PQEIL
a519		GAWGV	KVLR	YEIK	DLVP	PQEIL
	150	160	170	180	190	200
				RLSMQAQITA	EREKRARIAE	SEGRKIEQIN
				LA	SL	ASGOREAE
	100	110	120	130	140	150

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                |||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                |||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51  ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TCGGTTATCA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILVA VAVFGKFSV VIPOQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEIILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGCTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep  
1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF  
51 IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS  
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
201 GQREAEIQQS EGEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI  
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
301 ISAGMKIIDS SKTAK\*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGKIEQINLASQREAEIQSEGEAQAANASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASQREAEIQSEGEAQAANASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq  
1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA  
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG  
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT  
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT  
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG  
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCT  
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC  
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA

```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCGCG CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTGCGC CTTGTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFGEKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEEAI
251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

a519-1.pep	10	20	30	40	50	60
	MEFFIILLAAVVVFGEKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
	10	20	30	40	50	60
a519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
a519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
a519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
a519-1.pep	250	260	270	280	290	300
	LVAEANAEEAIRQIAAALQQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAEEAIRQIAAALQQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
a519-1.pep	310					
	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAC GCGGCGCCCG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTCCGG
551 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

```
m576.pep.. (partial)
1  ..MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLIVFDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

```
g576.seq.. (partial)
1  ..atgggctggtg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttctctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttcgggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgta ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggtgcgagg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaaa
601 gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa
```

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

```
g576.pep.. (partial)
1  ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGEAFLEK NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVY DGKEIKMTEE QAQEVMMKFLO
              |||

```



80

```

g576          MGVDIGRSLKQMKGEAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLO
                10      20      30      40      50

m576.pep      70      80      90      100     110     120
EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGEKQPTKDDIV
|||||
g576          60      70      80      90      100     110
EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGEKQPTKDDIV

m576.pep      130     140     150     160     170     180
TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
|||||
g576          120     130     140     150     160     170
TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE

m576.pep      190     200     210     220
QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN*
|||||
g576          180     190     200     210
QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAAATGAAG GAACAGGGCG CCGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC  CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC SGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGCGCA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

m576.pep      10      20      30
MQQASYAMGVDIGRSLKQMKGEAEIDLKV
|||||
a576          30      40      50      60      70      80
CGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGVDIGRSLKQMKGEAEIDLKV

m576.pep      40      50      60      70      80      90
FTEAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA
|||||
a576          90      100     110     120     130     140
FTEAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA

```

	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPFVTFPLSQ					
a576	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPFVTFPLSQ					
	150	160	170	180	190	200
m576.pep	VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
a576	VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
	210	220	230	240	250	260
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

g576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

```

701 CCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTGACGT GAAACTGGTC  
 751 AAAATCGGCG CACCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA  
 801 CATCAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASAA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ  
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPDQVDIKK VN\*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL TLSAALALSACGKKEAPASASEPAASAAQGDTSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL TLSAALALSACGKKEAPASASEPAASAAQGDTSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKAN GGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKAN GGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKAN GGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKAN GGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLV KIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLV KIGAPENAPAKQPDQVDIKKVN					
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC  
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC  
 101 CTGCCGCCG TTCTTCGCG CAGGCGACA CCTCTCGAT CGGCAGCAG  
 151 ATGCAGCAG CAAGCTATGC GATGGCGTG GACATCGGAC GCTCCCTGAA  
 201 GCAATGAAG GAACAGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG  
 251 CCATGCAGG AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG  
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT  
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT  
 401 TTCTGAAAGA AAATGCCGCC AAAGACGCGG TGAAGACCAC TGCTTCCGGC  
 451 CTGCAATACA AAATCACCAC ACAGGCGGAA GGCAACAGC CGACCAAGA  
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT  
 551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA  
 601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA  
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGGCG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep  
 1 MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASSA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ  
 101 AQEVMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ  
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPAQVDIKK VN\*

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

a576-1.pep	10	20	30	40	50	60
	MNTIFKISALTLSAALALSACGKKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAQEVMKFLOEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAQEVMKFLOEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	250	260	270			
	ATLVFDVKLVKIGAFENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAFENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq  
 1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT  
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA  
 101 CATCCGTCAT CAACGGCCCG GACCGGCCCG TCGGCATCCC CGACCCCGCC  
 151 GGAACGACGG TCGCGGCGCG CGGGGCCGTC TATACCGTTG TACCGCACCT  
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT  
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG  
 301 TCGGCCAAG CCTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT  
 351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG  
 401 CCGGTACGGT TACCGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

```

451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCcG ATTCCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCTTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGTATAGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAACCTCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTTG TCGCCACCGC CCATCCGGT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGCAGGAAG CCGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1  MKKYLFRAL YGIAAAILAA COSKSIOTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDBR
151 RTAQRFPFIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPOR LAEVLQNPNS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCGGCGCG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggT tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGGTAT TACGAACCGG TGCTGAAGGG CGACCGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCGCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGcgcgCTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tCGaacttTT TTTTATGCAC AtccaaggCT CGGGCCGCTT
801 GAAAACCCcG tccggcaaat acatCCGCat cgggTacgcc gacAAAAACG
851 AACatccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

```

g919.pep
  1 MKKHLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
 51 GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPVSI GRYMADKGYL
301 KLGOTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGVVWQL LPNGMKPEYR P*

```

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

```

m919/g919

      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g919      MKKHLRSALYGIAAAILAACQSRSIQTFPQDTSVINGPDRPAGIPDPAGTTVAGGGAV
          10      20      30      40      50      60

      70      80      90      100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKQFFER
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g919      YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKRFFER
          70      80      90      100     110     120

      130     140     150     160     170     180
m919.pep YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g919      YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYIGIPDDFISVPLPAGLRGGKN
          130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRFLPYHTRNQINGGAL
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g919      LVRIRQTGKNSGTIDNAGGTHTADLSRFPI TARTTAIKGRFEGRFLPYHTRNQINGGAL
          190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPVSI GRYMADKGYL
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g919      DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPVSI GRYMADKGYL
          250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGOTSMQGI KSYMQRNPORLAEVLGQNPSYIFFRELAYSNDGPVGALGTPLMGEYAGA
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g919      KLGOTSMQGI KAYMRQNPORLAEVLGQNPSYIFFRELAYSNDGPVGALGTPLMGEYAGA
          310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g919      IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          370     380     390     400     410     420

```

```

          430      440
m919.pep  QKTTGYVWQLLPNGMKPEYRPX
          |||||
g919      QKTTGYVWQLLPNGMKPEYRPX
          430      440

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCGTCAT CAACGGCCCG GACCGCCCG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGCGGCCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCTGCCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCCCCAAG CCTTCAAAC CCCGTCCAT TCCGTTAGG CAAAACAGTT
351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCTGCCG GTTTGGGAG CGGAAAAGCC CTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCGCTTCTCT CCCCTACAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCGATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCGCTGA TGGCGGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CTTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAAGT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAADFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPQR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

```

          10      20      30      40      50      60
m919.pep  MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKQFFER
          |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
          70      80      90      100     110     120

```

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLA3TVTGYE	PVLKGDDRR	TAQARFPIY	GIPDDFIS	SVPLPAGL	RSKGK
a919	YFTPWQVAGNGSLA3TVTGYE	PVLKGDDRR	TAQARFPIY	GIPDDFIS	SVPLPAGL	RSKGK
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGT	HTADLSRFP	ITARTTAIK	GRFEGSRFL	PHYHTRN	QINGGAL
a919	LVRIRQTGKNSGTIDNTGGT	HTADLSRFP	ITARTTAIK	GRFEGSRFL	PHYHTRN	QINGGAL
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMH	IQSGSRLK	TPSGKYIR	IGYADKNE	HPYVSIGR	YMADKGYL
a919	DGKAPILGYAEDPVELFFMH	IQSGSRLK	TPSGKYIR	IGYADKNE	HPYVSIGR	YMADKGYL
	310	320	330	340	350	360
m919.pep	KLQOTSMQGIKSYMQRNPOR	LAEVLGQN	PSYIFFRE	LAGSSNDG	PGVAGLGT	PLMGEYAGA
a919	KLQOTSMQGIKSYMQRNPOR	LAEVLGQN	PSYIFFRE	LAGSSNDG	PGVAGLGT	PLMGEYAGA
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPV	TRKALNRL	IMAQDTGS	AIKGAVRV	DYFWGYG	DEAGELAGK
a919	VDRHYITLGAPLFVATAHPV	TRKALNRL	IMAQDTGS	AIKGAVRV	DYFWGYG	DEAGELAGK
	430	440				
m919.pep	OKTTGYVWQLLPNGMKPEY	RXP				
a919	OKTTGYVWQLLPNGMKPEY	RXP				

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGC CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCGGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCGCTGCTG GCGxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxGAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCGGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```



1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG  
1101 A

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

m121.pep

1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL  
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ  
101 TVRHAPHEGY SIQLADLPLL Axxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
151 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx  
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL  
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV  
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK  
351 ATGASKPCIL XAGYYY\*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3077>:

g121.seq

1 ATGGAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG  
51 GGCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG  
101 AAGGGCACGC CTTTACCCCC TACCTGACC GGTGCGCCG CAAATTGCTG  
151 GATTTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC  
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA  
251 GTCAAACCT CGCTCCGTGC GACATTACCG CCTCGGGTG CCACGGGCAA  
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT  
351 GCCGCTGCTG GCGGAAGTga cgcggatttT TACCGTCggc gacttcCGCA  
401 GCCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCGCCTTT  
451 CACGAAGCCC TGTTCGCGCA TGACAGGGAA ACACGCGTGG TACTGAACAT  
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCGCGCGCA CCCGCCTTCG  
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca  
601 cacTGGcagc TGCCTTACGA CAAAAacggt gcAAAgcgag cacAAGGCAA  
651 catatTGCcg CAACTGCTCG gcaggctGCT CGCCcaccCG TATTCTCAC  
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggctc  
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgct  
801 ttcccgatcc accgcgcaaA ccgTttggga cgcggtctca CACGCAGCGG  
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT  
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG  
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATttg  
1001 cgtggttgG GCGGTGTTGG ATTAACCGCA TTCCCGGTAG TCCGCACAAA  
1051 GCGACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG  
1101 A

This corresponds to the amino acid sequence <SEQ ID 3078; ORF 121.ng>:

g121.pep

1 METQLYIGIM SGTSMGDADA VLVRMDGGKW LGAEGHAFTP YPDRLLRRKLL  
51 DLQDTGTDEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ  
101 TVRHAPHEGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAFLVPAF  
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA  
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL  
251 ETYLDGGENR YDVLRTLSRF TAQTVWDAYS HAAADARQMY ICGGGIRNPV  
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK  
351 ATGASKPCIL GAGYYY\*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW	LGAEGHAFTPYPGRLLRRQLLDLQDTGADEL				
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKW	LGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	:					

```

g121      HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
           70      80      90      100     110     120
           130     140     150     160     170     180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130     140     150     160     170     180
           190     200     210     220     230     240
m121.pep  XXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : |||||:||||| |||||:| |||||
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190     200     210     220     230     240
           250     260     270     280     290     300
m121.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121      GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDVSHAAADARQMYICGGGIRNPV
           250     260     270     280     290     300
           310     320     330     340     350     360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPQWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
g121      LMADLAECFGTRVSLHSTAE LNLDPQWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           310     320     330     340     350     360

m121.pep  XAGYYYYX
           |||||
g121      GAGYYYYX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGACACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCGCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGACGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCC
1001 CATGGATGSC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAEE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPDDA PAFGFDTGPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMDLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK  
 351 ATGASKPCIL GAGYYY\*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAF	TPYPGR	LRRQLLDLQDTGADEL	
a121	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAF	TPYPGR	LRRQLLDLQDTGADEL	
	10	20	30	40	50	60
m121.pep	70	80	90	100	110	120
a121	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	AXXX					
a121	AERTQIFTVGDFRS	RDLAAGGQ	GPLVPAFHEAL	FRDDRETRAVLN	IGGIANISVLP	PDPA
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
a121	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLD	GGENRYDVLRTLSR	FTAQTVCD	AVSHAAADARQ	MYICDGGIRNPV	
a121	GRELFAINWLETYLD	GGENRYDVLRTLSR	FTAQTVF	DAVSHAAADARQ	MYICGGGIRNPV	
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
a121	310	320	330	340	350	360
m121.pep	XAGYYYYX					
a121	GAGYYYYX					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

1	ATGGAAACAC	AGCTTTACAT	CGGCATCATG	TCGGGAACCA	GCATGGACGG
51	GGCGGATGCC	GTACTGATAC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCACGC	CTTTACCCCC	TACCCCGGCA	GGTTACGCCG	CCAATTGCTG
151	GATTTGCAGG	ACACAGGCGC	AGACGAACTG	CACCGCAGCA	GGATTTTGTC
201	GCAAGAACTC	AGCCGCCCTAT	ATGCGCAAAC	CGCCGCCGAA	CTGCTGTGCA
251	GTCAAAACCT	CGCACCGTCC	SACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTTAC	AGCATACAGC	TTGCCGATT
351	GCCGCTGCTG	GCGGAACGGA	CGCGGATTTT	TACCGTCGGC	GACTTCCGCA
401	GCCGCGACCT	TGCGGCCGGC	GGACAAGGCG	CGCCACTCGT	CCCCGCCCTT
451	CACGAAGCCC	TGTTCCGCGA	CAACAGGGAA	ACACGCGCGG	TACTGAACAT
501	CGCGGGGATT	GCCAACATCA	SCGTACTCCC	CCCCGACGCA	CCCGCCTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGACGCGTG	GACGCAGGCA
601	CACTGGCAGC	TTCTTTACGA	CAAAAACGGT	GCAAAGGCGG	CACAAGGCAA
651	CATATTGCCG	CAACTGCTCG	ACAGGCTGCT	CGCCCACCCG	TATTTGCGAC
701	AACCCACCC	TAAAAGCACG	GGGCGCGAAC	TGTTTGCCCT	AAATTGGCTC
751	GAAACCTACC	TTGACGGCGG	CGAAAACCGA	TACGACGTAT	TGCGGACGCT
801	TTCCCGTTTT	ACCGCGCAAA	CCGTTTGCGA	CGCCGTCTCA	CACGCAGCGG

```

851 CAGATGCCCC TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
  1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
  51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
 101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPF
 151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWTQA
 201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
 351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYISQLADLPLL					
g121	HRSRILSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPHEGYISQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	130	140	150	160	170	180
	AERTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
g121	AELTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
m121-1.pep	190	200	210	220	230	240
	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
g121	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDAYSHAAADARQMYICGGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121-1.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121-1.pep	XAGYYYX					
g121	GAGYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
  1 ATGGAAACAC ACCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAATG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGGCCGGC GGACAAGGCG CGCCGCTCGT CCCC GCCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGTGTA TGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACGTA TACGACGTAT TCGGACGCT
801 TTCCCGATT ACCGCGCAA CCGTTTTCGA CGCGCTCTCA CACGCAGCGG
851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTG
1001 CATGGATGCG GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGEG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAFWMAACW VNRIPGSPHK
351 ATGASKFCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW	LGAEGHAFTPYPGRLLRRQLDLQDTGADEL				
a121-1	METQLYIGIMSGTSMGDADAVLIRMDGGKW	LGAEGHAFTPYPGRLLRRQLDLQDTGADEL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHSYSVQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLITYLDGGENRYDVLRTLSRFTAQTVFDAVSHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLITYLDGGENRYDVLRTLSRFTAQTVFDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDLPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDLPQWVEAAAFWMAACWNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121-1.pep	XAGYYYY					
a121	GAGYYYY					

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```

m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACCAC
1  TACGCCAGCG AAAAAGTCG CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAyTCCCyG TCGGCAAwGT ATTAAACGGA CTGTTCCGCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGTC
151 TGGCACAAG ACGTGGCTA TtkTGAATTG CAACAAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCTACCT CGTCTGCAAC TTCGCCCCAC CCGTGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCTCT TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTcAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsg CGGCATGTT yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTCCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 3086; ORF 128&gt;:

```

m128.pep (partial)
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51  NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFPTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//
1  YASEKLREAK YAFSETXVK YFPVGXVLNG LFAQXKKLYG IGFTKTVPV
51  WHKDVRYXEL QONGEXIGV YMDLYAREGK RGGAWMNDYK GRRRFS DGTG
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFOXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQVVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDVAAT
301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHS GF DNAV*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

g128.seq

```

1 atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51 aatccaaacc gaagACatca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTC
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCT CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGGCGGATTT CGTATTGAGC GGGCGGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTGGCCGCC
601 GCCCGCGAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCGAGTTCC
651 GCACTACCTT GCCGTTATCC AATACGCCCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGcctaa ctGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCCGC CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCGCAGCCG TGGGACTTGA
1001 GCTACGCCCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTaca AAGGCCGCCG CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCTCACCC TCTTCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgtA GAATGGGACG CGGTCGAAC TCCAGCCAG
1501 TTTATGGAAG ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCTGCGCGAA AGAACTCTT GACAAAATGC
1601 TcgCGCCAA AACTTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGAGG CTATTACAGC TACGCATGGG CCGAAGTcct
1851 cAGCACCGAT GCCTACGCCG CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAACAG CTTCTGGCAA GAAatccttg ccgtcggcgg ctCCCGCAGC
1951 gcgCGGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTGCGC CAaagcggT TCGACAACGC gCcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

g128.pep

```

1 MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLPSPAQTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY PDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KPDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNFIHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSL YAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHBTGH GLHHLLTOVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHER TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLEKNW QQVLDSVRKE VAVIOPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRFWQ EILAVGGSRS

```

651 AAESFKAFRG REPSIDALLR QSGFDNAA\*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)  
from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQICTEDIKPAVQTAIAEARGQIAAVKAQTHGTWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPAQTATAEAREQIAAIKAQTHGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLSNVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep				YAGEKLREAKYAFSETEVKKYFPVGKVLG		
m128				YASEKLREAKYAFSETXVKYFPVGXVLNG		
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQNGKTIIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQNGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHLHLLTQVDELGV					
m128	GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSESDCRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQKEFALFDMMIYSEDDCRLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330



```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTAC CGACACGCCC GAACTGCGCG
251 CCGCTACAA TGAATTAATG CCGGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACACGATC
401 TGCGCGATTT CGTCCTCAGC GCGCGGGAAC TGCGCGCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAAATCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTGACGATG
551 CCGCACCGCT TGCGGCGATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCCGCGAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTACATC AATACGCCGA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCTA CGCCGAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCGC
1101 CCAAATCAA AACTCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGCGGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA SACGCGACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC SCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCACGA
1401 AACCGGACAC GGCCTCCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCGGCGAT CAACGGCGTA GAATGGGACG CAGTCGAAC GCCAGTCAG
1501 TTTATGGAAT ATTTGTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGCCCAA AACTTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAGAA GTCGCCGTG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWG
51  NTVPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLOIFHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLPLTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

```

551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKE VAVVREPEYN RFANSFGHIF  
 501 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS  
 551 AAESFKAFRG REPSIDALLR HSGFDNAA\*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPFRDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPFRDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIGVGVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIGVGVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSONVLDTDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep	-----					
a128	ARRAKPYAEKDLAEVKAFARESLGLADLPWDLGAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQKKLYGIGFTEKTVPVVHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGRKKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDSVRKEVAVVREPEYNRFANSFGHIF					
	550	560	570	580	590	600

```

400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||||||||||||||||||||||||||||||||||| |||: |||||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

460      470
m128.pep  REPSIDALLRHSGFDNAVX
          |||||||||||||||:
a128      REPSIDALLRHSGFDNAAX
          670

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEO ID 3091>:

m128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTTGGGC	GAAGAACCCC	GTTTGTATCA
51	AATCAAACCC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATCGCCGAAG
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA
151	AAACACTGTGC	AACCCTTGAC	CGCATCCACC	GAACGCGTCG	CGAGGATTTG
201	GGCGGTGGTG	TGCGACCTCA	ACTCCGTCGC	CGACACGCCC	GAACGTGGCG
251	CCGTCTATAA	CGAATCTGAT	CCCGAAATCA	CGGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCCAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAATTTCCC
351	CGAATTCGAC	ACCTCTCCC	CCGCAACAAA	AACCAAACTC	AACCACGATC
401	TGCGCGATTT	CGTCTCAGC	GGCGCGGAAC	TGCCGCCCGA	ACAGCAGGCA
451	GAACCTGGCAA	CTAGTCAAAAC	CGAAGCGCGC	CAACTTTCGG	CCAAATTTCT
501	CCAAAACGTC	CACAGCGCGA	CCGACCGGTT	CGGCATTTCAC	TTTGACGATG
551	CCGCAACGCT	TGCCCGCAAT	CCCGAAGACG	CGCTCGCAT	GTTTCCCGCC
601	GCCGCGCAAA	GCGAAAGCAA	AACAGGCTAC	AAAATCGGCT	TGCAGATTTCC
651	ACACTACCTC	GCCGTCATCC	AATACGCCGA	CAACCGCGAA	CTGCGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGCGCCA	GCGAACTTTC	AGACAGCGGC
751	AAATTCGACA	ACACGCCCAA	ACTCGACCGC	ACGCTCGCAA	ACGCCCTGCA
801	AACCGCCAAA	CTGCTCGGCT	TCAAAAACCTA	CGCCGAATTG	TGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAAGTTT	TAAACTTCTT	GCACGACCTC
901	GCCCGCCCGC	CCAAACCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCGCG	GAAAGCTGA	ACCTCGCGCA	TTTGCAACCG	TGGGAGTTGG
1001	GCTACGCCAG	CGAAAACTG	CGCGAAGCCA	AATACGGGTT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTATTAAACG	GACTGTTCCG
1101	CCAAATCAAA	AAACTCTAGC	GCATCGGATT	TACCGAAAAA	ACCGTCCCCG
1151	CTGTGCACAA	AGAGCTGCGC	TATTTTGAAT	TGCAACAAAA	CGCGGAAACC
1201	ATAGGCGGCG	TTTATATGGA	TTTGATACGA	CGCGAAGGCA	AACCGCGCGG
1251	CGCGTGGATG	AACGACTACA	AAGGCGCGCG	CGGTTTTTCA	GACGGCACGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	ACCGCTCGGG
1351	GGCAGGGAAG	CCCGGCTGAG	CCACGACGAA	ATCCTCATCC	TCTTCCACAT
1401	AACCGGACAC	GGGCTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAACGTGGCG
1451	TATCCGGCAT	CAACGGCGTA	GAATGGGACG	CGGTCGAACT	GCCCAGCCAG
1501	TTTATGGAAT	ATTTGGTTTG	GGAAATCAAA	GTCTTGCCAC	AAATGTCAGC
1551	CCACGAAGAA	ACCGGCGTTC	CCCTGCCGAA	AGAATCTTTC	ACAAAAATGC
1601	TCGCGGCCAA	AAACTTCCAA	CGCGGCATGT	TCTCTGTCGG	GCAAATGGAG
1651	TTCCGCCCTCT	TTGATATGAT	GATTTACAGC	GAAGACGACG	AAGGCCGCTC
1701	TAAAAACTGG	CACAGGTTTT	TGACGACCGT	GCGCAAAAAA	GTCCGCGTCA
1751	GACCGCCGCT	CGAATAACAAC	GCCTTCGCCCT	TGAGCTTCGG	CCACATCTTC
1801	GCAGGCGGCT	ATTCCGCAAG	CTATTACAGC	TACGCGTGGG	GCGAAGTATT
1851	GAGCGCGGAC	GCATACGCCG	CCTTTGAAGA	AAGCGACGAT	GTCGCGGCCA
1901	CAGGCAAAAC	CTTTTGGGAG	GAATATCTCG	CCGTGCGCGG	ATCGCGCAGC
1951	GCGGCAAGAT	CCTTCAAAGC	CTTCCGCGGC	CGCGAACCGA	GCATAGACGC
2001	ACTCTTGCGC	CACAGCGGTT	TGCACAACGC	GGTCTGA	

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

ml28-1.pep.  
1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA  
51 NTVEPLTGIT ERVGRINGVV SHLNSVADTP ELRAVYNELM PEITVFTEI

```

101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDI
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAFPVG
451 GREARLSHDE ILILFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFMMIYS EDDEGRKKNW QQVLDSVRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

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The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1 ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51 AATCAAAACC GAAGACATCA AACCAGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGGCGGATTT CGTATTGAGC GCGCGGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATCTCT
501 CCAAACCGTC CTAGACGCGA CCGACGCGTT CGGCATTATC TTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GEACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 CCGCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCCG GAACACCTCG GTCTCGCCGA CCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG SCCTGTTCGC
1101 CCAAATCAAA AAACCTTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGCTTGGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCGGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1 MIDNALLHLG EEPRFNQIKT EDIKPAVQTA IAEARGQIAA VKAOTHTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAFPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV K

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m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTGWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA_KAQHTGTGWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNREFTIKNSPEFA
m128-1	ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNREFTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHVLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHVLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPDLSYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPQPDLDGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTTGGGC	GAAGAACCCC	GTTTGTATCA
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATTGCCGAAG
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA
151	AACACTGTCG	AACCCCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTGGTG	TCGCACCTCA	ACTCCGTCAC	CGACACGCCC	GAACGCGCG
251	CGGCCTACAA	TGAATTAATG	CCCGAAATTA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAACCTCCC
351	CGAGTTCGAC	ACCCTCTCCC	ACGCGCAAAA	AACCAAACTC	AACCACGATC
401	TGCGCGATTT	CGTCCTCAGC	GGCGCGGAAC	TGCCGCGCCA	ACAGCAGGCA
451	GAATTGGCAA	AACTGCAAA	CGAAGGCGCG	CAACTTCCG	CCAAATTCTC

```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCGG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCAGAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CGGTTTTTCA GACGCGACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTACCCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGA CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAAGT GCCCAGTCAG
1501 TTTATGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCCGAA AGAAGTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCCAA CGCGGAATGT TCCTCGTCCG CCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 AGGSGAGAA CTTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTGA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMDATP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVY YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFS DGTQLQPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFWWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFO RGMFLVRQME
551 FALFDDMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

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m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

	10	20	30	40	50	60
a128-1.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA IKAQHTGTGWANTVEPLTGIT					
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA IKAQHTGTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a128-1.pep	ERVGRWGVVSHLNSVTDTP ELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
m128-1	ERVGRWGVVSHLNSVADTP ELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMAADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMAADTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESGLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGRLKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

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1  ATGTTTCCCC CCGACAAAAC CTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGSAaA ATCCCCGAcA GCCGcyTCAA
351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pep..

```

1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3099>:

g206.seq

```

1  atgttttccc cgcacaaaac ctttttctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaattccaa gccgtccgca tcagccacat cgccgcgaca
151 caaggctcgc aggaactcat gctccacagc ctccggactca tcggcacgcc
201 ctacaaatgg ggcgcgagca gcaccgcaac cggcttcgac tgcagcgcca
251 tgattcaatt ggtttataaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcgcgggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcggaat tcattccatgc ccccggcagc
451 ggcaaaaacca tcaaaaccga aaaactctcc acaccgtttt acgcaaaaaa
501 ctaccttggg ggcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	:					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPRTARDMAAASRKIPDSRXKAGD					
	:					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPRTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	:     :					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPFYAKNYLGAHTFFTE					



130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGCGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCAC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCCTTAA
351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACGTTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE+
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	70	80	90	100	110	120
	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	130	140	150	160	170	
	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GCGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCCT GTTGTCTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGCGCGCG CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGATCCG AATATGCTTG CCGGAAATAT GGAATCAAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGACGA TCCGTCGGCA GGCGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTGAGATCC CATCCCCGCG TCAAACCCCTG CACCTGCGAA TGGCGGTAGC
```

```

601 AATTTTGGAA GGGTTGATTG GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAAT CAGAATTGTA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATT CCAGCAGAAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGCAT GATTGCATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAAACGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTGCGCGCA
1451 AAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSPAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTFNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMAA
151 DGMQGGDDPSA GGQNAAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFGRVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRLPAE MPLIPVQAD TLIVDGEAVS LTCHSGNIFA PEGNYRYLTY
351 GAELPLGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDGFSK SVDGIIDSGD DLHMGTKQFK AADGNNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

```

g287.seq
1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcgggtggcg gatcgccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggcgcgcccc gttgttctg aaaatgccg ggaagggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcgggtg gcgcgcaayc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 ttctggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgcga
351 atccgcaaat caaacaggga acaaccaacc gcgcggttct tcagattccg
401 ccccgcgctc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgcgcg aaaaataaac
501 gttgaccac tgtaaaaggc attcttgtaa tggtagaat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaacgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaataatc atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggc
751 gagattccgc tgattccgt caatcaggcc gatacgtga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaagcgaaa tgcttggtg
951 cagggccgtg tacaacggcg aagtgtgca tttccatat gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaaattc aaagccgcca tcgatgaaa cggcttaag gggacttga
1151 cggaaaatgg cggcggggat gtttcggaa ggttttacg cccggccgc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaagg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

```

g287.pep
1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAP VVAENAGEGV

```

```

51 LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATTDNP
101 KNEDAGAQNQ MPQNAAESAN QTGNNQFAGS SDSAPASNPA PANGGSDFGR
151 TNVGNSSVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGNTKYI IFYTDKPPTR SARSRRSLPA
251 EIPLIPVNQA DTLIVDGEAV SLTGHSNIF APEGNYRYLT YGAEKLPFGS
301 YALRVQGEFA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVDDGIIDSG DDLHMGTKF KAAIDGNGFK GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

```

**m287/g287** ORFs 287 and 287.ng showed a 70.1% identity in 499 aa overlap

```

m287.pep      10      20      30      40      49
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEA
|||||         |||||         |||||         |||||         |||
g287          10      20      30      40      50      60
MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA
|||||         |||||         |||||         |||||         |||||

m287.pep      50      60      70      80      90      100      109
KEDAPQAGSQGQAPSAGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
||| :| | :|||         |||||         |||||         |||||
g287          70      80      90      100      110
AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTNPKNEDEVAQNMPQNA--

m287.pep      110     120     130     140     150     160     169
DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDFSGAGQNAGNTA
g287          -----

m287.pep      170     180     190     200     210     220     229
AQQANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLNGVLIDGPSQNTLTHCKGDS
::|||:|||| | |||| | ||||| ||||| ||||| ::|||:|||| | |||||
g287          120     130     140     150     160     170
-ESANQTGNNQFAGSSDSAPASNPAANGGSDFGRNTNVGNSSVIDGPSQNTLTHCKGDS

m287.pep      230     240     250     260     270     280     289
CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
|::|:||||: | ||||| :||| :||| : :||| | : | | |||||
g287          180     190     200     210     220     230
CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGNTKYIIFYTD

m287.pep      290     300     310     320     330     340     349
KPTSFAFRFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT
|| : | ||||| : ||||| ||||| ||||| ||||| ||||| |||||
g287          240     250     260     270     280     290
KPPT-----RSARSRRSLPAEIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT

m287.pep      350     360     370     380     390     400     409
YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFIITENGRPYPTRGRFAAKVDFGS
|||||         |||||         |||||         |||||         |||||
g287          300     310     320     330     340     350
YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS

m287.pep      410     420     430     440     450     460     469
KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGGSDVSGKFYGPAGEEVAGKYSYR
|||||         |||||         |||||         |||||         |||||
g287          360     370     380     390     400     410
KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGGSDVSGRFYGPAGEEVAGKYSYR

m287.pep      470     480     489
PTDAEKGFGVFAGKKEQDX

```

g287  
 PTD A E K G G F G V F A G K K D R D X  
 420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

a287.seq  
 1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC  
 51 CTGTGGGGGC GGCGGTGGCG GATCGCCCGA TGTTAAGTCG GCGGACACGC  
 101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG  
 151 CTGCCGAAAG AAAAGAAAGA TGAGGAGCG GTGAGTGGTG CGCCGCAAGC  
 201 CGATACGCAG CACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG  
 251 TTTCCGCGAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC  
 301 GAAAATAAAG ACGAGGGACC GCAAAATGAT ATGCCGCAAA ATGCCGCCGA  
 351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA  
 401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGC ACAACCGGCA  
 451 AACCAACCGG ATATGGCAAA TCGGCGGAC GGAATGCAGG GGGACGATCC  
 501 CTCGGCAGGG GAAAATGCCG SCAATACGGC AGATCAAGCT GCAATCAAG  
 551 CTGAAAACAA TCAAGTCGGC GGCTCTCAAA ATCCTGCCTC TTCAACCAAT  
 601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA  
 651 TGGCATCAAG CTGACAGCG GTTCGGAAAA TGAACGTTG ACACATTGTA  
 701 AAGACAAAGT ATGCGATAGA GATTTCTTAG ATGAAGAAGC ACCACCAAAA  
 751 TCAGAAATTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA  
 801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA  
 851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA  
 901 TCTTCATCTG CGCGATTCAG GCGTTCGCA CGGTCGAGG GGTGCGTCC  
 951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GCGGATACG CTGATTGTCG  
 1001 ATGGGGAAGC GGTCAGCCTG ACGGGGCATT CCGGCAATAT CTTCGCGCCC  
 1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG  
 1101 ATCGTATGCC CTCAGTGTGC AAGGCCAACC GGCAAAAGGC GAAATGCTTG  
 1151 CGGGCACGGC CGGTGACAAC GCGGAAGTGC TGCATTTCCTA TATGGAAAAAC  
 1201 GGCCGTCCGT CCCCCTCCGG AGGCAGGTTT GCCGCAAAAG TCGATTTCGG  
 1251 CAGCAAACTT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG  
 1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGCTT TAAGGGGACT  
 1351 TGGACGGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGCCCGGCG  
 1401 CGCGCAAGAA GTGGCGGGA AATACAGCTA TCGCCCGACA GATGCGGAAA  
 1451 AGGGCGGATT CGCGGTGTT GCCGCAAAA AAGAGCAGGA TTGA

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep  
 1 MFKRSVIAMA CIVALSCGG GGGSPDVKS ADTLSKPAAP VVTEDVGEEV  
 51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTNDP  
 101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA  
 151 NQPDMAAAD GMQGGDPSAG ENAGNTADQA ANQAENNQVG GSONPASSTN  
 201 PNATNGGSDF GRINVANGIK LDGSENVTL THCKDKVCDR DFLDEEAPPK  
 251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKUKSAS  
 301 SSSARFRRSA RSRRSLPAEM PLIPVQADT LIVDGEAVSL TGHSGNIFAP  
 351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN  
 401 GRPSPSGGRF AAKVDFCSKS VDGIIIDSGDD LHMGTQKFKA VIDNGNFKGT  
 451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD\*

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEA				
a287	MFKRSVIAMACIVALSCGGGGGGSPDVKSADTLSKPAAPVVTEDEVGEEVLPKEKKDEEA				
	10	20	30	40	60
	50	60	70	80	100
m287.pep	KEDAPQAGSQGQAPSQGSQDMAAVSEENTGNGGAVTADNPKNEDQVAQNMPQNAAGT				
a287	VSGAPQADTQ--DATAGKGGQDMAVSAENTGNGGAATTNDPENKDEGPQNDMPQNAADT				
	70	80	90	100	110

m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDDPSAGGQNAGNTA						
a287	: :          :                  :						
	120	130	140	150	160	170	
	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDDPSAG-ENAGNTA						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNIITLTHCKGDS						
a287	:        : : :  :    :    :    : : :  : : : : :						
	180	190	200	210	220	230	
	DQAANQAENNOVGGSQNPASSTNPATNGGSDFRINVANGIKLDSGSENVTLTHCKDKV						
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMGKINQYIIFYKP						
a287	: :      :       : : : :  : : : : :  : :  : : : :						
	240	250	260	270	280	290	
	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKD						
m287.pep	290	300	310	320	330	340	
	KP--TSFARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
a287	:						
	300	310	320	330	340	350	
	KSASSSARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
m287.pep	350	360	370	380	390	400	
	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF						
a287							
	360	370	380	390	400	410	
	LTYGAEKLSGGSYALSVOGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF						
m287.pep	410	420	430	440	450	460	
	GSKSVGGIIDSDDLHMGTTQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS						
a287							
	420	430	440	450	460	470	
	GSKSVGGIIDSDDLHMGTTQKFAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYS						
m287.pep	470	480	489				
	YRPTDAEKGFGVFAGKKEQDX						
a287							
	480	490					
	YRPTDAEKGFGVFAGKKEQDX						

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTC GCACTAGACA

```

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701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFABEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATCTTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAGG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTGCA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGACCC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CCGCACCCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTCTTCTCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACTT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFABEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFABEQELVAASARA	AVKMDLQALHGR				
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFABEQELVAASARA	AVKMDLQALHGR				

110

	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 . pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGGMGYRNETLTTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 . pep	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAYKENYALWMGPYKVS KGIKPT EGLMVD FSDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAYKENYALWMGPYKVS KGIKPT EGLMVD FSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCATCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGIATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406 . pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARA AVK
51  DMDLQALHGR KVALYIATMG DQSGSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVS PANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA

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251	AYKENYALWM	GPYKVS	SGIK	PTEGLM	VDFS	DIQPYG	NHMG	NSAPS	VEADN
301	SHEGYGYSDE	AVRRHR	QGQP	*					
m406/a406	ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap								
	10	20	30	40	50	60			
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARA AVKMDLQALHGR								
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARA AVKMDLQALHGR								
	10	20	30	40	50	60			
	70	80	90	100	110	120			
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTS GGLTG								
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTS GGLTG								
	70	80	90	100	110	120			
	130	140	150	160	170	180			
m406.pep	LTTSLSTLNAPALSRTQSDGSGSKSSLG LNIGMGDYRNETLTNPRDTAFLSHLVQTVF								
a406	LTTSLSTLNAPALSRTQSDGSGSKSSLG LNIGMGDYRNETLTNPRDTAFLSHLVQTVF								
	130	140	150	160	170	180			
	190	200	210	220	230	240			
m406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL								
a406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL								
	190	200	210	220	230	240			
	250	260	270	280	290	300			
m406.pep	IKPKTNAFEAA YKENYALWMGPYKVS								
a406	IKPKTNAFEAA YKENYALWMGPYKVS								
	250	260	270	280	290	300			
	310	320							
m406.pep	SHEGYGYSDEVVRQHRQGQPX								
a406	SHEGYGYSDEAVRRHRQGQPX								
	310	320							

## EXAMPLE 2

### Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm



that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 3

#### Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 4

#### Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

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were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

#### EXAMPLE 5

##### Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

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*Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 8

### Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

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## EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

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1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

**Table 2**

#### **225 gene variability: List of used *Neisseria* strains**

<b>Identification Strains number</b>	<b>Source / reference</b>
<b>Group B</b>	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
<b>Group A</b>	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 22491	R. Moxon / Maiden <i>et al.</i> , 1998
<b>Group C</b>	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

**Others**

zo26\_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998  
 zo27\_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998  
 zo28\_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998  
 zo29\_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

**Gonococcus**

zo32\_225 Ng F62 R. Moxon / Maiden *et al.*, 1998  
 zo33\_225 Ng SN4 R. Moxon

fa1090 FA1090 R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCS  
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z2491 <SEQ ID 3116>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA  
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSISTGFDCSGF  
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z001\_225 <SEQ ID 3117>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z002\_225 <SEQ ID 3118>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z003\_225 <SEQ ID 3119>  
 MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQPVLPINRAFAARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z004\_225 &lt;SEQ ID 3120&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z005\_225 &lt;SEQ ID 3121&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z006\_225 &lt;SEQ ID 3122&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z007\_225 &lt;SEQ ID 3123&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z008\_225 &lt;SEQ ID 3124&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z009\_225 &lt;SEQ ID 3125&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z010\_225 &lt;SEQ ID 3126&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z011\_225 &lt;SEQ ID 3127&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF  
MQHIKFRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z012\_225 &lt;SEQ ID 3128&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z013\_225 &lt;SEQ ID 3129&gt;



MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPNRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z014\_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z015\_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS  
GFMQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z016\_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z017\_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z018\_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z019\_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z020\_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPINRPARRAGNADELIGSAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLNEQPVLVPNRPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF  
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z021\_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z022\_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVPINRPARRAG  
NADELIGSAMGLNEQPVLVPNRPARRAGNADELIGNAMGLNEQPVLVPNRPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z023\_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z024\_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z025\_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z026\_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z027\_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z028\_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z029\_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z032\_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCS  
GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z033\_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCS  
GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z096\_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLFINRAPARRAG  
 NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGSAMGLNEQVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMCHIIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFERTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDPSRFLN\*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

### EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used <i>Neisseria</i> strains		
Identification Strains number		Reference
Group B		
gnmzq01	NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02	BZ198	Seiler <i>et al.</i> , 1996
gnmzq03	NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04	1000	Seiler <i>et al.</i> , 1996
gnmzq05	1000	Seiler <i>et al.</i> , 1996
gnmzq07	BZ169	Seiler <i>et al.</i> , 1996
gnmzq08	528	Seiler <i>et al.</i> , 1996
gnmzq09	NGP165	Seiler <i>et al.</i> , 1996
gnmzq10	BZ133	Seiler <i>et al.</i> , 1996
gnmzq11	NGE31	Seiler <i>et al.</i> , 1996
gnmzq13	NGE28	Seiler <i>et al.</i> , 1996
gnmzq14	NGH38	Seiler <i>et al.</i> , 1996
gnmzq15	SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16	NGH15	Seiler <i>et al.</i> , 1996
gnmzq17	NGH36	Seiler <i>et al.</i> , 1996
gnmzq18	BZ232	Seiler <i>et al.</i> , 1996
gnmzq19	BZ83	Seiler <i>et al.</i> , 1996
gnmzq21	MC58	Virji <i>et al.</i> , 1992
Group A		
gnmzq22	205900	Our collection

gnmzq23	F6124	Our collection
z2491	Z2491	Maiden <i>et al.</i> , 1998

**Group C**

gnmzq24	90/18311	Our collection
gnmzq25	93/4286	Our collection

**Others**

gnmzq26	A22	(group W) Maiden <i>et al.</i> , 1998
gnmzq27	E26	(group X) Maiden <i>et al.</i> , 1998
gnmzq28	860800	(group Y) Maiden <i>et al.</i> , 1998
gnmzq29	E32	(group Z) Maiden <i>et al.</i> , 1998
gnmzq31	<i>N. lactamica</i>	Our collection

**Gonococcus**

gnmzq32	Ng F62	Maiden <i>et al.</i> , 1998
gnmzq33	Ng SN4	Our collection

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.  
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279  
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGA'VNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

GNMZQ01 <SEQ ID 3150>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSA'VNQIANNLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ02 <SEQ ID 3151>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSA'VNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ03 <SEQ ID 3152>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMALST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSARARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVS AVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ28 <SEQ ID 3173>  
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ29 <SEQ ID 3174>  
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ31 <SEQ ID 3175>  
 MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGTS  
 YQILDSVTTVSARARLVDSRNGKVLWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT  
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ32 <SEQ ID 3176>  
 MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

GNMZQ33 <SEQ ID 3177>  
 MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

Z2491 <SEQ ID 3178>  
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

### EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

**Table 4**

#### **287 gene variability: List of used *Neisseria* strains**

Identification Strains number	Reference
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Group B		
287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992
Group A		
z2491	Z2491	Maiden <i>et al.</i> , 1998
Gonococcus		
fa1090	FA1090	Dempsey <i>et al.</i> 1991

### References:

- Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.  
Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279  
Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287\_14 <SEQ ID 3179>  
MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG  
QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADTDSLTPNHTPAS  
NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ  
TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGFSQNTLTHCKGDS CSGNNFLDEEV  
QLKSEFEKLSADAKISNYKKDGKNDKDFVGLVADSVQMKGINQYIIIFYKPKPTS FAR  
FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP  
GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFTENGRRPSPSRGRFAAKVDFGSKSV DGI I  
DSGDGLHMGTKQKFAAIDGNGFKGTWTENG GGDVSGKFYGPAGEEVAGKYSYRPTDAEKG  
FGVVFAGKKEQD\*

287\_2 <SEQ ID 3180>  
MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG  
QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADTDSLTPNHTPAS  
NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ  
TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGFSQNTLTHCKGDS CSGNNFLDEEV  
QLKSEFEKLSADAKISNYKKDGKNDKDFVGLVADSVQMKGINQYIIIFYKPKPTS FAR  
FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP  
GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFTENGRRPSPSRGRFAAKVDFGSKSV DGI I  
DSGDGLHMGTKQKFAAIDGNGFKGTWTENG GGDVSGKFYGPAGEEVAGKYSYRPTDAEKG  
FGVVFAGKKEQD\*

287\_21. <SEQ ID 3181>  
MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG  
QGAPSAQGSQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAAGTDSLTPNHTPDP  
NMLAGNMENQATDAGESSQPANQPDMAANTADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ  
AAGSSDPIFASNPAANGSGNFRVLDLGVLIIDGFSQNTLTHCKGDS CSGNNFLDEEV  
QLKSEFEKLSADAKISNYKKDGKNDKDFVGLVADSVQMKGINQYIIIFYKPKPTS FARFRRS



ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY  
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENG RPYPTRGRFAAKVDFGSKSV DGIIDSGD  
DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG GFGV  
FAGKKEQD\*

287\_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGGSPDVKSADTL SKPAAPVVTEDVGEEVLPKEKKDEEA  
VSGAPQADTQDATAGKGGQDMAAVSAENTGNGGAATT DNPENKDEGPQNDMPQNAADTDS  
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAAADGMQGGDDPSAGENAGNTADQA  
ANQAENNQVGGSQNPASSTNP NATNGGSDFG RINVANGIKLDSGSENVTLTHCKDKVCDR  
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRV EKNGTNKYVIIYKDKSAS  
SSSARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYG  
AEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS  
VDGIIDSGDDLHMGTKQFKAVIDGNGFKGTWTENG GGDVSGRFYGPAGEEVAGKYSYRPT  
DAEKG GFGVFAGKKEQD\*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA  
AGGAPQADTQDATAGEGSDMAAVSAENTGNGGAATT DNPKNEDAGAQN DMPQNAAESAN  
QTGNNQFAGSSDSAPASN PAPANGGSDFGRTNVGNSVVIDGPSQNTLTHCKGDS CNGDN  
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRV KKDGTNKYIIFYTDKPTR  
SARSRRSLPAEIPVLPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGS  
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGSKSV DGIIDSG  
DDLHMGTKQFKAAIDGNGFKGTWTENG GGDVSGRFYGPAGEEVAGKYSYRPTDAEKG GFG  
VFAGKKEQD\*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTL SKPAAPVVSEKETEAKEDAPQAGSOG  
QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN DMPQNAAGTDSSTPNHTPDP  
NMLAGNMENQATDAGESSQPANQPDMAAADGMQGGDDPSAGGQNAAGNTAAQGANQAGNNQ  
AAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNTLTHCKGDS CSGNNFLDEEV  
QLKSEFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYII FYKPKPTSFARFRS  
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY  
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENG RPYPTRGRFAAKVDFGSKSV DGIIDSGD  
DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG GFGV  
FAGKKEQD\*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

**Table 5**

#### **519 gene variability: List of used *Neisseria* strains**

Identification Strains	Source / reference
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**number****Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

**Group A**

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

**Others**

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

**Gonococcus**

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090\_519 <SEQ ID 3185>  
MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIC  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTQGGAGAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

Z2491\_519 <SEQ ID 3186>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV01\_519 <SEQ ID 3187>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV02\_519 <SEQ ID 3188>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV03\_519 <SEQ ID 3189>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV04\_519 <SEQ ID 3190>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV05\_519 <SEQ ID 3191>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV06\_519ASS <SEQ ID 3192>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERK  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV07\_519 <SEQ ID 3193>

MEFFIILLVAVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV11\_519 &lt;SEQ ID 3194&gt;

MEFFIILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV12\_519 &lt;SEQ ID 3195&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV18\_519 &lt;SEQ ID 3196&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV19\_519 &lt;SEQ ID 3197&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV20\_519ASS &lt;SEQ ID 3198&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM  
ISAGMKIIDSSKTAK\*

ZV21\_519ASS &lt;SEQ ID 3199&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV22\_519ASS &lt;SEQ ID 3200&gt;

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV26\_519 &lt;SEQ ID 3201&gt;

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV27\_519 &lt;SEQ ID 3202&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV28\_519 <SEQ ID 3203>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV29\_519ASS <SEQ ID 3204>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSIVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV32\_519 <SEQ ID 3205>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV96\_519 <SEQ ID 3206>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

### EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

#### 919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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**number****Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11	asbc NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

**Group A**

zm22	205900	R. Moxon
zm23	asbc F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

**Group C**

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

**Others**

zm26	A22 (group W)	R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26 (group X)	R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800 (group Y)	R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32 (group Z)	R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

**Gonococcus**

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon
fa1090	FA1090	R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.

Maiden et al., Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>

MKKHLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN  
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA  
IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

Z2491 <SEQ ID 3208>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM01 <SEQ ID 3209>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM02 <SEQ ID 3210>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM03 <SEQ ID 3211>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMQQNQRRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM07 <SEQ ID 3215>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM08N <SEQ ID 3216>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM09 <SEQ ID 3217>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL



KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM12 <SEQ ID 3220>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM13 <SEQ ID 3221>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQOTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM14 <SEQ ID 3222>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSRNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM15 <SEQ ID 3223>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDLAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNHQQWQDVCAQAFQTPVHVSQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM16 <SEQ ID 3224>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPGRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGHTADLSOFITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM17 <SEQ ID 3225>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM19 <SEQ ID 3227>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM20 <SEQ ID 3228>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM22 <SEQ ID 3230>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL  
KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL

KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK  
MKEPGYVWQLLPNGMKPEYRP\*

ZM24 <SEQ ID 3232>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM26 <SEQ ID 3234>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAAAILAACQSKSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK  
MKEPGYVWQLLPNGMKPEYRP\*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIPTDDFISVPLPAGLRSGKA  
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATTHPIRTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYVFFRELAGSGNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM32ASBC <SEQ ID 3239>

MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKA  
 LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGGDPVGALGTPLMGYSAGA  
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM33ASBC <SEQ ID 3240>

MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN  
 LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL  
 KLGQTSMQGIKSYMQRNPKLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA  
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGHTADLSRFEITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

**Table 7:** Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF	primer	Sequence	Restriction sites
001	Forward	CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGTCTTGCCAC	XhoI
003	Forward	CGCGGATCCCATATG-GTCGTATTCGTGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATCATGAACACGCGC	XhoI
005	Forward	CGCGGATCCCATATG-GACAATATTGACATGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCACATCCGCCC	XhoI
006	Forward	CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGTTCCGGCTTTGATGT	XhoI
007	Forward	CGCGGATCCCATATG-GCCGACAACAGCATCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGGCGTTCATGATATAAG	XhoI
008	Forward	CGCGGATCCCATATG-AACAACAGACATTTTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward	CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCTTTTGCCACGTTTT	XhoI
011	Forward	CGCGGATCCCATATG-AAGACACACCGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGGTCAGTACGGT	XhoI
012	Forward	CGCGGATCCCATATG-CTCGCCCGTTGCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward	CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGATTCGGCAAAAAATCT	XhoI
018	Forward	CGCGGATCCCATATG-CAGCAGAGGCAGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGAGGCGAACGCC	XhoI
019	Forward	AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	Eco RI
	Reverse	AAACTGCAG-TCAGCGGGCGGGACAATGCCCAT	Pst I
023	Forward	AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse	AAACTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward	AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse	AAACTGCAG-TCAGAACGCGATATAGCTGTTCCG	Pst I
031	Forward	CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATGTAAGACGGGGACAAC	XhoI
032	Forward	CGCGGATCCCATATG-CGGCGAAACGTGC	BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGA CTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTACTGCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGGAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAAACTCTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTCACCTTCGCCGC	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG- TTAATCCTGCAACACGAATTCGCCCGTCCG	Pst I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	BamHI-
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward	CGCGGATCCCATATG-GTCATCATACAGGCG	XhoI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	NdeI
	Reverse	AAACTGCAG-TCAAGATTGACGGGGATGATGCC	XhoI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Eco RI
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	Pst I
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	BamHI-
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	NdeI
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	XhoI
	Reverse	AAAAAAGTCGAC-TCAGGCGGCGTTTTTCACCTTCCT	Eco RI
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Sal I
			Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCCAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGTTCTGCCAGTTTCAG	XhoI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAAGTCAACACCCATTATCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTTT	Pst I
111	Forward	CGCGGATCCCATATG-TGTTCCGAACAAACCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAAA	XhoI
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTGAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	XhoI
122	Forward	CGCGGATCCCATATG-GTCATGATTAAAATCCGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATT	XhoI
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-



	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
			XhoI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Pst I
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Pst I
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA	XhoI
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCTTCAAAACCTTAATTTG	Eco RI
	Reverse	AAAAAACTGCAG-TCACCATGTCGGCATTTGAAAAAC	Pst I
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	XhoI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	XhoI
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCAATTCGATCC	Kpn I
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	Pst I
137a	Forward	AAAAAAGAATTC-GGCCGCAAAACACGGCATCGGCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAACAGCCGTGAATCACGCC	Pst I
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTCATG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	XhoI
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Pst I
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Eco RI
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Xba I
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAAACTGGG	Pst I
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTGGAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Xba I
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTTGAACACGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Xba I
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	BamHI-

	Reverse	CCCGCTCGAG-AAACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	NdeI
151	Forward	AAAAAAGAATTC-	XhoI
		ATGAAACAAATCCGCAACATCGCCATCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC-	Eco RI
		ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG-	Pst I
		TTACGCCGACGAAATACTCAGACTTTTCGG	
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTTCCAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTTGCCCCGCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTTCGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAAACGGGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTTGCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGTTTTTTCCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
			BamHI-
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	NdeI
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	NdeI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGTTCTAAGTTCCTGATATG	NheI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	NdeI
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	NdeI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTTG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	NdeI
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-CGACTTGGTTACCGCG	NdeI
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	NdeI
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	NdeI
248	Forward	CGCGGATCCCATATG-CGCAAACAGAACACT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	NdeI
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	NdeI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	XhoI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Eco RI
			Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	NdeI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	XhoI
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	BamHI-
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCCTG	NheI
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	NdeI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	XhoI
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	BamHI-
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCGC	NdeI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	XhoI
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	Eco RI
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	Pst I
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	BamHI-
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	NdeI
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	XhoI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGGG	Kpn I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Pst I
	Reverse	AAACTGCAG-CTATTCCCTGTTGCGCGTGTGCCA	Eco RI
267	Forward	AAAGAATTC-TTCTTCCGATTGATGTTAATCG	Pst I
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Eco RI
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Pst I
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Eco RI
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Pst I
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Eco RI
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTGCAATG	Pst I
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Eco RI
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	Pst I
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	BamHI-
			NdeI
			XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	XhoI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCCATCACGATGATGCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Pst I
277	Forward	AAAAAAGAATTC-ATGCCCGCTTTGAGGACAAGCTCGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	XhoI
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAACCAG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	Pst I
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Pst I
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	XhoI
284	Forward	CGCGGATCCCATATG-TTGCCTGCAAAAGAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAAGT	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTCCGAAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	EcoRI- NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTTGCC	XhoI
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGATTTTTGCGGATGATTT	NdeI
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	XhoI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	Eco RI
295	Forward	CGCGGATCCCATATG-AACCGGCCGCGCCTCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	NdeI
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	XhoI
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	Eco RI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	Pst I
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTCGCCTCCG	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	NheI
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	XhoI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	Eco RI
305	Forward	AAAAAAGGTACC-GAATTTTTACCGATTTCCAGCACCGGA	Pst I
	Reverse	AAAAAACTGCAG-TCATTCCCACTTATCCAGCCTGACAG	Kpn I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Pst I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Kpn I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	NdeI
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTTCAGTTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTTCATATTCCCTGCCTTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	NdeI
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCAFTTACCCTTGC	XhoI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Xba I
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Xba I
			BamHI-
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTCGGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTTCACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI



	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTCG	Eco RI
	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530	Forward	CGCGGATCCCATATG-AGTGCAGCGCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531	Forward	AAAAAAGAATTC-TATGCCGCCGCTACCAAATCTACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACAGCGCCGTGCCGACGACAAG	Pst I
532	Forward	AAAAAAGAATTC-ATGAGCGGTCAAGTGGGCAAAGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCCGGTATCAAA	Pst I
532a	Forward	AAAAAAGAATTC-TTGGGTGTGCGGTTTGAGCCGGAAGT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCCGGTATCAAA	Pst I
535	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539	Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
	Reverse	AAACTGCAG-TTACCGCAACCGGTCAGGAT	Pst I
543	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a	Forward	AAAAAAGAATTC-GGCAAACTCGTCATGAATTTGC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a	Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547	Forward	AAAGAATTC-ATGTTTCGTAGATAACGGATTTAATAAAAC	Eco RI
	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548	Forward	AAAGAATTC-GCCTGCAAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCCGCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCAAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTTCATTTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTCAATTCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTCTGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTGGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
			XhoI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Pst I
589	Forward	AAAAAAGAATTC- ATGCAACAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI- NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI- NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI- NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI- NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTGTGTTTTAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGCGTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTGCGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCCC	Eco RI
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Pst I
645	Forward	AAAAAAGAATTC-GTGAACAGAGCAACACGTAAATCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Pst I
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Pst I
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Pst I
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGCGGAACTGCCGCCGTC	Pst I
650	Forward	AAAAAAGAATTC-ATGTCCAAACTCAAACCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Pst I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTTGCCAGTTGGTAGAATGCGGC	Pst I
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCCGA	Pst I
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-CTACGATTTTCGGCGATTTCCACATCGT	Pst I
657	Forward	AAAAAAGAATTC-GCAGAAATTTGCCGACCGCCATTTGTGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	Pst I
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTGCGCGTCGGGC	Pst I
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTGCCGACGATTC	Pst I
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTTGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	Pst I

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAAAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAAACGCGTCGGAAGTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI-
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	NdeI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	XhoI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	BamHI-
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTGGATACTTC	BamHI-
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	NdeI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	XhoI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Eco RI
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	Pst I
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	BamHI-
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	NheI
	Reverse	AAAAAACTGCAG-TTAGTTTTGCCGGATAATATGGCGGGTGCG	XhoI
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	Eco RI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	Pst I
708	Forward	CGCGGATCCGCTAGC-CTTTTAAAGCCATCCAAAA	BamHI-
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	NheI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	XhoI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	BamHI-
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	NdeI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	XhoI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	BamHI-
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI-
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	NdeI
			XhoI



725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI-
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	NdeI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	XhoI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	BamHI-
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI-
	Reverse	GCCCAAGCTT-TTGTCGGTTTGGGTATC	NdeI
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	HindIII
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	BamHI-
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	NheI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	EcoRI-
	Reverse	CCCGCTCGAG-TCGCTTGCCTCCTTTAC	NdeI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	XhoI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	BamHI-
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI-
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	XhoI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGAGAAATT	BamHI-
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI-
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	NdeI
743	Forward	CGCGGATCCCATATG-GACGGTGTTGTGCCTGTT	XhoI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	BamHI-
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CGGGAATCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTTCCGCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	NdeI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	XhoI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	BamHI-
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
	Reverse	CCCGCTCGAG-TTCTGTACAGCAGGGG	NdeI
768	Forward	CGCGGATCCCATATG-GCCCCGAAAAACCCG	XhoI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	BamHI-
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTGAGATTTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	NdeI
772	Forward	CGCGGATCCCATATG-TTGCGGCGTTGGTGG	XhoI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	BamHI-
774	Forward	CGCGGATCCCATATG-TCCGTTTCACCCGTTCC	NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

900	Reverse	CCCGCTCGAG-GGCGTTGTTCGGATTTCG	XhoI
	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
901	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
	Forward	CGCGGATCCCATATG-CCCGATTTTTCGATG	BamHI- NdeI
902	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
	Forward	CCGGAATTCTACATATG-TTGCAC TTCAAAGGATAATC 2	EcoRI- NdeI
903	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
	Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
904	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
	Forward	AAAAAAGGTACC-ATGATGCAGCACAATCGTTTC	Kpn I
904a	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
905	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
907	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
908	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
909	Reverse	AAACTGCAG-TTAATATGGTTTTGTCTGTTG	Pst I
	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
910	Reverse	CCCGCTCGAG-TCGGTTTTGAACTTTGGTTTT	XhoI
	Forward	AAAGAATTC-GCATTGCGCGGCGACTCTGCCGAGCG	Eco RI
911	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTT	Pst I
	Forward	AAAGAATTC-GCTTTCGCGTGGCCGGCGGTGC	Eco RI
912	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
	Forward	AAAAAAGAATTC- CAAATCCGTCAAAACGCCACTCAAGTATTGAG	Eco RI
913	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCCTTTCGC	Pst I
	Forward	CGCGGATCCCATATG-GAAACCCGCCCCGC	BamHI- NdeI
915	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
914	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
	Forward	AAAGAATTC-GACAGAATCGGCGATTTGGAAGCACG	Eco RI
916	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCGCCTTACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTT	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAAACCGCCAATCCGCCGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTCTGGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTAGAACCGCATTGTC	NdeI
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	XhoI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	BamHI-
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	XhoI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-GGGTCGTTTGTGCGTC	NdeI
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward	AAAAAAGAATTC- TTGACTAACAGGGGGGGAGCGAAATTAAAAAC	XhoI
			Eco RI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Xba I
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAACCGAAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Pst I
982	Forward	CGCGGATCCCATATG-GCAGCAAAAGACGTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	XhoI
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	XhoI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	BamHI-
			NdeI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	HindIII
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	EcoRI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	XhoI
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	BamHI-
	2		NheI
	Reverse	CCCGCTCGAG-AAACAGCCATTTGAGCGA	XhoI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	XhoI
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
			NheI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```
g001.seq
1  ATGCTGCCGC AGGGGAAGGC GGC GCGGAGG GTGTCGGCGA ACGAGGTGTC
51  CGGCAGGGCT TGC GCCCGA TGGTGCTGGT CATCTGCCAG ACGCTGCCGA
101 AACGCGATAC TTAAACGGC TCGGGTACGC ATACTTTACC GGT TTGGGCG
151 ATTTGCGGA GGTCTTGCG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGGTCGGTTT GTA ACTCGGC GGC GCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCTGAAG CGATGTTGAG GAAGAGTTCG GCGAGAAAC ACAGCGTCCA
351 CGCGATTGC CCGCTTCAT CGGCAGGTG GGACAATACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```
g001.pep
1  MLPOGKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGHTLPVWA
51  ILPRSLRSKS TIITFSARFF GSVNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```
m001.seq
1  ATGCTGCCGC AGGGGAAGGC GGC GCGGAGG ATGTCGGCGA ACGAGGTGTC
51  CGGCAssCTT ss.GCTTGGA yGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGGTACGC ATACTGTGCC GGT TTGGGCG
151 ATTTGCGGA GGTCTTGCG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GGC GCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGAGAAAC ACAGCGTCCA
351 CGCGATTGC CCCTCCGCAT CGGCAGGTG GGACAAGACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```
m001.pep
1  MLPOGKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGHTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```
a001.seq
1  ATGCTGCCGC AGGGGAAGGC GGC GCGGAGG ATGTCGGCGA ACGAGGTGTC
51  CGGCAAGGCT TGGGCTTGGA TGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGGTACGC ATACTGTGCC GGT TTGGGCG
151 ATTTGCGGA GGTCTTGCG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GGC GCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGAGAAAC ACAGCGTCCA
351 CGCGATTGC CTTGTGCAT CGGCAGGTG GGACAAACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```
a001.pep
1  MLPOGKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGHTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PASGRWDKT A*
```

m001/a001 96.2% identity over a 131 aa overlap

	10	20	30	40	50	60
m001.pep	MLPOGKAARRMSANEVCGXLXAWXVLVICQ	TLPKRDTLNGSGHTVPVWAILPRSLRSKS				
a001.pep	MLPOGKAARRMSANEVCGKAWAWMVLVICQ	TLPKRDTLNGSGHTVPVWAILPRSLRSKS				

m001/g001

[illegible]

g003.seq

g003.pcp

```

1  MVVFAEGGVF GRAVLGHLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGFA DVDVAVAVGV FNQVVLMLVL GVVVFQRFV FNNEGQLVFL
101 LLAFFGGGDD GFFGGVGVVH AAVALRAGVV TLFVEAGRIN DAEIILQDVV

```

151 QAEFVGIVGH FDGLGMTRMA VGHFFVRVFR VAVGVTYRV NHAVIDALEIG  
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq  
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA  
51 CTTGsTATTG CTCTTCGGTC AGGGTGCCTT TGAGTTCGGC GTCACCTCGGT  
101 TTTTATACG TTGCCCGGTC GAAGCCTTTG CCTTGCCTGG CCGTCTTGGT  
151 TTTGCCCGGC AGCGGTTTCGT CAGCKTTGCG GATGTCGATG TGGCAGTAGC  
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG  
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG  
301 CTGCTCGCGT TTGAGGGCGk CCGCGATGAC GGCTTTTTTCG kCGGGGTCGG  
351 TGTAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCSTT GCCCTGTTTG  
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC  
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGTT TCGGCGTGGC  
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTT CGTGTGCGC  
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA  
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT  
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221  
1 MVVFVAEGIF GRAVLGNLXL LFGQGAFFEG VTRFFIRCRV EAFALRGGLG  
51 FARQRFVSXA DVDVAVAVGV FNQVVLVFL GIVEVFQRLV FNNEGQLVFL  
101 LLAFEGXGDD GFFXGVGVVH AAVLRTGVV ALFVEAGRIN DAEEILQDVV  
151 \*AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVIDALEI  
201 GFQAPEAAXG EVNGARVHDF \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq  
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA  
51 CTTGGTATTG CTCTTCGGTC AGGGTGCCTT TGAGTTCGGC GTCACCTCGGT  
101 TTTTATACG TTGCCCGGTC GAAGCCTTTG CCTTGCCTGG CCGTCTTGGT  
151 TTGCCCCGCG AGCGGTTTCGT CGGCTTTGCG GATATCGATG TGGCAGTAGC  
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG  
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG  
301 CTGCTCGCGT TTGAGGGCGG CCGCGATGAC GGCTTTTTTCG GCGGGGTCGG  
351 TGTAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG  
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC  
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGTT TCGGCGTGGC  
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTT CGTGTGCGC  
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA  
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGCG GAGGTAGATG GTGCGCGTGT  
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep  
1 MVVFVAEGIF GRAVLGNLVL LFGQGAFFEG VTRFFIRCRV EAFALRCGLG  
51 FARQRFVGFA DIDVAVAVGV FNQVVLVFL GIVEVFQRLV FNNEGQLVFL  
101 LLAFEGGGDD GFFGGGVVH AAVLRTGVV ALFVEAGRIN DAEEILQDVV  
151 \*AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVIDALEI  
201 GFQAPEAAG EVDGARVHDF \*

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXLFLFGQGAFFEGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVLFLFGQGAFFEGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60



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	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRITGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRITGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALIEIGFQAPEAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDALIEIGFQAPEAAGEVDGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVFVFAEGIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
g003	MVFVFAEGVFGRVVLGHLVLLFGQGAFFGVTRFFIRCRVEAFALRCGFGFARQRFVGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGVVEVFQRFVFNNEQQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRITGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVVTLEFVEAGRINDAEIILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALIEIGFQAPEAAXGEVNGARVHDFX					
g003	RVAVGVAGYRVNHAVDALIEIGFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTGAT
51  GCGCCCATGC CAACAagtga gccAAAtgtT CGGCGGCAGG GCCTacgatT
101 TCCGCGCCGA TAAagcgcc gGTGgctTTT tcgGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggtcg accttgaTTT TTGAACGATA
201 CTTGCGCCgaT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTCGga ctggttaaACA CCACGCCAAT
301 GGTgctgcgg cGCAAACCGC TGCCGATATt cgGgtagcgg ccccgcggtta
351 ttgcccggca atcttacctt ggtcggcggc ttcatGCAGC AGGGGCagtt
401 ggttggaagc gtcgcccga ataaAGATAT GCGGAATgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgcgcgc gcgtctttgT CGATATTGAT
501 GTTTTCCAAA CCGATATtgT CAACGTTTCGG ACGGCgACCT ACGGCTGCCA

```

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551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGETTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTCGCCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACCGAA AATTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

**g004.pep**

```

1 MVERHIQHLR NGHLMRCP QVVSQMFGR AYDFRADKAA GFFFGIQAHM
51 AFVYQHAAAA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAAQTAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTPR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMPP MIPKPKIST
251 FTPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

**m004.seq**

```

1 ATGGTAGAAC GGCATATCCA GCATTGCGG AACGGTCATC TTCATTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCTG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTAGAC CGACAAAGCC GATTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTTCG CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATTCCGCCCA AACCAGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

**m004.pep**

```

1 MVERHIQHLR NGHLMCP S QVVRQMFGR AYDFRADKAA GFFFGIQAHM
51 AFVHQHAAAA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAD
101 GAAPQTAADI RVAAALSPA I LPWSAASCSR GSWLDASPAM KICGILVCMV
151 SGSATGTPRA SFSILIFSKP ILSTFGRRPT AASIYSATNT PFSPPSCSQWT
201 STLPSASSLT SVLASRCSFN SSPNTAFASS ETTGSEMPPM IPPKPKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

**a004.seq**

```

1 ATGGTAGAAC GGCATATCCA GCATTGCGG AACGCTCATC TTCATTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCCG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTTCG CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCTC GAGTTTGCC TCGGTTTTAG CATCCAAATG
651 CAGTTTCAAT TCTTACCAGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATGCCACCCA AACCAGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

**a004.pep**

```

1  MVERHIQHLR NGHLMCPSS QQVRQMFGR TYDFCADEAA GGFFGIQAHM
51  AFVYQHAAAA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD
101 GAAAQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV
151 SGSATGTPRA SFSILMFSKP ILSTFGRRPT AASIYSATNT FFSPSCSQWT
201 STLPSASSLA SVLASKCSFN SSPNTAFASS ETTGSEMPPM MPPKPKISTF
251 TPKRCNA*

```

**m004/a004** 94.9% identity over a 257 aa overlap

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLMCPSSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQAHHAAA					
a004	MVERHIQHLRNGHLMCPSSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVYQHAAAA					
	10	20	30	40	50	60
m004.pep	70	80	90	100	110	120
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI					
a004	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGEHYADGAAAQTAADIRVAAALSPAI					
	70	80	90	100	110	120
m004.pep	130	140	150	160	170	180
	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFILIFSKPILSTFGRRPT					
a004	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFILMFSKPILSTFGRRPT					
	130	140	150	160	170	180
m004.pep	190	200	210	220	230	240
	AASIYSATNTFFSPSCSQWTSTLPSASSLSVLASRCFNSPNTAFASSETTGSEMPPM					
a004	AASIYSATNTFFSPSCSQWTSTLPSASSLSVLASKCSFNSPNTAFASSETTGSEMPPM					
	190	200	210	220	230	240
m004.pep	250					
	IPPKPKISTFTPKRCNAX					
a004	MPPKPKISTFTPKRCNAX					
	250					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

**m004/g004**

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLMCPSSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQAHHAAA					
g004	MVERHIQHLRNGHLMRPCQQVSMFGRAYDFRADKAAGGFFGIQAHMAFVYQHAAAA					
	10	20	30	40	50	60
m004.pep	70	80	90	100	110	119
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA					
g004	TLIFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHANGAAAQTAADIRVAAPRYCPA					
	70	80	90	100	110	120
m004.pep	120	130	140	150	160	179
	ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFILIFSKPILSTFGRRP					

g005.seq

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

g005.pap

1	MGMDNIDMF	PEQEETQSMW	KEILLNYGIF	<u>LLELLTVFGA</u>	IALIVLAIQV
51	SKKQSESGSV	VLTDFSENKQ	KQRQSFETFF	LSEETKFEQE	KKEKKKEKAE
101	AKAEKKRLKE	GGEKSAETQK	SRLFLVDFDG	DLAHAVEVSL	RHEITAVLLI
151	AKPEDEVLLR	LESPPGVVHG	YGLAASQLRR	LRERNIPLTV	AVDKVAASGG
201	YMMACVADKI	<u>VSAPFAVIGS</u>	VGUVAEVPMI	HRLLKKHIDV	VDVMTAGEFK
251	RTVTFMGENT	EKGKQKFRQE	LEETHQLFKQ	FVSENRPGLD	IEKIATGEHW
301	FGQALALNL	IDEISTSDML	LLKAFENKQV	IEVKYQEKRS	LQRIQLQAE
351	ASVEKLFACL	VNRRADVM*			

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 21>:

m005.seq

1	ATGGACAATA	TTGACATGTT	CATGCCTGAA	CAAGAGGAAA	TCCAATCAAT
51	CTGGAGGAAA	ATTTTACTGA	ATTACGGTAT	TTTCTCGTCT	GAAGTGTCTA
101	CGGTGTTCCG	CGCAATTGCG	CTGATTGTGT	TGGCATGTCT	ACAGAGTTAG
151	AAACATCTCG	AwAGCGGCAG	TGTCGTACTG	ACGGATTTTT	CGGAAAATTA
201	TAAAAAATCA	CGGCAATCGT	TTGAAGCAAT	CTTTTAAAGC	GGGGAAGCAG
251	CACACATACA	GGAAAAAGAG	GAAAAAGAAA	AGGAAAAGGC	GAAGGCCAAA

```

301 GCAGAGAAAA A.CGTTTGAA GGAGGTTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGCGGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATCCGACA
801 GGAACGTGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGCGGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHKEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
351 VEKLEAKLVN RRADV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCGTACTG ACGGATTTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GAAAAAGAG GAAAAGAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGTTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCCGC CTTTTGTGT TGGATTTTGA CGGCGATTTG TATGCACACG
401 CCGTAGAATC CTTCGCTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGAA AGTCCGGGCG GCGTGGTTCA
501 CGGTACCGGT TTGCGCGCTT CGCAGCTTAG GCGTTTGC GCACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGCGGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATCCGACA
801 GGAACGTGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGCGGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHKEKE EKKKEKAEAK
101 AEKXRLKEGG EKSSSETQKSR LFVLDFDGL YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS  
 351 VEKLFKLVN RRADM'

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	10	20	30	40	50	60
	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSVL					
a005	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSVL					
	10	20	30	40	50	60
m005.pep	70	80	90	100	110	120
	TDFSENYKKQSQSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKXRLKEGGEKSAETXKSR					
a005	TDFSENYKKQSQSFEAFFLSGEEAKHQEKEKKKEKAEAKAEKXRLKEGGEKSSSETQKSR					
	70	80	90	100	110	120
m005.pep	130	140	150	160	170	180
	LFVLXX					
a005	LFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLES?GGVVHGYGLAASQLRRLR					
	130	140	150	160	170	180
m005.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSGVVAEVPNIHRLKKHDIDVD					
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSGVVAEVPNIHRLKKHDIDVD					
	190	200	210	220	230	240
m005.pep	250	260	270	280	290	300
	VMTAGEFKRTVTFMGENTKKGKQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG					
a005	VMTAGEFKRTVTFMGENTKKGKQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG					
	250	260	270	280	290	300
m005.pep	310	320	330	340	350	360
	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN					
a005	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN					
	310	320	330	340	350	360
m005.pep	RRADMVX					
a005	RRADMVX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	10	20	30	40	50
	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSV				
g005	MGMDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSV				
	10	20	30	40	50
m005.pep	60	70	80	90	100
	VLTDFSENYKKQSQSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKXRLKEGGEKSAETXK				
g005	VLTDFSENYKKQSQSFETFFLSEETKHQEKKEKKKEKAEAKAEKXRLKEGGEKSAETQK				
	70	80	90	100	110
					120

	120	130	140	150	160	170
m005.pep	SRLFVLXX					
	:					
g005	SRLFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRR					
	130	140	150	160	170	180
	180	190	200	210	220	230
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
	190	200	210	220	230	240
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTEGKGKQFRQELEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTEGKGKQFRQELEETHQLFKQFVSENRPGLDIEKIATGEHW					
	250	260	270	280	290	300
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFaki.					
g005	FGRQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKRSIQRIGLQAEASVEKLFaki					
	310	320	330	340	350	360
	360					
m005.pep	VNRRADVmx					
g005	VNRRADVmx					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

**g006.seq**

```

1   ATGCTGCTGG TGCTggaatt ttggttcGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCT CCTGAACAAC AGCTTGAAC gcgACAACCA CTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCG
251 CGGCGATGGG TATTTGTTC GGCTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACGGCA GCGCGGGGCA TATTTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGGACG ATGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAACCT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

**g006.pep**

```

1   MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRVL ISNREAFGYL CVGAAMGILF GFAPVMTLK
101 GYGSAGHIYS VGTYLWMPAM SLDDVPRLVE QYSNLKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

**m006.seq**

```

1   ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCGTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCT CCTGAACAAC AGCTTGAAC GCGACAACCA CTTATCCGA
151 AAAGGCGACC GCGGCAGCT GTACCGCCAT TACGGACTGC TTGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCA
251 CGGCGATGGG TATTTGTTC GGCTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT

```

```

351 GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

**m006.pep**

```

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51 KGDRLQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMTLK
101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSLNKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

**a006.seq**

```

1 ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51 TCGGTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGATTTCCG CCTGAAGAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GGACCGCCAT TACGGAATGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCA
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAACCT GA

```

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

**a006.pep**

```

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
51 KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMTLK
101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSLNKDIGQ RIEWSKRNIK
151 AGT*

```

**m006/a006** 96.7% identity over a 153 aa overlap

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS					
a006	MLLVLEFWVGVS					
	10	20	30	40	50	60
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
m006.pep	SLDDVPRLVEQYSLNKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSLNKDIGQRIEWSKRNIKAGTX					
	130	140	150			
m006.pep	SLDDVPRLVEQYSLNKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSLNKDIGQRIEWSKRNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

**m006/g006**

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS					



q006-1.seq

This corresponds to the amino acid sequence <SEQ ID 32; ORF 006-1.ng>:

q006-1.pcp

1	MWKMLKHIAR	THRKRRLICTF	SPVGLENLLM	LGYPVFGGWA	INAVIAGRWW
51	<u>QALLVALVSR</u>	LMWLVGGAARR	IDIATRTFTRI	YTEIAVPPVL	EQRQSRQVHS
101	AVTARVALVSF	EFVSFEEHEL	PIATRSVSIS	FGACIMLLVL	EFVWVGSGVA
151	<u>ILALFLWLLP</u>	RFAAISENLY	FRLNNSLERD	NHFIRKGDGR	QLYRHYGLVS
201	RLRLVISNR	AFGYLCVGAH	MDGLFGFAFV	MMTLKGYGSA	GHIYSVGTYL
251	WMFAMSLDDV	PLRVEOYSNL	KGILGRIEVS	ERNIKAGT*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 33>:

m006-1.seq

1	ATGTGGA AAA	TGTTGAAACA	CATAGCCCAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACATTT	TCCCTGGTCG	GACTTGA AAA	CCTTTGTATG	CTGGTGTATC
101	CGGTGTTTGG	CGGCGGGGCG	AGTATCCCG	TGATTGCCGG	GGAGGTGTGG
151	CAGGCGTTGC	TGTCAGCTTT	GGTGTGCTT	TTGATGTGCC	TGGTGGGTGC
201	GGTGCGGCGG	ATTGCCGATA	CGCGCACGTT	TACCGGGATT	TATACCGAAA
251	TCGGCGTGCC	GGTCGTGTTG	GAACAGCGGC	AGCGACAAGT	CCCGCATTCG
301	CGGGTAACTG	CGCGGGTTCG	CTGTTCGGT	GAGTTTGTCA	GCTTTTTTGA
351	AGAAACCTGC	CCGATTGCCG	CGACATCCGT	CGTATCCATA	TTCGGCCGCT
401	GCATCATGCT	GCTGGTGCTG	GAATTTTGGG	TCGGCGTGTC	GCGGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTGTCCG	CCATCAGCGA
501	AAACCTGTAT	TTCCCGCTGA	ACACAGACTT	GGAACGCGAC	AACCATTTA
551	TCCGAAAAGG	CGACCGGCGG	CAGCTGTAGT	GCCATTACGG	ACTGCTTGGC
601	CGCCTGCGTG	TGCTGATTTC	CAACCGCGAA	GCGTTCCGCT	ATCTCTGCGT

m006-1.pep

	1	MWKMLKHIAQ	THRKRLIGTF	SLVGLENLIM	LVPVFGGRA	INAVIAGEVM
51		QALLYLVLVL	LMWLVGAVRR	IADTRTFTRI	YTEIAMFVVL	EQRQRQVSAS
101		AVTARVALSR	EEVSEFEELH	PIAATSVFSI	FGACIMLVLL	EFWVGVSAPH
151		<u>ILALFLWLLP</u>	RFAAISENLY	FRLNNSLERD	NHFIRKGDRR	QLYRHYGLLA
201		RLRVLSINRE	APFLVCVSTA	MGILFGFAFW	MMTLKGYSSA	GHVYSVGTYL
251		WMFAMSLDDV	PRLVEQSYNL	KDIGORIEWS	ERNIKAGT*	

1/q006-1

		10	20	30	40	50	60
m006-1.pep	MWKMLKHIAQTHRKRLIGTFSVLGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVV						
	:           :           :           :           :						
g006-1	MWKMLKHIAKTHRKRLIGTFSPVGLENLLMLGYPVFGGWAINAVIAGRNVQALLYALVVF						
	10 20 30 40 50 60						
		70	80	90	100	110	120
m006-1.pep	LMWLVGAVRRIADTRTFTTRIYTEIAVPVVLEQRQRQVPHSAVTARVALSREFVSFFEEHL						
	:           :           :           :           :						
g006-1	LMWLVGAAARRIADTRTFTTRIYTEIAVPVVLEQRQRQVPHSAVTARVALSREFVSFFEEHL						
	70 80 90 100 110 120						
		130	140	150	160	170	180
m006-1.pep	PIAATSVVSIFGACIMLLVLEFWVGVSavgILALFLWLLPRFAAISENLYFRlNNSLERD						
	:           :           :           :           :						
g006-1	PIAATSVVSIFGACIMLLVLEFWVGVSavgILALFLWLLPRFAAISENLYFRlNNSLERD						
	130 140 150 160 170 180						
		190	200	210	220	230	240
m006-1.pep	NHFIRKGD RRQLYRH YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFM MT LKGYS SA						
	:           :           :           :           :						
g006-1	NHFIRKGD ERQLYRH YGLVSR LRVLISNREAFGYLCVGA AMGILFGFAFM MT LKGYS A						
	190 200 210 220 230 240						
		250	260	270	280	289	
m006-1.pep	GHVYSVGTYLWMFAMS LDDV PRLVEQYSNLKD IGQRIEWSERNIKAGTX						
	:           :           :           :           :						
g006-1	GHIYSVGTYLWMFAMS LDDV PRLVEQYSNLKD IGQRIEWSERNIKAGTX						
	250 260 270 280						

a006-1.seq (partial)

1	AGCCAAAACC	ACCGAAGCG	ATTGATTGGC	ACATTCTTTC	TGTCGGGACT
51	GGAAABACCT	TTGATGCTGG	TGTATCCGGT	GTTTGGCCGC	TGGGCGATTA
101	ATGCGCGTAG	TGCGGGGACG	CGCTGGCAGG	CGTTGCGTGA	CCGCTTTGGTT
151	GTGCTTTTGA	TGTGCGTGGT	CGGTGCGCGC	CGCGGGAATTG	CGCATACCGC
201	CACGCTTACG	CGGATTTATA	CCGAAATCCG	CGTCCCGGTT	GTGTTGGAAC
251	AGCGGCGAGC	GCAAGTCCCG	CATTGCGCGC	TAACTGCGCG	GGTTGCCCTG
301	TCGCGTGAGT	TTGTGACGTT	TTTTGAAGAA	CACCTGCCGA	TGTCCGCGAC
351	ATTCGCTCGTA	TCCATATTCG	GCGCGTGCAT	CATGCTGCTG	GTGCTGGAAT
401	TTTGGGTCCG	CGTGTCCGGT	TGCGGCATAC	TTGCGTTGTT	TTTATGGCTT
451	TTGCGCAGTT	TTGCCCGCCG	CAGCGAAATC	CTGTATTTCC	GCCTGAAGAA
501	CAGCTTGGAA	CGCGACAACC	ACTTTATCCG	AAAAGGCCAG	GAGCGCGAGC
551	TGGACCGCCA	TTACGGGATG	CTTGCGCCGC	TGCGTGTGCT	GATTTCCAAC
601	CGCGAAGCCT	TCGGCTATCT	CTCGCTCGGC	ACGGCGATGG	GTATTTTGTT
651	CGGCTTTGCT	TTTGTGATGA	TGACGCTCAA	AGCTACAGC	AGCGCGGGGG

701 ATGTCTATTC GGTCCGCACT TATCTGTGGA TGTTTGCCAT AAGTTTGGAC  
 751 GACGTGCCGC GATTGGTCGA ACAATATTCC AATTTGAAAG ACATCGGACA  
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)

1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV  
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL  
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWVGVS VLGILALFLWL  
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN  
 201 REAFGYLCVG TAMGILFGFA FVMMTLKGY SAGHVYSVGT YLWMFAISLD  
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT \*

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENLLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRLIGTFFSLVGLNLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
m006-1	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
m006-1	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKERNIKAGTX				
m006-1	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq

1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTGTGCT GCCTCTGcgC  
 51 CGCGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT  
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC  
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa  
 201 cgTCctgctg cacagcaatg tcaaaggcAt cgacgggaca ttcaaagtgg  
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC  
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep

1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG  
 51 TAFPLFRSD CIMNKPHVLL HSMVKIDGT FKVERQNLRR IYARNRHQRC  
 101 GHCRRRHLYH ERL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

## m007.seq

```

1 ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCGGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTC.
251 AACGGCAAAA CCTACAACGG ATTCATGCCC GCAACCGCCA TCAGCGATGC
301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

## m007.pep

```

1 MNTRLPTAL VLGCFCFAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARNRHQRC
101 GRCRRRHLHY ERL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>:

## a007.seq

```

1 ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCGGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTC.
251 AACGGCAAAA CCTACAACGG ATTCATGCCC GCCACTGCCA TCAGCGATGC
301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

## a007.pep

```

1 MNTRLPTAL VLGCFCFAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARNRHQRC
101 GRCRRRHLHY ERL*

```

m007/a007 97.3% identity over a 113 aa overlap

	10	20	30	40	50	60
m007.pep	MNTRLPTALVLGCFCFAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD					
a007	MNTRLPTALVLGCFCFAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD					
	10	20	30	40	50	60
	70	80	90	100	110	
m007.pep	FIMKKPQVLLHSMVKGINGTIKVXRQNLQRIHARNRHQRCGHCRRRHLHYERLX					
a007	FIMKKPQVLLHSMVKGINGTIKVXRQNLQRIHARNRHQRCGHCRRRHLHYERLX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

## m007/g007

	10	20	30	40	50	60
m007.pep	MNTRLPTALVLGCFCFAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD					
g007	MNTRLPTAFILCCLCAAASAADNSIMTKGQKVYESNCIACHGKKGEGRGTAFFPLFRSD					
	10	20	30	40	50	60
	70	80	90	100	110	
m007.pep	FIMKKPQVLLHSMVKGINGTIKVXRQNLQRIHARNRHQRCGHCRRRHLHYERLX					

g007                    CIMNKPHVLLHSMVKGIDGTFKVERQNLRRRIYARNRHQRCGHCRRLYHERL  
                               70                80                90                100                110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)  
       1    ATGAACACAA    CCCGACTGCC    GACCGCCTTC    ATCTTGTGCT    GCCTCTGCGC  
      51    CGCCGCTTCT    GCCGCCGACA    ACAGCATCAT    GACAAAAGGG    CAAAAAGTGT  
     101    ACGAATCCAA    CTGCATCGCC    TGCCACGGCA    AGAAAGGGGA    AGGGCGCGGC  
      151    ACTGCGTTTC    CTCCGCTTTT    CCGGTCGGAC    TATATTATGA    ACAAAACGCA  
      201    CGTCCTGCTG    CACAGCATGG    TCAAAGGCAT    CAACGGTACA    ATCAAAGTCA  
      251    ACGGCAAAAC    CTACAACGGA    TTCATGCCCG    CAACCGCCAT    CAGCGATGCG  
      301    GACATTGCCG    CCGTCGCCAC    TTATATCATG    AACGCCTTTG    ACAACGGCGG  
      351    CGGAAGCGTT    ACCGAAAAAG    ACGTAAACA    GGCAAAAGGC    AAAAAAAC.

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)  
       1    MNTTRLPTAF    ILCLCAAAS    AADNSIMTKG    QKQYESNCIA    CHGKKGEGRG  
      51    TAFPPLFRSD    YIMNKPHVLL    HSMVKGINGT    IKVNGKTYNG    FMPATAISDA  
     101    DIAAVATYIM    NAFDNGGGSV    TEKDVQAKG    KKN...

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq  
       1    ATGAACACAA    CCCGACTGCC    GACCGCCCTC    GTCTTGGGCT    GCTTCTGCGC  
      51    CGCCGCTTCT    GCCGCCGACA    ACAGCATCAT    GACAAAAGGG    CAAAAAGTGT  
     101    ACGAATCCAA    CTGCGTCGCC    TGCCACGGCA    AAAAGGGCGA    AGGCCGCGGA  
      151    ACCATGTTTC    CGCGCTCTA    CCGCTCCGAC    TTCATCATGA    AAAAACCGCA  
      201    GGTGCTGCTG    CACAGCATGG    TCAAAGGCAT    CAACGGTACA    ATCAAAGTCA  
      251    ACGGCAAAAC    CTACAACGGA    TTCATGCCCG    CAACCGCCAT    CAGCGATGCG  
      301    GACATTGCCG    CCGTCGCCAC    TTATATCATG    AACGCCTTTG    ACAACGGCGG  
      351    CGGAAGCGTT    ACCGAAAAAG    ACGTAAACA    GGCAAAAGC    AAAAAAACT  
     401    AA

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep  
       1    MNTTRLPTAL    VLGCFCAAAS    AADNSIMTKG    QKQYESNCVA    CHGKKGEGRG  
      51    TMFPPLYRSD    FIMKKPQVLL    HSMVKGINGT    IKVNGKTYNG    FMPATAISDA  
     101    DIAAVATYIM    NAFDNGGGSV    TEKDVQAKS    KKN\*

m007-1 / g007-1    91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	AAADNSIMTKGQKQYESNCVACHGKKGEGRG	TMFPPLYRSD			
g007-1	MNTTRLPTAFILCLCAAAS	AAADNSIMTKGQKQYESNCIACHGKKGEGRG	TAFPPLFRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVN	KGTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV				
g007-1	YIMNKPHVLLHSMVKGINGTIKVN	KGTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV				
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKN					
g007-1	TEKDVQAKGKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)  
       1    ATGAACACAA    CCCGACTGCC    GACCGCCTTC    GTCTTGGGCT    GCCTCTGCGC  
      51    CGCCGCTTCT    GCCGCCGACA    ACAGCATCAT    GACAAAAGGG    CAAAAAGTGT  
     101    ACGAATCCAA    CTGCGTCGCC    TGCCACGGCA    AAAAGGGCGA    AGGCCGCGGA

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAAC3GA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAACA GGCAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1 MNTTRLPTAL VLGCLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCLCAAAS	AAADNSIMTKG	QKVYESNCVA	CHGKKGEGRG	TMFPPLYRSD	
a007-1	MNTTRLPTALVLGCLCAAAS	AAADNSIMTKG	QKVYESNCVA	CHGKKGEGRG	TMFPPLYRSD	
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNG	FMPATAISDA	DIAAVATYIM	NAFDNGGGSV	
a007-1	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNG	FMPATAISDA	DIAAVATYIM	NAFDNGGGSV	
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
a007-1	TEKDVQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1 ATGAACAACA GACATTTTGC CGTCAtcgCC TTGGGCAGCA ACCTTGACAA
51 CCCCACACAA CAAATAcgCG gCGcattaga cgcgcctctcg tcccatcctg
101 acatccggtc tgaaCaggtt tcctcaactgt aTatgaccgc acctgtcggt
151 tacgAcaatC agcccgATTT CATCaatgcc gTCTgcaccg TTTCACCAC
201 CtTGGACGGC ATTGccctGC TTGCCgaACT CAAccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGCC TTACCCTGCC
351 GCATCCGCGC GCGCAGCAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTtTG GGAAAATACG GAAAGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGCTT TTACCGGACA GGTA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1 MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTTLDG IALLAELNRI EADFRGRSF RNAPRTLDD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKYGKVVELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGCG CCGCATTGGA CAGCTGTGCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT TGTCAATGCC GTCTGCACCG TTTCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAct CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTtGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACctTGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTGTTTTA GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHGKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAC CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTTGGAC
301 ATATCGACTT TTGACGGCAT CTCAGCGAC GACCCCGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERSF RNAPRTLDLD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKHGKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
	10	20	30	40	50	60
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

```

m008/g008
      10      20      30      40      50      60
m008.pep MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA
g008     MNNRHFAVIALGSNLDNPAQQIRGALDALSSHPDIRLEQVSSLYMTAPVGYDNQPDFINA

```

183

	10	20	30	40	50	60
m008.pep	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
g008						
	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
m008.pep	130	140	150	160		
	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008						
	AHERSFVIRPLAEILPDFILGKYGVVVELSKRLGNQGIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

**g009.seq**

```

1  ATGCCCCGCG CTGCCGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAT TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGTTGTGCG cGTCCAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AaaGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

**g009.pep**

```

1  MPRAAFAFER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARNQSVMAV
51  QLPLVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

**m009.seq**

```

1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAT TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC CGGTCGCCTT TTCGGATAAA GTGTTGTGCG CGTCCAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

**m009.pep**

```

1  MPRAAFAFER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPPVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

**m009/g009**

	10	20	30	40	50	60
m009.pep	MPRAAFAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009						
	MPRAAFAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
m009.pep	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009						
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
	70	80				



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTTCTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
1  MPRAAVAFER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

```

              10      20      30      40      50      60
m009.pep      MPRAAVAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK
              |||||
a009           MPRAAVAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK
              10      20      30      40      50      60

              70      80
m009.pep      VVVAFAQVQAEIQVFADGGKTWQKXPX
              |||||
a009           VVVAFAQVLQAEIQVFADGGKTWQKXPX
              70      80
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
1  ATGGGGTTTC CTGTTGCGAA GTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGACGCC TCCAATTAT CAAATCCGGT TTGAATTGTG
101 CCGTTTGTGC TAAAGTGTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCG TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTGAacgc
801 cgacggcgaa cgcTTATGG AAcgctatgc GCcgACCGta aAgaCTTGG
851 CTTCCTGCGa cgtGGTTTCA CgcgcGatgG CGatggaAat ctatgaaggt
901 cgcggctgTG GtaaaAaaca agaCCacgtC TTA CTGAAAA TCGACcAtAt
951 cggTGcAGAA AAAATATATG AAAAAGTCCG GGCATCCGC GAGATTTCCA
1001 TTcagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc cgttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTccg aCCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTc cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGSWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QONVRANTQF FVEWTAODLI RDENGDVVG TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

```

m010.seq (PARTIAL)
1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCCCTCn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAA ATTTATCAGC GTCCTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GYCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCGTGCCA
401 ATACGCAATT CTTTGTGGAA TGGACGGCAC AAGATTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACC GCCATG GAAATGGAAA CCGCGCAAGT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCG CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATCCAGCCG ACCGGCGTGG CGGGTGC GGTGTTGATT ACCGAA...

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

```

m010.pep (PARTIAL)
1  ..XQLSKSGLNC AVLSKVFPTTR SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSWDLGDDQ AIEFMCRAAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQON VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMEFWQFQP TGAVAGAVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

```

a010.seq
1  ATGGGCTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTGCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CGGCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTTGGA AGCGGTAAAA TTTATCAGCG
351 TCCTTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCGG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGCGT ACGCGCGGAG GCGGTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCETA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTCCC GGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCACT ATATGATGGG CGGTATCCG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTCTT CAAGGCGACG AATACGAAGT GCCTGTAATA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCTGCTA

```

```

1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGACAGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGGCAGCGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTGTGCCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
  1 MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVLF PTRSHTVAAQ
  51 GGISASLGNV QEDRWDDHMY DTVKGSDDLW GDQDAIEFMCR AAPEAVIELE
 101 HMGMPFDRVE SGKIQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
 151 QQNVVRANTQF FVEWTAQDLI RDENGDDVGV TAMEMETGEV YIFHAKAVMF
 201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
 251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
 301 RCGGKNDHV LLKIDHIGAE KIMEKLGIR EISIQFAGID PIKDPIPVVP
 351 TTHYMMGGIP TNYHGEVVPV QGDEYEVVPK GLYAAGECAC ASVHGANRLG
 401 TNSLLDLVVF GKAAGDSMIK FIKESDWWK LPANAGELTR QRIERLDNQT
 451 DGENVDALRR ELQRSVQLHA GVERTDEILS KGVREVMAIA ERVKRTEIKD
 501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
 551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                      XQLSKSGLNCVLSKVFPTRSHTVAAQGGISASXGNV
                                |||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWDDHMYDTVKGSDDLWGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                |||
a010      QEDRWDDHMYDTVKGSDDLWGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADRTGHAMLHTLYQQNVVRANTQFFVEWTAQDLIRDENGDDVGV
                                |||
a010      GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVVRANTQFFVEWTAQDLIRDENGDDVGV
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |||
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pep/g010.pep

m010.pep				10	20	30	
				XQLSKSGLNCAVL	SKVFPTR	SHTVAAQGGISASXGNV	
g010	MGFPVRKFD	DAVIVGGGGAGL	RALQLSKSGLNCAVL	SKVFPTR	SHTVAAQGGISASLGNV		
	10	20	30	40	50	60	
m010.pep	40	50	60	70	80	90	
	QEDRW	DWHMYD	TVKGS	DWLG	QDAIE	FMCR	AAPEAVIE
g010	QEDRW	DWHMYD	TVKGS	DWLG	QDAIE	FMCR	AAPEAVIE
	70	80	90	100	110	120	
m010.pep	100	110	120	130	140	150	
	GHTAE	HGKRA	VERXC	AVADR	IGHAM	LHTLY	QQNVR
g010	GHTAE	HGKRA	VERXC	AVADR	IGHAM	LHTLY	QQNVR
	130	140	150	160	170	180	
m010.pep	160	170	180	190	200	210	
	TAMEM	TGEVY	IFHAK	AVMF	TGGGG	GRIYAS	STNAY
g010	TAMEM	TGEVY	IFHAK	AVMF	TGGGG	GRIYAS	STNAY
	190	200	210	220	230	240	
m010.pep	220	230					
	FQPTG	VAGAG	VLITE				
g010	FHPTG	VAGAG	VLITE	GVRGE	GGILL	NADGER	FME
	250	260	270	280	290	300	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1  ATGGGTTTTTC CTGTTTCGCAA GTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTTGT CTAAGTGTTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCAGGATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGCC GACCAAGATG
251 CGATTGAGTT TATGTGTCTG GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCGGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GCGGTATTTC TGTGTAACGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTGGTTTCA CGCGCGATGG CGATGGAAAT CTATGAAGGT
901 CCGGCTGTG GTAAAAACAA AGACCACGTC TTAATGAAAA TCGACCATAT
951 CCGTGCAAG AAAATTATGG AAAAAGTGGC GGCATCCGCG GAGATTTCCA
1001 TTCAGTTTGC CGGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTGCGCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMFPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGCKNKDHF LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

g010-1 / P10444

sp|P10444|DHSA\_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT  
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942  
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588  
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169  
 Identities = 191/303 (63%), Positives = 238/303 (78%)

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKSLNCVLSKVF PTRSHTVAAQGGISASLGNV 60  
 M PVR+FDVAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN  
 Sbjct: 1 MKLPVREFDAVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMFPDRVESGKIYQRPFG 120  
 ED W+WHMYDTVKGSD++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG  
 Sbjct: 61 HEDNWEWHMYDTVKGSDYIGDQDAIEYMCKTGPEAILEHMG LPPSRLLDDGRIYQRPFG 120

Query: 121 GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENG DVVG V 180  
 G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL+++++G VVG  
 Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNHTTIFSEWYALDLVRNQDGA VVGC 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240  
 TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+C+ RAG+P++DME WQ  
 Sbjct: 181 TALCIETGEVVYFKARATVLATGGAGRIYQSTTNAHINTGDGVGM AIRAGVPVQDMMEMWQ 240

Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300  
 FHPTG+AGAGVL+TEG RGEVG LLN GERFMERYAP KDLA RDVV+R++ +EI EG  
 Sbjct: 241 FHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLA GRDVVARSIMIEIREG 300

Query: 301 RGC 303  
 RGC  
 Sbjct: 301 RGC 303

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169  
 Identities = 53/102 (51%), Positives = 62/102 (60%)

Query: 309 HVLLKIDHIGAEKIMEKLPGIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368  
 H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +  
 Sbjct: 310 HAKLKLHLGKEVLESRLPGILELSRTFAHVPVKEPIPIPTCHYMMGGIPTKVGTQAL 369

Query: 369 VPQGEYEVVVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410  
 +V V GL+A GE AC SVHGANRLG NSLLDLVVF  
 Sbjct: 370 TVNEKGEDVVVPG LFAVGELACVSVHGANRLG CNSLLDLVVF 411

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTTC CTGTTTCGAA GTTTGATGCC GTGATTGTGC GCGGTGGTGG
51  TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTGC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

```

```
451 CAACAAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAC CGCGGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 ECTACCGCGC GCGGCGGTGCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGCG GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGATATTC TGTGAATGC
801 CGACGCGGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTCCG GGGCATCCGC GAGATTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTCGTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCAGGTGA GTTGACCCGC CAACGTATCG AGCGTTTGGG CAACCAAACC
1351 GATGGTGAAG ACCTTGATGC ATTGCGTCGC GAACTGCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCGGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA
```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

```
1 MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51 GGISASLGNV QEDRWDMHY DTGKSDWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRANTQF FVEWTAQDLI RDENGDVVG TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLSRDRVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPKIR EISIQFAGID PIKDPFVVP
351 TTHYMMGGIP TNYHGEVVPV QGEDYEVVK GLYAAGECAC ASVHCANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMIAA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAAH SDDHEERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*
```

m010-1 / g010-1 99.5% identity in 410 aa overlap

```
10 20 30 40 50 60
m010-1.pep MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
g010-1 MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
10 20 30 40 50 60
70 80 90 100 110 120
m010-1.pep QEDRWDMHYDTGKSDWLGDDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
g010-1 QEDRWDMHYDTGKSDWLGDDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
70 80 90 100 110 120
130 140 150 160 170 180
m010-1.pep GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVG
g010-1 GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVG
130 140 150 160 170 180
190 200 210 220 230 240
m010-1.pep TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDDGLGICARAGIPLDMEFWQ
g010-1 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDDGLGICARAGIPLDMEFWQ
```

190

	190	200	210	220	230	240
	250	260	270	280	290	300
m010-1. pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
g010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m010-1. pep	RGCGKNKDHVLLKIDHIGA EKIMEKLP GIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
g010-1	RGCGKNKDHVLLKIDHIGA EKIMEKLP GIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m010-1. pep	TNYHGEVVVPQGEDYEVVPVKGLYAAGECASCASVHGANRLG TNSLLDLVVF GKAA GDSMTK					
g010-1	TNYHGEVVVPQGEDYEVVPVKGLYAAGECASCASVHGANRLG TNSLLDLVVF RPTPRX					
	370	380	390	400	410	
	430	440	450	460	470	480
m010-1. pep	FIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQRSVQLHAGVFRTDEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1. seq..

```

1  ATGGGGCTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCC GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATCGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGTTTGGG GTATTGTGTC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGCGGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGCGGAG GCGGTATTCT TGTGAATGC
801 CGACGCGCAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTA CTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAA CTGCC GGCATCCG GAGATTCCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATCCG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAAGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCTT TTGCCTGCTA
1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGGA CAATCAAACCT
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GGCGTGTTCG GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCATTGCCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA ECACGTAAAG
1601 AATCACGCGG TCGGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTT GAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1. pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF FTRSHTVAAQ
51  GGISASLGNV QEDRDWDHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101  HMGMFPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNVRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF  
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG  
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG  
301 RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPVPVVP  
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVPK GLYAAGECAC ASVHGANRLG  
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT  
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMIAA ERVKRTEIKD  
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERODE  
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY\*

m010-1 / a010-1 99.3% identity in 567 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFDIVGCGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
a010-1						
	10	20	30	40	50	60
	MGFPVRKFDIVGCGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
	70	80	90	100	110	120
a010-1.pep	QEDRWDMHYDTVKGSDWLGEQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
m010-1						
	70	80	90	100	110	120
	QEDRWDMHYDTVKGSDWLGEQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	130	140	150	160	170	180
a010-1.pep	GHTAEHGKRAVERACAVADRTGHAMLTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
m010-1						
	130	140	150	160	170	180
	GHTAEHGKRAVERACAVADRTGHAMLTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
	190	200	210	220	230	240
a010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
m010-1						
	190	200	210	220	230	240
	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
	250	260	270	280	290	300
a010-1.pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
m010-1						
	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
	310	320	330	340	350	360
a010-1.pep	RCGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPVPVPTTHYMMGGIP					
m010-1						
	310	320	330	340	350	360
	RCGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPVPVPTTHYMMGGIP					
	370	380	390	400	410	420
a010-1.pep	TNYHGEVVVPQGDEYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVF GKAAGDSMIK					
m010-1						
	370	380	390	400	410	420
	TNYHGEVVVPQGDEYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVF GKAAGDSMIK					
	430	440	450	460	470	480
a010-1.pep	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRELQRSVQLHAGVFRTEILS					
m010-1						
	430	440	450	460	470	480
	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRELQRSVQLHAGVFRTEILS					
	490	500	510	520	530	540
a010-1.pep	KGVREVMIAAERVKRTEIKDKSKVWNTARIEALELDNLIEVAKATLVSAEARKESRGAHA					
m010-1						
	490	500	510	520	530	540
	KGVREVMIAAERVKRTEIKDKSKVWNTARIEALELDNLIEVAKATLVSAEARKESRGAHA					
	550	560	570	580		
a010-1.pep	SDDHPERDDENWMKHTLYHSDANTLSYKPVHTKPLSVEYIKPAKRVYX					



m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVIYX  
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq  
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC  
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA  
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA  
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA  
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA  
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT  
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT  
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG  
401 CCGTCGAAGC AGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGGATATG  
451 GGCAAAGTGA TGGTCGTATT GAAAACccGC CTCGCCGGCA AAGccgATAT  
501 GGGCGAAGTC AACAAAATCT TGAAAaccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep  
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK  
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT  
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM  
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)  
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC  
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA  
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA  
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA  
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA  
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT  
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT  
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG  
401 AGGTCAAGC TGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGGATATG  
451 GGTAAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)  
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK  
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT  
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM  
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSAV	VCFAFQTASKPA	VSIRHPSE	DIMSLKIRLT	EDMKTAMRAK	DQVSLGTIRL
g011	MRTHRKTCSAV	VCFAFQTASKPA	VSIRHPSE	DIMSLKTRLT	EDMKTAMRAK	DQVSLGTIRL
	10	20	30	40	50	60
m011.pep	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDSAKIY	TEAGRQDLAD	KENAEIEVLHR
g011	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDGAKIY	TEAGRQDLAD	KENAEIDVLHR

193

	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGMGLLKLRLAGKA					
g011	YLPQMLSAGEIRTAVEAAVAETGAAGMADMGMVVLKTRLAGKADMGEVNLKLTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

```

g012.seq
1  ATGCTCGCCC GTCGCTATTT TTTCAATATC CAACCCGGGG CGGTTTTCAC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 gGcggTGGAT ATTcGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAAACAAT TTTATCCGcC acacacgcca tcatatagcc
301 gCcgCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAGCACCC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GCAGATTTCT CCCCGCCCTC CTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTC CTGATGTTT GTCTCTTCCT
651 CGCTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

```

g012.pep
1  MLARRYFFNI QPGAVETDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRHFRHHTHR TDDRKRSGNN FIRHTRHHIA
101 AACRDLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LREGRFLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFLFLA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

```

m012.seq
1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTcGGTACT TCCGCCACCA CACCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnnnnnnnn AACACAAAAA GGCGTGATT nTGCGTTTCG
551 GCAGATTTCT CCCCACCTC CTCAAACGT TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTGT GCCTCTTCCC
651 CGCTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

```

m012.pep
1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTHR TDRKRSGSN FIRHTRHHIT
1C1 AARXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXQHKKA*F XREGRFLPTL LQTFFLCFGF
2C1 RLFLFLFLFF LMFLFLA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
  1 ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
 51 TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGTGGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGCGGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GAAGATTTCT CCCACCTTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
  1 MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
 51 KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSNGN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKRRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFF LMFLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYERHHHTHRTDNRKRSNGNFIRHTRHHITAARXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQAVDIRYFRYNTHRTDNRKRSNGNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
m012.pep	130	140	150	160	170	180
	XXXQHKKAXF					
a012	PKLRSRQTVTQNHAARTFQSKQNLIFRLGNQKRRRLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
m012.pep	190	200	210	219		
	XRFGRLPTLLQTLFLCFGRFLFLFLFLFLMLCLFPAX					
a012	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMLCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

195

	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKRSNFIHRTRHHITAARXXXXXXXXXXXXXXXXXXXX					
	:     :     :     :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNFIHRTRHHIAAACRDLIDGDGQRNIAFAQT					
m012.pep	130	140	150	160	170	180
	XXXQHKKAXF					
	:	:	:	:	:	
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
m012.pep	190	200	210	219		
	XRFGFRLPTLLQTFFLCFGRFLFLFLFLFLMLCLFPAX					
	:     :     :     :					
g012	190	200	210			
	LRFGFRLPALQLTFLCFGRFLFLFLFLFLMFLCLFLAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAACTG  CTGAACAAC  TGATGCGTTT  CCTCCAGTTC  CTGTCGGAAT
101 TTCTGTTTGC CCTTTCCGT  ATTTTCACCC  ATAAAAGTAA  CCGTGCCTT
151 AAATTCGCCC GCGTCATCA  CATCCACATC  AATATCATGT  TTTTCAACA
201 GGCGGTGGAT ATTCCGTACT TCCGCCACCA  CACCCACCGA  ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC  ACACACGCCA  TCATATAACC
301 GCGCTCGCC  GCCACCTAT  CGACGGCGAC  GGTGAGCGGA  ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA  AACCCTAACC  GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC  TCATCTTCAG  GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA  GGATCTACG  GCGTGTGCAT
501 ACAATCGCC  GTCAAAATCC AACACAAAAA  GGCGGATT  TTGCGTTTCG
551 GCAGATTCT  CCCCACCCTC CTTCAAACGC  TTTTCTCTG  CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT  CCTCTTTTTC  CTGATGTTTT  GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR FTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTHR TDNRKRSNFI FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT XKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKRRNLMTQ  GFYGVCIQIA VKIQHKKAGF LRFGFRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFLFLFA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKILLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	:     :     :     :					
g012	10	20	30	40	50	60
	MLARRYFFNIQPGAVFTDKILLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
m012-1.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKRSNFIHRTRHHITAARRHLIDGDGQRNIAFAQT					
	:     :     :     :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNFIHRTRHHIAAACRDLIDGDGQRNIAFAQT					
m012-1.pep	130	140	150	160	170	180
	XKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	:     :     :     :					
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	:     :     :     :					
g012	LRFGRLPALQLTLFLCFGRFLFLFLFFLMFCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCGGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 CGCGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCAGC
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAATACC AACACAAAAA GGCGGGATT TTGCGTTTCG
551 GAAGATTTCT CCCCACCTTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSNGN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVDIRYFRYNTHRTDNRKRSNGNFIRHTRHHITARRHLIDGDGQRNIAFAQT					
	:     :     :     :					
m012-1	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKHRRLMTQGFYGVCIQIAVKIQHKKAGF					
m012-1	XKLSRQTVT VNHAARTFQSEQNLIIFRLGNQKHRRLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
m012-1	LRFGRLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTTtgt tcataataca
51  gtCcagaccGG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCCTTTCT
101 TGCCGTGGCA GGCGATGCag tTgGATTcGT ACACCTTTTG CCCTTTtGtc

```

197

```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaagtgtt
251 tgaaaccttg ttttttgatt Ttgcctttac ggggtgaaaa gtttttTtg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng>

## g013.pep

```

1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
51 MMLLSAAEAA AQRQHKMKAV GSRVVFIGVS PNVLKPCFLI LPLRGEKFFW
101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

## m013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGTTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCAGCGCAG TTGGATTCTG ACTTTTTTGC CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTCA TGGTGTTCCT TTCATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTGCCGAAT
301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

## m013.pep

```

1 MPLTMLCSST CGFFMMKSER XSGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIGVS FMFETLLLLI RSGXKIFLPN
101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

## a013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGTTTTTT ICATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCAGCGCAG TTGGATTCTG ACTTTTTTGC CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTCA TGGTGTTCCT TTAATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTGCCGAAT
301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

## a013.pep

```

1 MPLTMLCSST CGFFMMKSER *SGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIGVS LMFETLLLLI RSG*KIFLPN
101 R*

```

m013/a013 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
m013.pep	AQRQPKTRAVGSRVVFIGVSFMFETLLILRSGXKIFLENQX					
a013	AQRQPKTRAVGSRVVFIGVSLMFETLLILRSGXKIFLENRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPRSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	:   :   :   :					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNAVPRSPFLPWAQMLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIGVSF-MFETLLLILR-SGXKIFLPNQX					
	:     :                   : :   :             :					
g013	AQRQHMKMAVGSRVVFIGVSPNVLKPCFLILPLRGEEKFFWPKGIX					
	70	80	90	100		

q015.seq

1	ATGCAGTATC	TGATTGTCAA	ATACAGCCAT	CAAACTCTCG	TTACCATCAC
51	CATTTTGGTA	TTCAACATCC	GTTTTTTCCT	ACTTTGGAAA	AATCCAGAAA
101	AGCCCTTTGGT	CGGCTTTTGG	AAGCACTGAC	CCCCACTCAA	CGACACCGATG
151	CTGCTGTTTA	CGGGATTGTG	GCTGATGAG	ATTACCATCT	TTCCTCCGTT
201	CAACGCGCCT	TGGCTCGGCA	CAAAAATCCT	GCTCCTGTTT	GCCTACATCG
251	CACCTGGGCA	GGTAATGAT	CGCGCCCGTC	CGCGTTGAC	CAAGTTCTAC
301	ACCGTTTACC	TGCTCGCTAT	GTTGTGCATC	GCCTGCATCG	TTTACCTTGC
351	CAAAACAAA	GTCCTGCCAT	TCTGA		

q015.pep

1 MQYLIVKYSH QIFVTITILV FNIRFLLWK NPEKPLVGFW KALPHLNDTM  
51 LLFTGLWLWK ITHFSPFNAP WLGTKILLF AYIALGMVMM RARPRSTKPY  
101 TVYLLAMCCI ACIVYLAKTK VLPF\*

m015.seq (partial)

```

1      . AAAATCAGAA AAGCCTTGCG GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51     CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101    TCTCCCGTT CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCGCTC
151    GCCTATATCG CATTTGGTAT GATGATGATG CGCGCCCGTC CGCGTTTCGAC
201    CAAGTTCTAC ACCGTTTACC TGCTGCCATT GTGTTCGCTG GCCTGCATCG
251    TTTACCTTGC CAAAACCAA GTCCTGCCTT TCTGA

```

m015.pep (partial)

1 ..KIRKALAGFW KALPHLNDTM LLFTGLWLMM ITHFSPFNAP WLGTKILLLL  
51 AYIALGMMTMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF\*

a015.seq

```

1   ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTGTTTTCNT AC'TTTGGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGCACTGCT CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGA'TTGTG GATCGATAAA ATTACCCATT TCTCCCAGTT
201 CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGAT CGGCCCGCTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGGCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAAACAAA TGCTGCTT TCTGA

```

a015.pap

199

1 MQYLIVKYSH QIFVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM  
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY  
 101 TVYLLAMCCL TCIVYLAKTK VLPF\*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDT	MLLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDT	MLLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCLTCIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDT	MLLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFLLWKNPEKPLVGFWKALPHLNDT	MLLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
g015	FSPFNAPWLGTKILLLLFAYIALGMVMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG  
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg  
 101 tctttgTCGA TATTGATGTT TTCCAACCG ATATTgTCAA CGTTCGGACG  
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTCGC  
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC  
 251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT  
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT  
 51 ATYGQHFIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFSEHGF



200

101 RLV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

```
m018.seq
1  ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51  GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCCACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

```
m018.pep
1  MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51  AAHGCQHIFG NKYAFAILL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

```
a018.seq
1  ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCCGCAATA AAGATATGCG
51  GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCTTACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGGCC
251 TCGGTTTTAG CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGGTTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

```
a018.pep
1  MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51  AAYGCQHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFTEHGF
101 RLV*
```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCQHIFG					
	10	20	30	40	50	60
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFQTDIVNVRTAAYGCQHIFG					
	70	80	90	100		
m018.pep	NKYAFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX					
	70	80	90	100		
a018	NKYAFAILLPMDFYIAVCVEFDLGFSIQMQFQFFTEHGFRLVX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

```
m018/g018
10 20 30 40 50 60
m018.pep MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCQHIFG
g018 MQQGQLVGRVARNKDMRNAGLHGQRVGNRYAARVFDIDVFQTDIVNVRTATYGCQHIFG
10 20 30 40 50 60
```

201

	70	80	90	100
m018.pep	NKYAFFAILLEPMDFYIAVCIEFDLGFSIQMQFFFAEHGVRVLVX			
g018	NKYAFFAILLEPMDFYIAVCIEFDLGFSIQMQFFSEHGFRVLVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

g019.seq (partial)

```

1  ..ctgctggcgg ccctgggtgct tgccgcggtgt tcttcgACAA ACaactTGCC
51  AGCCGGCAAG ACCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTTCCAC cgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151 GGCGGCTACC CGTCCGCACT GGATGCAGTG AAACAGAAC ACGATGCGGC
201 AGCCGCGGCC TATTTGGAAA Acgcaggaga cagCGcgatg gcGGAAtg
251 tccgcaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

g019.pep (partial)

```

1  ..LLAALVLAAC SSTNTLPAGK TPAADNIETAD LSASVPTRPA EPEGKTLADY
51  GGYPSALDAV KQNNDAASAA YLENAGDSAM AENVKRWEL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

m019.seq (partial)

```

1  ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
51  GCTTGCCGCG TGTCTCTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGCGGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCGCG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCGAG ACAGTGGACG CTGTTTGAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CGGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTGTTTGGAC GGCAACGACG CCTGGAGGCG CGTGGCGGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTTGCCGCCT TGGACTATTA
801 CGGCAAGGTT GCCGACC3CC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCCTTGCGC ECCCAGCGTT GGGACGAGCT GGCCTCCGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCAGCG AGCCGCGCGC CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GGCGGCAGCG ACGGGCAGGA ATTTTATGC GGTGCTGGCA
1051 GGGGAAGAAT TGGGTGCGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAAACGG
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTGCC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGTT CGACCAAGGT TTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTG
1351 CGCTATATTT CGCCGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCGGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

m019.pep (partial)

```

1  MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51 AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARROWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGVL
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAALR ARRWDELASV
301 ISHMPEKLQK SPTWLYWLR SRAATGNTQE AEKLYKQAAA TGRNIFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQN SQSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNLYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

```

a019.seq
1 ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCTGGT
51 GCTTGCCGCG TGTTCCTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCNGCCCT
151 GCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGCG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCCG AACTGGTCAA AAATACGGCG
451 AAAGTGCCTT CGGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAGAGG GCACGCAAA' CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAGCGCG TTAAAGCCTC GAACAACGCA GTTTCGCGTG EGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCTT TGGAATATTA
801 NGGCAAGGTT GCCGACCGCC ECCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCANNNNNGC NNNCGNNGTT NGNANGANNNT GGCNNCCGNN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCACGC AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAC
1001 TNTACAAACA GCGCGCAGCA NCGGGCANGA ATTTTATGCT NGTGCTGNCN
1051 GGGCAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCTCTC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGTGTGCT GTCCGAAAC AGCCGAACCG CCGCGGATGC GAAAATGCGC
1201 CGTCNGGCTC AGGCGGAATG GCGTTTCGCC ACACGCGGCT TCATGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGT CGACCAAGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTG
1351 CGCTACATTT CGNNNNNTNA NGACACGSTA ATCGCCACG CGAAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGCG AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCGGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCCGCTTG CAAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCGG GCGCGCGCGA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCGG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCTT ACTACGCTC CCTCTTCGGC
1801 GCGCCGCACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

```

a019.pep
1 MYPPSLKHS LLLVXLVLA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51 AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARROWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGVL
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAAXX XXXXXXXXXX
301 XXXXXXXXXX XXXXXXXXXX SRAATGNTQX AXKLYKQAAA XGNIFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFN SRTAGDAKMR
401 RXAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNLYTL

```

451 RYISXXD TV IRHAQNVNVD PAWVYGLIRQ ESRFVMGAQS RVGAQGLMQV  
501 MPATAREIAG KIGMDAAQLY TADGNIRMG T WYMADTKRRL QNNEVLATAG  
551 YNAGPGRARR WQADTPLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG  
601 APHIPLKQRM GIVPAR\*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSNTLTPAGKTPADNIETADLSASVPTRPAPERKTLAD					
a019	MYPPSLKHSLPLLVXLVLAACSXTNTLSADKTPADNIETADLSASVPTXPAPEPKTXAD					
	10	20	30	40	50	60
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTLFAQEYAKLE					
a019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTLXAXEYAKLE					
	70	80	90	100	110	120
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLEQAAASGLLDGNDAWRRVRG					
a019	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLEQAAASGLLDGNDAWRRVRG					
	130	140	150	160	170	180
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
	190	200	210	220	230	240
m019.pep	250	260	270	280	290	300
	EQR SFAWGLGHYQSQNLNVPAALDYXGKVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	EQR SFAWGLGHYQSQNLNVPAALDYXGKVADRRQLTDDQIEWYARAAXXRXRXRXAXX					
	250	260	270	280	290	300
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQEAELKLYQAAATGRNFYAVLAGEELGRKIDT					
a019	XXXXXXXXXXXXXXXXXARSRAATGNTQXAKLYQAAAXGXNFYAVLXGEELGRKIDT					
	310	320	330	340	350	360
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWR FATRGFDEDKLL					
a019	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRSRTAGDAKMRRXAQAEWR FATRGFDEDKLL					
	370	380	390	400	410	420
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLN YTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	TAAQTAFDHGFYDMAVNSAERTDRKLN YTLRYISXXD TVIRHAQNVNVDPAWVYGLIRQ					
	430	440	450	460	470	480
m019.pep	490	500	510	520		
	ESRFVIGAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	ESRFVIGAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMG TWYMADTKRRL					
	490	500	510	520	530	540
a019	QNNEVLATAGYNAGPGRARRWQADTPLEGA VYAETIPFSETRDYVKKVMA NAAYYASLFG					
	550	560	570	580	590	600

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

q019/m019

10 20 30 40 49  
 g019.pep LLAALVLAACSSNTLPAAGKTPADNIETADLSASVPTRPAPPEGKTLAD  
 |||||  
 m019 MYLPSMKHSLPLLAALVLAACSSNTLPAAGKTPADNIETADLSASVPTRPAPPERKTLAD  
 10 20 30 40 50 60  
 50 60 70 80 89  
 g019.pep YGGYPSALDAVKQNNDAAAAAYLENAGDSAMAENVRKEWL  
 |||||:|||||:|||||:|||||:|||||:  
 m019 YGGYPSALDAVKQNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTLFAQEYAKLE  
 70 80 90 100 110 120

q023.seq

1	ATGGTAGAAC	GTA AATTGAC	CGGTGCCCAT	TACGGTTTGC	GC GATTGGGT
51	AATGCACCGT	GC GATCGCGG	T TATTATGTT	GATTATACCC	GT TGCACTTT
101	TAGTGGTTCT	ATT TGCCTG	CCTAAAGAA T	ATCCGGCATC	GCAGGCATTT
151	TTTAGTCAAG	CT TGGGTAAA	AGTATTATACC	CAAGTGAGCT	TTATCGCGGT
201	ATTCTTGCAC	GCTTGGGTGG	GTATCCGCGA	TTTGTGGATG	GACTATATCA
251	AACCCTTCCG	CTGCGTGTG	TTTTTGCAGG	TGCCCACCAT	TGcttGGCTG
301	CTGGCGTGCC	TCGTGTATT C	AGTTAAAGTG	ATT TGGGGGT	AA

q023 . pep

1 MVERKLTHGAY YGLRDWVMQR ATAVIMLIYT VALLVVLFLAL PKEYPANQAF  
51 FSQAVVKVFT QVSFIAVFLH AWVGTRDLWM DYIKPFGVRL FLQVATIVWL  
101 VGCLVYSVKV IWG\*

m023.seq

1	ATGGTAGAAC	GTA AATTGAC	CGGTGCCCAT	TACGGTTTGC	GCGATTGGGT
51	GATGCACAGT	GCGACATCGG	TTATTATGTT	GATTTATAAC	GTTCACACTTT
101	TAGTGGTTCT	ATTTTCCCTG	CCTAAGAAGT	ATTCGGCATG	CGAGGCATTT
151	TTTAGTCAAA	CTTGGGTAAA	AGTATTTACC	CAAGTAGCTT	TCATCGCCGT
201	ATTCTTGCAC	GCTTGGGTTG	GTATCCGCAG	TTTGTGGATG	GACTATATCA
251	AACCCCTTCG	GCTGCGTTTG	TTTTCGCGAG	TTGCCACCAT	CGTTTGGCTG
301	GTCGGCTGTC	TCGTGTATTG	AGTTAAAGTG	ATTTTGGGGT	

m023 . pep

1 MVERKLTGAH YGLRDVWMQR ATAVIMLIYT VALLVVLFSL PKEYSAWOAF  
51 FSQTVWKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFCVRL FLQVATIVWL  
101 VGCLVYSVKV IWG\*

a023.seq

1 ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GGGATTGGGC  
51 GATGCAACGT GCGACCGCGG TTATTATGTT GATTTATACC GTTGCACTTT  
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT  
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

205

201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA  
 251 AACCTTTCGG CGTGCGTTTG TTTTGCAGG TTGCCACCAT CGTCTGGCTG  
 301 GTCGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep  
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVL FAL PKEYSAWQAF  
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPFVRL FLQVATIVWL  
 101 VGCLVYSIKV IWG\*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYT	VALLVVL FAL PKEYSAWQAF	FSQTWVKVFT			
a023	MVERKLTGAHYGLRDWVMQRATAVIMLIYT	VALLVVL FAL PKEYSAWQAF	FSQTWVKVFT			
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL VGCLVYSIKVIWGX				
a023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL VGCLVYSIKVIWGX				
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYT	VALLVVL FAL PKEYPAWQAF	FSQAWVKVFT			
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYT	VALLVVL FSLPKEYSAWQAF	FSQTWVKVFT			
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL VGCLVYSIKVIWGX				
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL VGCLVYSIKVIWGX				
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq  
 1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TGCCCGCTCT  
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTcATT GCAGGCAATT  
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA  
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC  
 201 CGTGCAAact gcgcgggttT ATTGCCTCC TGCTTATGTT CCGCcgCTG  
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC  
 301 aacgCGGCGa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTc  
 351 caaAcgCtac CATATCTCTC AAGACGATT TCCGTGCGTGG AACGGCATGA  
 401 CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCaggA  
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC  
 501 TGCCGCGCAA ACCCTGTGA AACCGCCGC gcaACCGCCC GTTCAGTCCG  
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC  
 601 GCGCCGCCCC CGCAATCTCC TGCCGCTTCG CTTCCGCA CGCGTTCGGT  
 651 CGCGGCATT GTTTGGCAGC GTCCGACCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAAA TTGCTGGTTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTCAGC AGGTTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTC GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
1   MLKQTTLLAA CTAVAALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51  TPNNAAPAAAN DAPYVPVQQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFRW NGMTDNTLSI QQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAAO TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEQQQVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
1   ..GTGCGGCGG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTC
51  GCCGTCTGCA CCTGCCGTTT CGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGATC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCACCG AAAGCCGCG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGATC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACGCGC CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCTGTGAAA CCGCGCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TGCGGAAAAT AAAGCGGTTT CCGCGCCCGC
651 CCGCAATCT CCTGCCGCTT CGCTTCCGG CACGCGTTTG GTGCGCGGCA
701 TTGTTTGGCA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCGCGGCG
751 AACAAACAAG GTGTGCATAT TGCCGGTAAT GCGGGACAGC CCGTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGGTCA
951 GCAGGTTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
1   ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51  NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNLSIGQIV KVKPAGYAAP KTAAVESRPA VPAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRP QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSGL RGYGNLVIIQ HNSSF LTAYG
301 HNQKLLVGEG QQVKRQQQVA LMGNTDASRT QLHFEVRQNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
1   ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACGCCC TTGCCGCTCA
51  GTTGGGCGGA TGCCCCACCC AACACCCTTC TCCTGTCAAT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

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207

```
151  ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201  GGTGCAAAGC GCGCCGGTTT ATANGCCTCC TGCTTATGTT CCGCCGCTCTG
251  CACCTGCCGT TTCGGGTACA TACGTTCTTT CTTACGCANC CGTCGACATC
301  AACCGCGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351  CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
401  CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA
451  TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501  TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551  CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601  CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651  GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701  CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751  ACCCGTGTGA AACCCGCCGC GCAACGCCTT GTGCAGTCCG CGCCGCAACC
801  TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCGCAAT
851  CTCCTGCCGC TTCGCTTCC GGCACGCGTT CCGTCGCGCG CATTGTTTGG
901  CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951  GGGTGTTCGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTTC GCGGCGGCTG
1001 ACGGCAAAGT GGTTTATGCA GGTTCCGGTT TGAGGGGATA CGGCAATTTG
1051 GTCATCATCC AGCATAATTC TTCCTTCTTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTCCAGGTG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

```
a025.pep
1  MLTPTTL*VA CTALAAQLGG CPTQHPSPVI AGNSGMQTVP SAPVYNPYGA
31  TPNAAAPAA DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATHTIVRG DTVYKISKCY HISQDDFRAW NGMTDNTLSI GQIVKVKPAG
131 YAAPKAAAVK SRPAVPAAQ PLVQSAPVDI NAATHTIVRG DTVYNISKRY
201 HISQDDFRAW NGMTDNTLSI GQIVKVKPAG YAAPKAAAVK SRPAVPAAVQ
231 TPVKPAAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIIV
301 QRPTQGVVVA DFGGNNKGVD IAGNAGOPVL AAADGKVVYA GSGLRGYGNL
331 VIIQHNSFL TAYGHNQKLL VEGEQQVKRG QQVALMGNTE ASRTQLHFEV
401 RQNGKPVNPN SYIAF*

m025/a025 97.4% identity over a 351 aa overlap

                                10      20      30
m025.pep                                VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                |||:|||:|||:|||:|||:|||:|||:|||
a025  GMQTVPSAPVYNPYGATPNAAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
                                40      50      60      70      80      90

                                40      50      60      70      80      90
m025.pep  YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
            |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025  YAXVDINAATHTIVRGDTVYKISKCYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
            100     110     120     130     140     150

                                100     110     120     130     140     150
m025.pep  KAAAVKSRPAVPAAQPPVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMT
            |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025  KAAAVKSRPAVPAAQPLVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMT
            160     170     180     190     200     210

                                160     170     180     190     200     210
m025.pep  DNMLSIGQIVKVKPAGYAAPKTAAVESRPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
            |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025  DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
            220     230     240     250     260     270

                                220     230     240     250     260     270
m025.pep  KAVPAPAPQSPAASPSGTRSVGGIIVQRPTQGVVADFGGNNKGVDIAGNAGQPVLAAD
            |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
```



Homology with a predicted ORF from *N. gonorrhoeae*

m025/q025

```

m025.pep                                10          20          30
                                VPPVQSAPVYTTPAYVPPSAPAVSGTYVPS
                                |||||:||||:|||||
g025    GMQTVSSAPVYNPYGATFYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
          40          50          60          70          80          90

          40          50          60          70          80          90
m025.pep    YAPVDINAATHTIVRGDTVYNISKRYHISQDDFFRAWNGMTDNTLSIGQIVKVKPAGYAAP
          |||||:||||:|||||
g025    YAPVDINAATHTIVRGDTVYNISKRYHISQDDFFRAWNGMTDNTLSIGQIVKVKPAGYAAP
          100         110         120         130         140         150

          100         110         120         130         140         150
m025.pep    KAAAVKSRPAVPAQAAPPVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFFRAWNGMT
          |
g025    K-----

          160         170         180         190         200         210
m025.pep    DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVAAVQTPVKPAAQPPVQSAPQPAAPAAEN
          |||||:||||:|||||
g025    -----TAAVESRPAPVAAQTPVKPAAQPPVQSAPQPAAPAAEN
          160         170         180         190

          220         230         240         250         260
m025.pep    KAVPAPAP--QSPAASPSGTRSVGGIIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
          |||||:||||:|||||
g025    KAVPAPAPAPQSPAASPSGTRSVGGIIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
          200         210         220         230         240         250

          270         280         290         300         310         320
m025.pep    ADGKVYVYAGSGLRGYNLVIIOHNSFLTAYGHNQKLLVGEGQOVKRGQQVALMGNTDAS
          |||||:||||:|||||
g025    ADGKVYVYAGSGLRGYNLVIIOHNSFLTAYGHNQKLLVGEGQOVKRGQQVALMGNTDAS
          260         270         280         290         300         310

          330         340         350
m025.pep    RTQLHFEVRONGKFPVNPNSYIAFX

```

g025                    |||||  
                       RTQLHFEVRQNGKPVNPNYSYIAFX  
                       320            330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq  
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC  
 51 TGACAATTTC CTTTTCGCC AGCCAAATAT CATGCGTATC TTTCGGTTCG  
 101 GGCTTGTGG GCATGGCAAC CTTCAACAGC CGCGCCATCA CAGGAATCGT  
 151 CGTTCCTGTA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA  
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC  
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC  
 301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC  
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCCGCCCTG  
 401 TCCAACACGC CGGCGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT  
 451 TGCTGCGGCC AGCCAAGCCA AACCTCCAT CACACGCAA ACCTGTTCCG  
 501 TcgcACGGTT GCGCTGGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC  
 551 AAAAAGCCGC TGCCGCCTAT GGTATTGGTA AACGCAACA CAAGCAGCCC  
 601 CCCCAGACACA ATCATCAGCG CGTACAGACC TTCCGtacac acctccaatt  
 651 cccaatcaac gtcatagetg tctcccggtg taaaatgttc ttcacttcag  
 701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta nacctgtggg  
 751 tgccccaacg gatttagtaa cctcccaatg actctgcttg tcgccccctt  
 801 cgcccgcttt ctccttcgag gaaaacttgt tgtcccgctc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep  
 1 MVSLRFRFGN HFRRHSDFN LFRQPNIMRI FRFGLVGHGN LQQRHHRNR  
 51 RSLNQQRQHH HGKRHIKQOV RIGNAHQHRH HRQRNRYGSS QAQPTDIRLF  
 101 TQAVIEFPQT AEHCQTRDQ HQERRNRQGF RRPVQHAGGR NQQTEDHDEQS  
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAAY GIGKRKHQKP  
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPPSSQ PETFMCXTLG  
 251 CPNGFSNLPM TLLVAPFARF LLPGKLVVEV LH\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)  
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTC TATTCGGCTA TACGCCTTTT  
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA  
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CCGCCGCCCT  
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAACGTG  
 201 CGGACAAAGT GGTGAAACC ACGCTCAGAA ACAACAGTGC GCCACCCGGC  
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)  
 1 ...RLKHGVLHF YSAIRLFTQA VIEFPQTAEH CRRTRDQHQE RNRQGFRRP  
 51 VQHVGRNRNQ QRHSQTCGQS GRNHAQKQOC ATRQ....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq  
 1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTTCCACAAA CCGCCGAACA  
 51 CTGCCGCGCG ACGCGCGACC AGCATCAGGA ACGCGCAAT CGCCAAGGCT  
 101 TCCGCCGCCG CGTCCAACAC GTTGGCAGGA GAAACCAGCA GCAAAGGCAT  
 151 TCCCAAACGT GCGACAAAG TGGTGAAAC CACGCTCAGA AACACAGTG  
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)  
 1 IRLFTQAVIE FPQTAEHCRH TRDQHQERRN RQGFRFPVQH VSRNRQQQRH  
 51 SQTCCQSGRN HAQKQCATR Q

210

m031/a031 100.0% identity over a 71 aa overlap

	10	20	30	40	50	60
m031 . pep	RLKHGVLH	FYSAIRLFTQAVIEFPQTAEHCRRTRDCHQERRNRQGFRRPVQHVGRNRQQ				
a031		IRLFTQAVIEFPQTAEHCRRTRDCHQERRNRQGFRRPVQHVGRNRQQ				
		10	20	30	40	
	70	80				
m031 . pep	QRHSQTCGQSGRNHAQKQQCATRQ					
a031	QRHSQTCGQSGRNHAQKQQCATRQ					
	50	60	70			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

		10	20	30
m031 . pep		RLKHGVLH	FYSAIRLFTQAVIEFPQTAEH	
g031	NQQRQHHHGKRHIKQVVRICNAHHQRHHRQNRNYGSSQAQPTDIRLFTQAVIEFPQTAEH			
	60	70	80	90
	40	50	60	70
m031 . pep	CRRTRDCHQERRNRQGFRRFVQHVGRNRNQQRHS-QTCGQSGRNHAQKQQCATRQ			
g031	CQTRDCHQERRNRQGFRRFVQHVGRNRNQTEHDEQSLRQPSQTVHHTQNVFRRTVALV			
	120	130	140	150
	160	170		
g031	TDNDAGKVNROKAAAAYGIGKRKHQPARHNRQVQTFRTHLQFPINVIASVRVKMFFTS			
	180	190	200	210
	220	230		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032 . seq

```

1  ATGCGGCGAA  ACGTGCTGCG  CGTCGCCGTA  TTGCGCCGCC  CACGATTCTGA
51  GCGGTTTTTG  GATTTGCGGT  TGGCTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101  AACAGGGCTT  TGCCGTCCGA  TGCCGTCTGA  CGCAGCGGCA  GATAGTTTTT
151  CAAGGCTTCC  ACGCTTTTGC  CGGTCAGCGG  AACCTGACGC  TGCTTGCGCC
201  CTTTGCCGGT  AACGTGTACC  CACGCTTCGT  CCAAATATAC  ATCATCTGCA
251  TTCAAGCCGT  GTATCTCGCT  CACGCGCAA  CCGCTGCCGT  ACATCAGCTC
301  GAACAGCGCG  TGGTCGCGCA  CCGCCAGCGG  GTCGCCGCCG  TCCACGGGCA
351  AATCCAACAT  CCGGTTTCAG  CATTCTGCG  GCAGGGCTTT  GGGTACGCGC
401  TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  CGGCATCAG
451  CCCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCACGCC  GACAGCTTGC
501  GCGCCAGCGT  CCGACCGTCC  AAACGCGGCT  GCGACAGCCG  CCGCAACGCC
551  GccgTAAAT  CGCGCCGCGA  CAAGTCCTGC  GGCACGCcgc  ctgcatCTTC
601  AGACGGCATT  TGTGCCAACA  GTGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651  ATGCCGCAAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701  TAAGCGTCAA  AATacgcgc  AAACccgTCC  AAAACCATAA  CCGTCCACA
751  CAAATATCAA  AAAACAGTG  A

```

This corresponds to the amino acid sequence &lt;SEQ ID 110; ORF 032.ng&gt;:

g032 . pep

```

1  MRRNVPAAVAV  LRRPRFEAF  L  DLALAAQARAV  PAGKQGF  AVR  CRLTQRQIVF
51  QGFHAFAGQR  NLTLAPFAG  NVYPRFVQIY  IICIQAVYLA  HAQTA  AVHOL

```

```

101 EQRVVAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGAHQ
151 PAFDQPGAIL PPRRLARQR PTVQTALRQP PQRRRKIAPR QVLRHAACIF
201 RRHLCQQCKQ FFQIAPVCRN RVLRLALAH D VFQISVKIRR KPVQNHNRPT
251 QISKNQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

m032.seq (partial)
  1 ATGCGGCGAA ACGTGCmTGC mGTGCGCGTT kTGCGCCGCC CATTGCGCCA
  51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGACCAGCGG CACCTGCCGC TgTT.GCGCC
201 CTTTGCCGAT AACGTGTACC CACGcyTCGT CCAAATAGAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGGGCG TGGTCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTACG CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGCGG GTCGGGTCGG CGTGCAATCAG
451 GCCGCGCTTT ACCAGCCAAA CGCAATACTG CCGCCAAGAC GAAAGCTTGC
501 GAGCCAGCGT CCGTTCCTCC AAACCGCG...

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```

m032.pep (partial)
  1 MRRNVXAVAV XRRPLRQTF L DLALAQARAV PAGKQGFVR CRLTQRQIVF
  51 QGFHAFADQR HLPLXAPFAD NVYPRXVQID IICIQAVYLA HAQTAAVHQF
101 EQGVVAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGVHQ
151 AALYQPNAIL PPRRKLASQR PFPQTA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```

a032.seq
  1 ATGCGGCGAA ACGTGCCTGC CGTCGCCGTT TTGCGCGGCC CATTGCGCCA
  51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGGTCAGCGG AACCTGCCGC TGCTTGCGTC
201 CTTTGCCGGT AACGTGTACC CACGCCTCGT CCAAATATAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGCGCG TGATCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTACG CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGCGG GTCGGGTCGG TATGCAGCAG
451 ACCGCGTTTG ACCAGCCAGG CGCAATACTG CCGCCAAGAC GACAGCTTGC
501 GCGCCAGCGT CCGCGCATTC AAACCGCGCT GCGACAGCGG CCGCAACGCC
551 GCCGTAAAT CGCGCTGCGA CAAGCCCTGC GGCACGCCGC CTGCATCTTC
601 AGACGGCATT TGTGCCAACA GCGCAAACAG TTCTTCCAAA TCGCGCGGGT
651 ATGCCGCCAC CGTGTGCTCC GACTTGCCCT CGCGCACGAT GTTTTCCAAA
701 TAAGCGTCAA AATGCGCGC AAACCCGTCC AAAACCATAA CCGCCCCACA
751 CAAATATCAA AAAACAGTG A

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```

a032.pep
  1 MRRNVPAAVAV LRRPLRQTF L DLALAQARAV PAGKQGFVR CRLTQRQIVF
  51 QGFHAFAGQR NLPLASFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHQF
101 EQRVIAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGAIL PPRRLARQR PRIQTALRQP PQRRRKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAH D VFQISVKMRR KPVQNHNRPT
251 QISKKQ*

```

m032/a032 88.1% identity over a 176 aa overlap

```

          10      20      30      40      50      60
m032.pep MRRNVXAVAVXRRPLRQTF L DLALAQARAVPAGKQGFVR CRLTQRQIVFQGFHAFADQR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a032     MRRNVPAAVAVLRRPLRQTF L DLALAQARAVPAGKQGFVR CRLTQRQIVFQGFHAFAGQR
          10      20      30      40      50      60

```

212

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAAHQAATAAVHQFEQGVVAHRQRVAAVHGQIQH					
a032	NLPLLASFAGNVYPRLVQIYIICIQAVYLAAHQAATAAVHQFEQRVIAHRQRVAAVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPERRKLASQRPFQTA					
a032	PVQPFLLRQGFYALGLLRRFDVGGRVGMQQTAFDQPGAILPERRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVRLALAHDFQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng)

from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFDLALAAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFADQR					
g032	MRRNVPAVAVLRRPRFEAFDLALAAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAAHQAATAAVHQFEQGVVAHRQRVAAVHGQIQH					
g032	NLTLLAPFAGNVYPRFVQIYIICIQAVYLAAHQAATAAVHQLEQRVVAHRQRVAAVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPERRKLASQRPFQTA					
g032	PVQPFLLRQGFYALGLLRRFDVGGRVGAHQPAFDQPGAILPERRQLARQRPVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCQQCKQFFQIAPVCRNRVRLALAHDFQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1  ATGGCGGCGG CGGACAACT CTTGGGCGGC GACCGCCGCA GCGTCGCCAT
51  CATCGGAGAC GCGCGGATGA CGGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCGGCGCA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CGGCGCGTTG CCCAAATATC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAAA GCGCAAacgg
251 GCAAGGTATT AGACAAAATA CCCGCGCGCA TGGagtTTGC CCAAAAAGTC
301 GAACAcaaa TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCGCTG TTTGAAAATT TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAGAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCcg tcaAATACCA CGCGTCGcC aACCTGCcta
551 AAGAAGGCGG GGCGCAAATg ccGTCTGAAA AAGAACCCAA GCCCGCCgCc
601 aaaccgACCT ATACCAAGT ATTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCATGCGC GAGGGCAGCG

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701 GACTGGTGGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGTTTGG CGTGCGAAGG
801 CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCGT TTTGTTTGCC
901 GTCGACCGTG CCGGCATCGT CGGCGCGGAC GGTCCGACCC ATGCCGGCTT
951 GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCTGTCTGC TTTGACCTG CTATCAGGCG
1051 GATGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAT CGGCAAGGCG ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TTcatTGCCT TCGGCAGTAT GGTGCGCCAC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTt
1251 cgtcaaacCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACg
1301 accGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGTCTTGG AAGTGTGGC GAAACACGCC ATCTGCAAC CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CGGCGATCCG AAAAAACTTT
1451 TGGACGATTG GGGTTTGTAGT GCCGAAGCGG TGGAAACGCC GGTGCGCGAG
1501 TGGCTGCCGG ACCGTGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

**g033.pep**

```

1 MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISENVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLLKDLRSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPPTYQVFGK WLCDRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAT
401 ALAVAELKNA TVADMRFVKP IDEBLIVRLA RSHDRIVTLE ENAEOGGAGG
451 AVLEVLAKHG ICKPVLLIGV ADTVTEHGDP KKLLDDLGLS AEAVERVRRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

**m033.seq**

```

1 ATGGCGCGCG CAGACAAACT CTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGCGGAC GCGCGGATGA CGCGCGGCA GCGCTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGTt GATTTGCTtG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CGGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGCGCGCA TGGAGTTTGC CCAAAAAGTC
301 GAACACAAAA TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCTTTG TTTGAAAACT TCGGCTTCCG CTACACCGGC CCGGTGGACG
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCCG TCAAATACCA CGCCGTGCGC AACCTGCCTA
551 AAGAAAGCGC GCGCAAAATG CCGTCTGAAA AAGAACCCAA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAAA TGGCTGTGCG ACCGGCGGCG
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT C3ATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA C3CGCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCGGT TTTGTTTGCC
901 GTCGACCGCG CCGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTCG GCTGCGTGCC GAACATGATT GTCGCGCGCG
1001 CGAGCGATGA AAACGAATGC CGCTGTGTC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAT CGGCAAGGCG ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG

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1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAG3CGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCCG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pap

```

1 MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVLA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 LAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAP
401 ALAVAEKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLGLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1 ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GGC GCGATGA CGGCGGGTCA GCGCTTTGAA GCCTTGAAC
101 GCGCGGCGCA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTGCGATT CCCCAACGT CGGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGCGCGCA TGGAGTTTGC CCAAAAAGTC
301 GAACATAAAA TCAAAACCTT TGCCGAAGAA GCCGAACACG CCAAAACAGTC
351 ACTGTCTTTT TTTGAAAAC TCGGCTTCCG CTATACCGCG CCCGTGGACG
401 GACACAACGT CGAAAATCTG ETCGATGTAT TGGAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGGCA ACGCTACAA
501 ACTCGCCGAA AACGATCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAATG CCGTCTGAAA AAGAACCCTA GCCGCGCGC
601 AAACCGACCT ATACCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTGCGC
751 ATCGCCGAGC AGCAGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCAC CTTTTTACAA CGCGCTACG
851 ACCAAGTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTTGGC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGTTT
951 ATCGATTTA AGCTTTTTC GCTGCATTCC GAATATGATT GTCGCGCGC
1001 CGAGCGATGA AAATGAATG CGCCTGCTG TTTGACCTG CTATCAGGCA
1051 GACGCGCCG CCGCGTCCG CTATCCGCG GGCACGGSTA CCGCGTGCC
1101 GGTTCAGAC GGCATGAAA CCGTGAAAT CGGCAAGGCG ATATCCGCC
1151 GCGAAGGTGA GAAAACGCA TTCATTGCT TCGGCAGTAT GGTGCCCCCT
1201 GATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTGCGC ATATGCGCTT
1251 CSTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG
1301 ACCGCATCGT TACCCTTGAA GAAAACGCC AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCCG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pap

```

1 MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVLA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA  
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAP  
 401 ALAVAGKLN TVADMRVFKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS  
 451 AVLEVLAHKG ICKPVLLLG ADTVTGHGDP KKLLDDLGLS AEAVERRVRA  
 501 WLSDRDAAN\*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISPNVGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISPNVGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAHQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAHQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPVDGHNVENLVDVLEDLRGRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREGKTAFFIAFGSMVAPALAVAELNATVADMRVFKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREGKTAFFIAFGSMVAPALAVAGKLNATVADMRVFKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAHKGICKPVLLLGVDVTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAGVLEVLAHKGICKPVLLLGVDVTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			



Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISPNVGAL	60
g033	MAAADKLLGSDRRSVAIIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISPNVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKITLAEEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKITLAEEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPKQLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPKQLLHVITKKGNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALONLPVLFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALONLPVLFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPMNIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPMNIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAPGSMVAPALAVAELNATVADMRFVKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAPGSMVATALAVAELNATVADMRFVKP	420
m033 . pep	IDIELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
g033	IDIELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
m033 . pep	KKLLDDLGLSAEAVERRVRANLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVRENLPDRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

1	ATGAGCCGTT	TATGGTTTTT	TGCCGTAAAA	AACATTATAA	TCCGCCTTAT
51	TTACCTATTG	CCCAAGGAGA	CACAAATGGC	ACTCGTATCC	ATGCGCCAAC
101	TGCTTGACCA	CGCCGCCGAA	AACAGCTACG	GCCTGCCCGC	GTTCAACGTC
151	AACAACCTCG	AACAAATGCG	CGCCATTATG	GAAGCCGCCG	ACCAAGTCAA
201	CGCGCCCGTC	ATCGTACAGG	CGAGCGCAGG	TGCGCGCAAA	TACGcgGCG
251	CGCCGTTTTT	GCGCCACCTG	ATTCTGGCGG	CAGTCGAAGA	ATTTCCGCAC
301	ATCCCCGTCG	TGATGCACCA	AGACCACGGC	GCATCGCCCG	ACGTgtGCCA
351	ACGCTCCATC	CAACTGGGCT	TCTCCTCCGT	GATGATGGAC	GGCTCTTTGC
401	TCGAAGACGG	CAAAACCCCT	TCTTCTTACG	AATACAACGT	CAACGCCACC
451	CGTACCGTCG	TCAACTTCTC	CCAGCCCTGC	GGCGTGTCG	TGAAGGCCGA
501	AATCGGCGTA	TTGGGCAACC	TCGAAACCGG	CGAAGCAGGC	GAAGAAGACG
551	GAGTGGGCGC	GGCAGGCAAA	CTCTCACACG	ACCAAATGCT	CACCAGCGTT
601	GAAGATGCCG	TGCGTTTCGT	TAAAGATACC	GGCGTTGACG	CATTGGCGAT
651	TGCCGTCGGC	ACCAGCCACG	GCGCATACAA	ATTCACCCGT	CCGCCACAG

```

701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAT CAAACCTGTT TCGTTGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQSI QLGFSVMMD GSLLEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIAVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKVI NEYGGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA WACAGCTACG GCyTGCCGCG GTTCAACGTC
151 AACAACTCG wACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAAA TATCGGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGGCGG CTGTGCAAGT ATTTCCACAC
301 ATCCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTTCT CCACGCTTGC GCGGTATCCG TTGAAGCGCA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGCGCG AGTGGGCAAA CTTTCCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGGTGACG CATTTGGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLXQMRAIM EAADQVDAPV IVQASAGARK YAGAPFLRHL ILAAVEVFPH
101 IPVVMHQDHG ASPDVCORSI OLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAIAVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCGC ACCAAGTCAA
201 CGCGCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGGCGG CTGTGCAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TTTCTCTCGT GATGATGGAC GSCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

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218

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451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TGCCTTTCGT TAAAGATACC GCGGTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCGTACAA ATTCACCCGT CCGCCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTCCGC AAGAAATGGCT
801 GAAAGTCATC AACGAATACG CCGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGGC TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

a034.pep

```

1 MSRLWFFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIAGV TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPKYL SKTIEAMKQI CLDRYLAFCG
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

	10	20	30	40	50	60
m034.pep	MSCLWFFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM					
a034	MSRLWFFFAAKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM					
	10	20	30	40	50	60
m034.pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI					
a034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI					
	70	80	90	100	110	120
m034.pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI					
a034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI					
	70	80	90	100	110	120
m034.pep	QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLNLETGDAG					
a034	QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLNLETGEAG					
	130	140	150	160	170	180
m034.pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
a034	EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
	190	200	210	220	230	240
m034.pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
a034	EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
	190	200	210	220	230	240
m034.pep	RIKEIHQALPNTHIVMH					
a034	RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVKRVN					
	250	260	270	280	290	300

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

## m034/g034

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILA AVEVFPHPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILA AVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034 . pep	QLGFSSVMMDGSLMEDGKTPSSYEYNVNATRTVNFSSHACGVSVGEIGVLGNLETGDAG	180
g034	QLGFSSVMMDGSLEDGKTPSSYEYNVNATRTVNFSSHACGVSVGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

## g036 . seq

```

1  ATGCTGAAGC CGTGTGTTGGT ATACAGTGCC TGTGCGGCGG cgttgcCTGC
51  GCGGACTTCG AGCAGCAGGC GTTGCCTGCC TTCGGGCAGA TGTGCGTACC
101 AATATTCGAG CAGGGCGGAC GCAACGCCCC GTCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCTGCCGT CTTTTCCTCG AAGGAAAACC TGTTCGGACG
251 GCGAAACAAG CGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGTAT CGAGCGCGGC CAGTGCAGCG CAGTCCGACG GTGAGGCTGG
351 GCGGATGTTT ATGTTCTGTC CTTCCGTTCC GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAGTTC GGCGTGTGCC GCGCCAGTTG
451 CGGATAGGCC GCGGCGGAGG GCGAGCGCGA GAAATCGGC GCGGTCGCGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGTG CGAACGCACT
551 GCCGATGCCG TCTGAAAAGA CGTACCCCTC GGGGAGGGCA ATGTCTGCCG
601 CCCTACCGAC TTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGGAAC
651 CCGACATAAA ACACTTCGCC CATACGCGCG TCCGACGCGG CGAGTATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGTG GGGATGCCGA
751 TTAAAGGCGT GTCGAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

## g036 . pep

```

1  MLKPCLVYSA CAAALPARTS SSRRCVPSGR CAYQYSSRAD ATPRRRHSGA
51  VAIRCSSDSS GRFCQTIKAA ILPSFSARKT CSDGETSADS NWRCVHADGL
101 QTVSSAASAA QSDGEAGRMF MFVPSVPPVL WQSGRFCCGR RAVRRVPRQL
151 RDSRRRRGRAR ENRRRSAYRV CLRRADGFPV RTHCRCLRK R*PRGGQCLP
201 PYRLDNRSNG GGSACRTTHK TLRPYARPQR RVCSFAAAAA RRRHRAWGCR
251 LKACRTALPN LAPRRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

## m036 . seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGCTG
51  ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCGA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCG .CGT CTTTTCCTCG AAGGAAAACC TGTTCGGACG
251 CCGAAACCCAG TCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGC3GC CAGCTCCTCA CAATCGGCAC AAACGGCAGC

```

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351 GCGGATGTTT ACAGGCGCGC TCTCCGTTCT GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAAACC GCGGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTG3CT GCCAATGCCA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGCTTGCCG
601 CCCGCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTTCGCC CACACGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCA3CG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGT ATCAAAC3GC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

m036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNREWLPMR ESRQSAYPV CLRTAELLPA RTRCLRLKR RIFPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

a036.seq

```

1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGTC
51 ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCGCGCGT CTTTTCGCG AAGGAAAACC TGTTCCGACG
251 CCGAAACAGC TGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGGCGCGC CCTCCGTTCG GCCTGTTCTT TGGCAGTCAA
401 GCGGATTTTG TTGCGGACGT AGAGCAGCTC GCGGTGTGCC GCAGCGACGG
451 CCGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGGC GGCGGTCGCG
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTCCAGCG CGAACGCATT
551 GCGGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGCTTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGCAAC
651 CATGCATAAA AACTTTCGCC CACACGAGCG TCCGACGCG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGAGT ATCAAACGCG GTTGCCAAAC CTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

a036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRFFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFFA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
a036	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
m036.pep	GRFCQTIKAAIPXSFSAKRTCSDETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
a036	GRFCQTIKAAIPPSFSARKTCSDETSADSNWRCVHADGLQTASSAASAAQSAXTARRMF					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPLPMRESRRQSAYPVCLRTAELLPA					
a036	TGAPSVPPVLWQSGRRFCCGRRRAARVPQRRRENRLQPPDXGSRRRSAYRVCLRRADGFPA					
	130	140	150	160	170	180
m036.pep	RTRCLCRLKRRIPPAAGCLFPARPDNRSNGGSSAYRTMHKTLRPYERPXQGCSEFAAAAA					
a036	RTHCRCLKRRILPAAGCLFPDRPDNRSNGGGSACRTMHKTLRPYVRPQRCSEFAAAAA					
	190	200	210	220	230	240
m036.pep	RRRHRARVRRRLRGYQTALPNPELHRCRYAVRX					
a036	RRRHRARVRRRLKEYQTALPNLAPRRCRYAVPX					
	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNYSSRADAIPWRRHSGAVAIRCSSDSS					
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAYQYSSRADATPRRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
m036.pep	GRFCQTIKAAIPXSFSARKTCSGGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
g036	GRFCQTIKAAILPSFSARKTCSGGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	70	80	90	100	110	120
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPLPMRESRRQSAYPVCLRTAELLPA					
g036	MEVPSVPVLWQSGRFCCGRRAVRRVPRLDRSRRRGRARENRRRSAYRVCLRRADGFVP					
	130	140	150	160	170	180
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERPXQGCSEFAAAAA					
g036	RTHCRCLKRRTPRGQCLPPYRLDNRSNGGGSACRTTHKTLRPYARPQRRVCSFAAAAA					
	190	200	210	220	230	240
m036.pep	RRRHRARVRRRLRGYQTALPNPELHRCRYAVRX					
g036	RRRHRAWGCRLLKACRTALPNLAPRRCRYAVRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGTC
51  ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCTGTC GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCC GCCGT CTTTTCCTCGC AAGGAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGCGGC CAGCTCCTCA CAATCGGCAC AAACGGCAGC

```

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCCTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGCTC GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTCGCC CATAAGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

m036-1.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMP ESRRQSAYPV CLRTAELLPA RTRCLRLKR RIPPAAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

	10	20	30	40	50	60
m036-1.pep	MLKPCAVYSACAAVL	PARTSSSRRCVSSGR	CVNQYSSRADAI	PWRRHSGAVAI	IRCSSDSS	
g036	MLKPCLVYSACAAAL	PARTSSSRRCVPS	SGRCAYQYSSRA	DATPRRRHSGAV	AIRCSSDSS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m036-1.pep	GRFCQTIKAAIPPS	FSAKRTCS	DGETSADSNWRC	VHADGLQTASSA	ASSSQSAQTARR	MF
g036	GRFCQTIKAAILPS	FSAKRTCS	DGETSADSNWRC	VHADGLQTVSSA	ASAAQSDGEAGR	MF
	70	80	90	100	110	120
	130	140	150	160	170	180
m036-1.pep	TGALSVRPVLWQSG	RFCGRRANRRVR	HGRQDNRPWLP	MRESRRQSAYP	CLRTAELLPA	
g036	MFVPSVPPVLWQSG	RFCGRRVRRVP	RQLRDSRRRGR	ARENRRRSAYR	VCLRRADGFPV	
	130	140	150	160	170	180
	190	200	210	220	229	
m036-1.pep	RTRCLRLKRRIPPA	AGCLPPARPDNR	SNGGSSAYRTM	HKTLRPYERPX		
g036	RTHCRRLKRRTPR	GQCLPPYRLDN	RSGGGSACRTH	TKTLRPYARPQ	RRVCSFAAAAA	
	190	200	210	220	230	240
g036	RRRHRAWGCRLK	ACRTALPNLAP	RRCRYAVRX			
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

g038.seq

```

1 ATGACTGATT TCCGCCAAGA TTCTCTCAAA TTCTCCCTCG CCCAAAATGT
51 TTTGAAATTC GGCGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCTCTTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151 AAATTCATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCTACAAAG GCATTATTTT GGCGGGCGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351 GCGCGTGTG ATTATCGACG ACGTGATTC CGCCGGCACA TCCGTACGCG
401 AATCAATCAA ACTGATTGAA GCGGAGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAATTTGT CCGCCGTTCA
501 GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTGTT TATCCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GCACCTACCG CCGGCAGTAC GCGTAGAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDRGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GKLSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GGCGAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGTCCC GCCTACAAAG GCATTATTTT GGCGGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCcGC CGGTGTCGCC
451  ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAa AAACAATACG GkCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GGCGAATTTA CCACCAAGGC CGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GGCGGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCcGC CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAa AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

              10      20      30      40      50      60
m038.pep    MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
```



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```

|||||
a038      MTDFRQDFLKFSLAQNVLFKGFETTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
           10      20      30      40      50      60
           70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
|||||
a038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           70      80      90      100     110     120
           130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
|||||
a038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
           130     140     150     160     170     180
           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
|||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

           10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLFKGFETTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
|||||
g038      MTDFRQDFLKFSLAQNVLFKGFETTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIES
           10      20      30      40      50      60
           70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
|||||
g038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
           70      80      90      100     110     120
           130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
|||||
g038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQEVEKQYGLPVAPI
           130     140     150     160     170     180
           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
|||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1   ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51  CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCGCCT
101 CTGGGTCAAA GAAAcccagC TCAAcytCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaagct gtttcgggat gTcaaaCTCG

```

225

```

251 TccaccgcacT cggcagcgac gccattagca aGAaacagat gtccccgcgac
301 gaaatCgccc atatacctcaa cggcgggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGCaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

```

g039.pep
  1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
 51 KNAKCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGE NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

```

m039.seq
  1 ATGCCGTCCG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CGnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCC GTGACGAAAT CGCCGGCATC CTCAACGGCG GTACAACCCA
351 GCGCGATATT CCGCCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCCGCG CCGCCCGGTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTCGCCCT TATCGTCCTC ATTATGCAGC TTTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

```

m039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPPXXXXXX
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTQPD I PPATAATPAA APQVTVPAA PARQDGFNWT
151 IATLFAIIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

```

a039.seq
  1 ATGCCGTCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCACGAAA
201 GAACCATAT TCAACGATT. TGCCCGAAGC TGTTCGGAT GTCAAACCTG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTCC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

```

a039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
 51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVIL*

```

m039/a039 79.4% identity over a 170 aa overlap

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPN	SMSPPXXXXXXXXXXXXXXXXXX				
a039	MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPN	SMSPKASSSAKNAKECLKPK				

		10	20	30	40	50	60
m039.pep	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTR	AI	GKKQISRDEI	AGIL	NGGTTQ	PDI
a039	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTR	AI	GKKQISRDEI	AGIL	NGGTTQ	PDI
		70	80	90	100	110	120
m039.pep	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTR	AI	GKKQISRDEI	AGIL	NGGTTQ	PDI
a039	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTR	AI	GKKQISRDEI	AGIL	NGGTTQ	PDI
		70	80	90	100	110	120
m039.pep	PPATAATPAAAPQVTVP	PAAPARQDGFNWTIAT	LFALIVLIMQLSYLVILX				
a039	PPATAATPAAAPQVTVP	PAAPARQDGFNWTIAT	LFALIVLIMQLSYLVILX				
		120	130	140	150	160	

m039/g039

```

      10      20      30      40      50      60
m039.pep  MPSEPPYASDGIKPDTHEEIPCPVVSAPTAKPVSGSKKPNSMSPXXXXXXXXXXXXXXXXXX
          ||||| |||||  :  |||||: |||||: |||||: ||
g039       MPSEPPAASDGIKPHTHTEKSCPPVSVRTAKPASGSKKPSSTSPKASSAKNAKGLKPK
          10      20      30      40      50      60

      70      80      90      100     110     120
m039.pep  XXXXXXXXXXXXXXXXXXXXPEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD
          :          :          :  ||||| |||||: ||: ||: ||||| ||||| |
g039       TIWQARKNLYSTIG-----PKLFRDVKLVHRIGTHAISKQMSRDEIADI LNNGGTTLHDT
          70      80      90      100     110

      130     140     150     160     170
m039.pep  PPATAAT-PAAAPQVTVPAAAPARQDGFNWTIATLFLALIVLIMQLSYLVILX
          |||||: |||||: ||||  ||: ||||| ||||| ||||| ||||| ||||
g039       PPATAAAAPAAAPQVSVPPA---RQEGLNWTIATLFLALIVLIMQLSYLFILX
          120     130     140     150     160

```

g040.seq

1	ATGAACGCGC	CCGACAGCTT	TGTCGCCAC	TTCGCGAAG	CCGCCCCCTA
51	CATCCGCCAA	ATGCGCGGTA	CGACACTGGT	CGCGCGCAT	GAcggCCGCC
101	TGCTCAAGG	CGGCACCTTA	AATAAGCTCG	CCGCGGCAT	C3GGCTGTTG
151	TCGCAACTGG	GACATCCGACT	CGTCTCATC	CAGCGCGGT	ACACTTCTT
201	CGAaccgCCTC	GCCGCCGCGC	AAGgccGCAC	GCCGCATTAT	TGCCGgggtt
251	tCGCGGTTAC	CGACGaaAaCc	tGctcgGAG	AGGCGCAGC	GtttGCCGGC
301	AccgTCCGCA	GCCGTTTTGA	agcCGCATG	tgcggcagCG	tttcaggatt
351	cgcgCGCGCG	CCTTCGCTG	CGCTGATc	ggcgaacttc	ctgacCGGCC
401	GTCcgatggg	cgtgattgac	ggaACGata	tggaatacgc	gggggttata
451	cgcaaaaccg	ACACCGCCGC	CCTCGTTTTC	CAACTCGAC	CGGGCAATAT
501	CGTCTGGATG	CCCGCGCTCG	GGCATTCTTA	CGGCGCGAAA	ACCTTCAATC
551	TCGATATGGT	GCAGCGCGCC	GCTTTCGTG	CGGTTCGCT	TAGGCGCGAA
601	AAACTCGTTT	ACCTGACCCT	TTCAGACGGC	ATTCCC GCC	CCGACGGCAC
651	GCTCGCGGAA	ACCTCTCTCG	CACAGAGAC	GCAATCGTG	GCGGAACACG
701	CGCCGACGA	AACCCGACGA	CTGATTTCGT	CCGCCGTTC	CGCGCTCGAA
751	GCGCGCGTGC	ATCGCGTCCA	AATCTTCAAC	GGGGCGCGC	ACGGCAGCA
801	GCTGCAAGAA	CTCTTCACCC	GCAACGGCAT	CGGCACGTCC	ATTGCCAAAG
851	AAGCTTCTGT	CTCCATCCGT	GAGGAGACAC	GCGCGCATAT	CCCGCACATC
901	GCGCGCCTCA	TCCGCTCCG	CAGGCGCAG	GGCGTCTAT	TGCACACGAT
951	CCGCGAATAC	CTCGAAAACC	ACATTTCCGA	ATTTTCATC	CTCGAACACG

```

1001 ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051 TCGGCGGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGg
1101 ctACGCGGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTOGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

g040.pep

```

1 MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLLEGGL NKLAADIGLL
51 SQLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDET SLGQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
201 KLVYLTSLDG ISRPDGTAE TLSAQEAQSL AEHAASETRR LISSAVAAL
251 GGVHRVQILN GAADGSLLE LFTNRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHDGDLYGC AALKTFEAD
351 CSEIACLAVS POAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNGRNPHIL VRLRHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

m040.seq

```

1 ATGAGCGCGC CCGACCTCTT TGTGCGCCAC TTCCGCGAAG CCGTCCCCTA
51 CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCGCTC AAGCCCGCAC GCCGCATTAT TGCCGGGGCT
251 TCGCGCTTAC CGACGAAACC TCGCTCGAAC AGGCGCAgCA GTTGCCGGC
301 ACCGTCCGCA GCCGTTTTGA AGCCGCATG TCGGCGAGCG TTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGGAAATACG GGGCGTTATC
451 CGCAAACCG ACACCGCCGC CCTCCGTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCGGCTCG GACATTCTTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCGC CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTTT ACCTGACCTT TTCAGACGGC ATTCCCGCC CCGACGGCAC
651 GCTCGCGGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCGGGGCA AACGCGACGG CTGATTTCGT CCGCCGAAC CTTCACCCGC
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCGCAywgG G.CGACATCC CGCACATCG CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCTGCTG CACCGCAs.c GCGAATACCT CGAAAACAC
901 ATTTCCGAAT TTTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCGC
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAAGC CnTGCTTGCC
1051 CACATTATCG ATAAGGCGCG CGGCATAGGC ATAAGCAGGC TGTTGCGACT
1101 GTCCACAAAT ACCGGCGAAT GGTTCGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAATCGC ATATTCTGGT ACGTCGCGCT CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

m040.pep

```

1 MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLEGDTL NKLAADIGLL
51 SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTSLDG ISRPDGTAE TLSAQEAQSL AEHAGGQTRR LISSAELFTR
251 NGIGTSIAKE AFVSIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

```

1  ATGATCGTGC CCGACCTCTT TGTGCGCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCGCGC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TGCGCGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTGGCCGGC
301 ACCGTCCGCA GCCGTTTGA AGCCGCATTG TGCGGCASCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATAACGC GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCGCGCTC GACATTCCCTA CAGCGGCAAG ACCTTCCATC
551 TCGATATGCT TCAAACCGCC GCCTCCGTCG CCGTCTCGCT TCAGGCCGAA
601 AAATCGTTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGTA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCGCGCGA AACGCGACGG CTGATTTCTG CCGCCGTTGC CGCGCTCGAA
751 GCGCGCGTGC ATCGCGTCCA AATCCTCAAC GGAGCCGCGC ACGGCAGCCT
801 GCTGCAAGAA CTCTTCACCC GCAACGGCAT CGGCACGTC ATTGCCAAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCACAT CCCGCACATT
901 CCGGCCCTCA TCCGCCCGCT GGAAGAACAG GGATCCTGC TGCACCGCAG
951 CCGCGAATAC CTCGAAAACC ACATTTCCGA ATTTTCCATC CTCGAACACG
1001 ACGGCAACCT GTACGGTTGC GCCGCCCTGA AAACCTTTCG CGAAGCCGAT
1051 TGCGGCGAAA TCGCCTGCCT TCGCGTCTCG CCGCAGGCAC AGGACGGCGG
1101 TCACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTCGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGTTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGGAATC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 152; ORF 040.a>:

a040.pep

```

1  MIVPDLFVAH FREAAPYIRQ MRGKTLVAGI DDRLLEGDTL NKFAADIGLL
51  SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFHLDMLQTA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGT LAV TLSAQEAQSL AEHAGGETRR LISSAVAAL
251 GGVRHVQILN GAADGSLLOE LFRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GILLHRSREY LENHISEFSI LEHDGNLYGC AALKTFEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNSHIL VRRLHR*

```

m040/a040 91.5% identity in 436 aa overlap

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI					
a040	MIVPDLFVAHFREAAPYIRQMRGKTLVAGIDDRLLEGDTLNKFAADIGLLSQLGIRLVLI					
	10	20	30	40	50	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
	70	80	90	100	110	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK					
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK					
	130	140	150	160	170	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGT LAETLSAQEAQSLAEHAGGQTRR					
a040	TFHLDMLQTAASVAVSLQAEKLVYLTLSDGISRPDGT LAVTLSAQEAQSLAEHAGGETRR					
	190	200	210	220	230	240

229

	190	200	210	220	230	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI					
a040	LISSAVAALGGVHRVQILNGAAGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI					
	250	260	270	280	290	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
a040	AALIRPLEEQGILLHRSREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
	310	320	330	340	350	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
a040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
	370	380	390	400	410	420
m040.pep	RSNGRNSHILVRRRLHRX					
a040	RSNGRNSHILVRRRLHRX					
	430					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*.

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAAPYIRQMRGTTLVAGIDGRLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAQGRTPHYCRGLRVTDETSLQAQQFAGTVRSRFEALCGSVSGFARA	120
g040	HGAYHFLDRLAAQGRTPHYCRGLRVTDETSLGQAQQFAGTVRSRFEALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALGGVHRVQILNGAAGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSNGRNSHILVRRRLHRX	413
g040	RSNGRNPILVRRRLHRX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
  1 ATGAGTTCGC CCAAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGCCT
 51 GATTACCGCC GCCGCCTTCG TGC GCGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTC AAGTT GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCGG CTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCGGAC AAACCTGCCT GCGTGTGCT GTTTTGGAAA
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
  1 MSSPKHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETS PQSW LYS PDGGGHT NGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
  1 ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGACT
 51 GATTACTGCC GCCGCCTTCG TGC GCGAACC GCAAAGCATC GGCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTC AAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCGGAC GAACTCGCCT GCGTCTTGCT GTTTTGGAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
  1 ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETS AQSW LYS PDGGGHT NGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
  1 ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGACT
 51 GATTACTGCC GCCGCCTTCG TGC GCGAACC GCAAAGCATA GGCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTC AAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCGGAC GAACTCGCCT GCGTGTGCT GTTTTGGAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
  1 ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETS PQSW LYS PDGGGHT NGTQREAAD ELACVLLFLK
```

151 EFLG\*

m041/a041 98.7% identity over a 154 aa overlap

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
a041	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQPSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTCRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTCREAADELACVLLFLKEFLGX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
g041	MSSPKHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
g041	PQKYEACKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQPSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

```

1  ATGAAATCCT ACCCGACCC CTACGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCG CGCGCACTT CAGACGGCAT TTTGAATCAA
151 ATGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCAGCGGGAT
201 GTACCATTTT CATCAGAATG CGGAATATCC GAAGGGCGTG TACCGCATGT
251 GTACGGCGGC GACCTACCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTTCGATG GTTGCTCGGC GACGATGTGT ATTTGGGCGG
351 CGTGTCGCAC TTGGTGGAGC AGCCCAACCG CGCGCTGCTG ACTTTGAACA
401 AATCGGGCGG CGATACGGCG TATACGCTGG AAGTGGATT GGAAGCAGGG
451 GAATTGGTAG AGGGCGGTTT TCACTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAAG TGTGGCTGGT GGAACGCGGC

```



```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCG
751 TCCGAAGGCG GGGCGAAACC GTTGAACTTG CCTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCAATTGGA AGCGTGGAAA GACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GCGGTTTGC CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACCTGGTTTA TCTTGCCGCC AGCGATTTC A
1151 CCACGCGCGT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTGAAC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGT TCAGACGGCA TCGAAGTGCG
1251 GCAGTTTGG GCGGTGTCGT CCGACGGCGA ACGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTCGGCA TTCCTGAATT GCCGATTAT CTGGGCAGCG TCGGCAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GGCAACATC CGCGCGGCG
1451 GAGAATTCGG CCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAAAC
1501 AAAAGCGTTG ATGATTICTT GGCAGTCGTG CGTGATTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGCC
1601 TGATTACCGC CGCCCGCTTC GTGCCGAAC CGCAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGAT CGTTATCCGC TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCCG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTCGCG GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGGTGTTGC TGT'TTTTGAA
2001 AGAATTTTTG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1 MKSYDPYRHF FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51 MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSOGDTA YTLEVDLEAG
151 ELVEGGFHFAP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDGCVVGYL AGHLLLTLRK DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQP WGGDVVYLAA SDETTPLTLF ALDLNVMELT
401 VMRLQPQQFV SDGIEVRQFW AVSSDGERIP YFHVGNKNAAP DPTLVYAYG
451 GFGIPELPHY LGSVGYWLE EGNAEVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGMSS PKHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDRVHFA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1 ATGAAATCCT ACCCGGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGCGACA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGGTGCGCAC TTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCAG CGATACGGCG TACACGCTGG AAGTGGATTG GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT CCCTGTGTAT CAAATCGCGC AAGACGGCAT
651 GATGGTGAAC GCGTGGC3TT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGAC3GT TTTTACACCA AAACCTATTT GCGGGTCTCA

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751 GCCGAAGGCG AGGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTGGT
801 CGGCTATCTG GCGGGGCATC TTTTGCTGAC GCTGCGCAAG GACTGGAACC
851 GCGCGAACCA AAGCTATCCG AGCGGCGCGC TGGTGGCGGT GAAGCTGAAT
901 CCGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCGAGCCTGT
1001 TGGAGAACGT ACAAGGCCGT CTGAAAGCAT GCGGGTTTGC CGACGGCAAA
1051 TGGCAGGAAG TCGAATTGCC GCGCCTGCCT TCGGGGCGGT TGGAATGAC
1101 CGACCAACCT TGGGGCGGCG ACGTGGTTTA CCTTGCCGCC AGCGATTTCa
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAACTGACC
1201 GTCATGCGCC GCCAGCGCGA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTTGG ACGACTTCGG CTGACGCGCA GCGCATTCTT TATTTCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTTCGGCA TTCCCGAATT GCCGCATTAT CTGGGCGAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GCGCAACATC CGCGGCGGCG
1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG CCGGATTGTG CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CGGCGCGCTG
1651 GTGTGCCAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCTT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCGCCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCCG
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CGAACTCGCC TCGCTCTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

m041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKG VYRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSLKLGSDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW NERQLTQSGY PREVWLVERG
201 KSFEESLPVY QIGEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLRVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRK DWNRRANQSY SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADGK
351 WQEVLPRLP SGALEMTDQP WGGDVVYLA SDFTPLTLF ALDLNVMEIT
401 VMRRQPQQFD SDGINVQQFW TTSADGERIP YFHVGNAAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAPVLANI RGGGEFGPRW HQAAOGISKH
501 KSVDDLLAVY RDLSEGRIS PEHIGLOGGS NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCRRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSAQSWLYS PDGGGHTGNG
651 TQRESADELA CVLFLKEFL G*

```

m041-1/g041-1 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYPDPYRHFENLDSAETQ	NFAAEANAET	RARFLNDKA	RALSDGILAQ	LQDTRQIPFC	
g041-1	MKSYPDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILNQ	MDTRQIPFC	
	10	20	30	40	50	60
m041-1.pep	QEHRARMYHFHQDAEY	PKG VYRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
g041-1	QEHRARMYHFHQNAEY	PKG VYRMCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
	70	80	90	100	110	120
m041-1.pep	LVEQPNRALLTSLKLG	SDTAYTLEVDLEAG	ELVEGGFHFP	AGKNHVSWRD	ENSVWVCPAW	
g041-1	LVEQPNRALLTLNKSG	GD TAYTLEVDLEAG	ELVEGGFHFP	AGKNHVSWRD	ENSVWVCPAW	
	130	140	150	160	170	180
m041-1.pep	NERQLTQSGYPREVWL	VERCKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
g041-1	NERQLTQSGYPREVWL	VERCKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
	190	200	210	220	230	240
m041-1.pep	NERQLTQSGYPREVWL	VERCKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
g041-1	NERQLTQSGYPREVWL	VERCKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	

sp|P55577|Y4NA\_RHISM PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4nA [Rhizobium sp. NGR234] Length = 726  
Score = 370 bits (940), Expect = e-101  
Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFPAGKNHVSWRDENSVMVCPAW 180  
L N L+ LS G D E D+ GE V+ GF P GK V+W DEN+++V W

Sbjct: 162 LPPTSNLCLIRLS DGGKDADVREFDIAKGEFVKEGFVLPEGKQSVTWVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPOGSPI 232  
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTS SSGYAYVTKVVRGQSLDQAVEIFRGQKKDVSAERGVLRDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDWNANOS-YPS 291  
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELA FYPNGH----PDTRKVVLPLPTTAVFSGYKQAIYWLKSDWTS AKGTVFHN 337

Query: 292 GALVAVKLN RGE LGAAQL----LFAPDETQALESVETTKRFVVASLLENVQGR LKAWRFA 347  
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIAFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQEV ELPRLPSGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQ 407  
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KCGWSSFKLALPENSTLSLTSSDDES DQLFVFSEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDS DGINVQQFWTTSADGERIPYFHVGNAAAP---DMPTLVYAYGGFGIPELPHYL GSI 464  
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGISKHKSVDDLLAVVRDLSE RGISSPEHI 524  
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DU AV +DL - ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWHDAGLKTNRQRYVDDFQAVAQDLIAKKVTS TPHL 577

Query: 525 GLQGG SNGGLITAAAFVRE PQSIGALVCEVPLTDMIRYPLLSAGSSWTEYGNPQKY EVC 584  
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRPDLWNAVVIQVPLLD MVNFTMSAGASWQAEY GSPDD-PVE 636

Query: 585 KRRLGELS PYHNLS DGI DYPALITTSLSDDR VHPAHALKFYAKLRETS AQSWLYSPDGG 644  
 L +SPYHN+ G+ YP TS DDRV P H A K A + + Y G

Sbjct: 637 GAFLRSISPYHN V KAGVAYPEPFETSTKDDR VGPVHARKMAALFEDMGLPFYYENIEG 696

Query: 645 GHTGNGTQRESADELACVLLFL 666  
 GH +E A A +++

Sbjct: 697 GHAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1   ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAAAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAAGATG CGGAATATCC GAAAGCGGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CTGTGTCGAC TGTGTGGAAC AGCCCAACCG CGCGTTGTTA ACACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTAG AAGCGCGTTT TCACTTTCGG GCAGGCCAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGTAC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 CCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CCGCTATCTG GCCGGACATC TTTTGCTGAC CTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTCTGT GCGAGCCTGC
1001 TGGAAAACGT ACAGGGTCGT CTGAAAGCGT GCGGTTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCCGCC AGCGATTCCA
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAACGTACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GCGGAACATC CGCGGCGGCG

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1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG AGCGATTGTG CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TGCCTGTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKG VYRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSKSGGDTA YTLVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRK DWHRANQSY PSALVAVKLN
301 RGE LGAAQLL FAPNETQALE SVETTKRFVV ASLLENVQGR LKAWRFTDGK
351 WQETELPRLP SGALEMTDQP WGGDVVYLAA SDFTPPLTLF ALDLNMELT
401 VMRRQPQDFD SDGINVQQFW TTSADGERIP YFHVGNAAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGRW HQAAQGISKH
501 KSVDDLLAVV SDSLSEGISS PEHIGLQGS NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCRRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILAQ	LQDTRQIPFC	
m041-1	MKSYDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILAQ	LQDTRQIPFC	
	10	20	30	40	50	60
a041-1.pep	QEHRARMYHFHQDAEY	PKG VYRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
m041-1	QEHRARMYHFHQDAEY	PKG VYRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
	70	80	90	100	110	120
a041-1.pep	LVEQPNRALL	TSKSGGDTAY	TLEVDLEAGEL	VEGGFHFP	AGKNHVSWRD	ENSVWVCPAW
m041-1	LVEQPNRALL	TSKSGGDTAY	TLEVDLEAGEL	VEGGFHFP	AGKNHVSWRD	ENSVWVCPAW
	130	140	150	160	170	180
a041-1.pep	DERQLTESGY	PREVLVERGK	KSFEESLPVY	QIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG
m041-1	DERQLTESGY	PREVLVERGK	KSFEESLPVY	QIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG
	190	200	210	220	230	240
a041-1.pep	FYTKTYLQVS	AEGEAKPLNL	PNDCDVVGYL	AGHLLTLRK	DWHRANQSY	PSALVAVKLN
m041-1	FYTKTYLQVS	AEGEAKPLNL	PNDCDVVGYL	AGHLLTLRK	DWHRANQSY	PSALVAVKLN
	250	260	270	280	290	300
a041-1.pep	RGE LGAAQLL	FAPNETQALE	SVETTKRFVV	ASLLENVQGR	LKAWRFTDGK	WQETELPRLP
m041-1	RGE LGAAQLL	FAPNETQALE	SVETTKRFVV	ASLLENVQGR	LKAWRFTDGK	WQETELPRLP
	310	320	330	340	350	360

	370	380	390	400	410	420
a041-1.pep	SGALEMTDQFWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
m041-1	SGALEMTDQFWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
	370	380	390	400	410	420
	430	440	450	460	470	480
a041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
	490	500	510	520	530	540
a041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDLLAVVSDLSERGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
	550	560	570	580	590	600
a041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSYPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSYPYHNLSDG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a041-1.pep	IDYPPALITTSLSDDRHPAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRHPAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA					
	610	620	630	640	650	660
	670					
a041-1.pep	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

```

g042.seq
1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TGCGGTCGAT GATGAAAATC CAGCCGGGGT TTTCTCTTT GATGTATTCTG
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG cggCTTCGCG CTTTGGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCGTTGTC CACCGTCAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCTG
501 CCCGCCGTA ATGACAAACT GCGATTGTG GCGGTGCAGG GATTGCGAAT
551 CGGGCTCAA CAGCGTCCCC ACCGTGCGC CCTGTCAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

```

g042.pep
1  MTMICLRFOA FVPHTSALS N TSTAAGPSCP MAAVRSMKI QPGFFSLMYS
51  KETGCPCLSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRFA NSASICAFNS ATRASLPKIR DRVSICFSL VRILPLSTVK
151 SMVVAFFANC SYASAPGPV MTNCGLWRCR DSQSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

## m042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CCGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCGTAACCG ACAGCACCAG CCGCGTCCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

## m042.pep

```

1 MTMICLRFOA FVPTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAENS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

## a042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCGGCGCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CCGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCGTAACCG ACAGCACCAG CCGCGTCCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

## a042.pep

```

1 MTMICLRFOA FVPTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAENS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAGC
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
a042	MTMICLRFOAFVPTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTPRPLPLAASRVWANSASICAENS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTPRPLPLAASRVWANSASICAENS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
	130	140	150	160	170	180
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					

239

```

|||||
a042      AARASLPKIRAKVSICFSPVLRLPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
           130      140      150      160      170      180

           190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
           |||||
a042      ASXSGSNSVPTVAALSNAGCKX
           190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

           10      20      30      40      50      60
m042.pep  MTMICLRFOAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
           |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      MTMICLRFOAFVPHTSALNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL
           10      20      30      40      50      60

           70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRVWANSASICAFNS
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRFWANSASICAFNS
           70      80      90      100     110     120

           130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPVLRLPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
           |:||||| |:||||| |:||||| |:||||| |:||||| |:|||||
g042      ATRASLPKIRDRVSICFSPVLRLPLSTVRSMVVAFFANC SYASAPGPPVMTNCGLWRCR
           130     140     150     160     170     180

           190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
           | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCT
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCGTAACCG ACAGCACCAG CCGCGCTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1  MTMICLRFOA FVERTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCPVKADTLL PVTDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSP LRLPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap



240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFAQFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	:					
g042	MTMICLRFAQFVPHTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPILVRILPLSTVRSMVVAFFANCYSASAGPPVMTSX					
	:     :					
g042	ATRASLPKIRDRVSICFSPILVRILPLSTVKSVMVVAFFANCYSASAGPPVMTNCGLRRCR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

```

a042-1.seq
1  ATGACGATGA  TTTGCTTGCG  CTTCCAAGCG  TTCGTGCCGC  GTACCAGCGC
51  GTTATCCAAT  ACTTCGACAG  CCGCCGGCCC  TTCCTGCCCG  ATGGCGGCGG
101  TACGGTCGAT  GATGAAAATC  CAATCGGGGT  TTTTCTCTTT  GATGTATTCT
151  AAGGAAACAG  GCTGCCCGTG  CCCCTCGTTG  CGTAAAGATT  CGTCTACAGG
201  CGGTAGGCCG  ATGTCGCCGT  GTATCCAAC  TGCCAACCGC  GACTGCGTGC
251  CGAAGGCGGA  CACCTTGTTG  CCCGTAACCG  ACAGCACCAG  CCCGCGTCCT
301  TTGCCTTTGG  CGGCTTCGCG  CGTTTGGGCG  AACAGCGCGT  CAATCTGCGC
351  CTTCAATTCC  GCCGCGGCGG  CTTCTTGCC  GAAATCCGC  GCCAAGGTCT
401  CCATCTGCTT  TTCGCCGCTG  GTGCGGATAT  TGCCGTTGTC  CACCGTCAGA
451  TCTATGGTGG  TCGCGTTTTT  CGCCAACGTG  TCATACGCTT  CCGCGCCCGG
501  CCCGCCGTA  A

```

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

```

a042-1.pep
1  MTMICLRFAQ  FVPRTSALSNTSTAAGPSCP  MAAVRSMMKI  QSGFFSLMYS
51  KETGCPGPSL  RKDSSTGGRP  MSPCIQLANR  DCPKADTLL  PVTDTSPRP
101  LPLAASRVWA  NSASICAFNS  AARASLPKIR  AKVSICFSP  VRILPLSTVR
151  SMVVAFFANC  SYASAGPPV  MTS*

```

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFAQFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
a042-1	MTMICLRFAQFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGREMSPCIQLANRDCVPKADTLLPVTDTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGREMSPCIQLANRDCVPKADTLLPVTDTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPILVRILPLSTVRSMVVAFFANCYSASAGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPILVRILPLSTVRSMVVAFFANCYSASAGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

241

```

g043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
101 CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151 GCCCGATTCTG ATGAGGGGcga gcGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201 GTCCGGCGAC GGTttCGCCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCTGTCA GCCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301 GGCGAATTCG CTGTTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

```

g043.pep
1  MVVSNQNIYA VGPSALFHIR RQKSVMPER FVEPSRVAVA AKVHRGLDGA
51  ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQPD AAGDFDGGQRA
101 GEFVQNIIGG FVYAPAAVAV VVAAEGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

```

m043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151 CCCGATTCTG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CGGCGCagGC
201 ATCCGGCGAC GGTttCGCCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCTGTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAAACGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

```

m043.pep
1  MVVSNQNIYA AGPSALLHIR RQKSVMPER FVEPSRVAVA AKVHGGLDGA
51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AAGDFDGGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPERFVEPSRVAVAAKVHRGLDGAARFDEGERVF					
	10	20	30	40	50	60
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFDGGQRTGEFVLQDVGGFVYAPTAVTV					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAAAGDFDGGQRAGEFAVQNIIGGFVYAPAAVAV					
	70	80	90	100	110	120
m043.pep	VVAEGEAQX					
g043	VVAEGEAXX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

```

a043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

242

```

151 GCCGGATTCTG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CGGCGCAGGC
231 ATCCGGCGAC GGTTCGCGG GTTTGCCTT TGAATAGCG TTTCAGGTAG
251 CATTCTGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCTG TGTTCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
  1 MVVSNQNIYA AGPSALLHIR RQKSVMPSE FVEPSRVAVA AKVHGGLDGA
  51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
 101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSE	FVEPSRVAVA	AKVHGGLDGA	AGFDEGERVF		
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSE	FVEPSRVAVA	AKVHGGLDGA	AGFDEGERVF		
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDA	AGDFGDGQRTGE	FVLQDVGGFVYAPTAVTV			
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDA	AGDFGDGQRTGE	FVLQDVGGFVYAPTAVTV			
	130					
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
  1 ATGCTGCCCC ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGCGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTCAGCCC TTCGATAACG GCGGTCAGCT
 201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
 251 CGGCTGCCGT AGCGCATTA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
  1 MLPDQSVEFL PQVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
  51 GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
  1 ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTCAGTCC TTCGATGACG GCAGTCAGTT
 201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
 251 TGGCTACCGT AGCGCAyTAa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
  1 MPSDXSVEFF PEVVFDGLF GGGFPAVALP TVYPVFHAIF DVLRVGADDD
  51 GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
1  GTGCCGTCCG ACCAGCGCGT CGAGTTCTTT CCACAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GCGGCGGTTT TTCCAGCCGT TCGGCTTCCA ACCGTGTATC
101 CAGTTTTCCT TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGTCC TTCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGTT TCGGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGCTGCCGT AGCGCATTA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
1  VPSDQRVVEFF PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

```
m044.pep      10      20      30      40      50      60
MPSDXSVEFFPEVVVFDGLFGGGFFAVALPTVYPVFHAI FDLRVGADDDGAAAFERFQS
:| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
a044          10      20      30      40      50      60
VPSDQRVVEFFPQVVVFDGLFGGGFFAVALPTVYPVFHAV FDLRVGADDDGAAAFERFQS

m044.pep      70      80      90
FDDGSQFHAVVGGLRFAAEKFFVFATVAHX
| | | | | :| | | | | :| | | | | :| | | | |
a044          70      80      90
FDDGGQFHTVVVGGLRFAAEKFFFAVAHAX
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

m044/g044

```
m044.pep      10      20      30      40      50      60
MPSDXSVEFFPEVVVFDGLFGGGFFAVALPTVYPVFHAI FDLRVGADDDGAAAFERFQS
| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
g044          10      20      30      40      50      60
MLPDQSVEFLPQVVVFDGLFGGGFFAVALPTVYPVFHAV FDLRVGADDDGAAAFERFQP

m044.pep      70      80      90
FDDGSQFHAVVGGLRFAAEKFFVFATVAHX
| | | | | :| | | | | :| | | | | :| | | | |
g044          70      80      90
FDNGGQLHAVVGGLRFAAEKFFFAVAHAX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
1  ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGCGcc gCGCCTGTAT
51  GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGTTTT CGTTATGCC gaATATGGAA AGGCTGCCgt TTtcGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT ECAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGagaGCGCG AGcagcaagt cggcatcttC
351 CgcgcggcgC Cgttataatg tgAAGGGGGA TGCGccgttg ccgaAAACGG
401 TTTGGacatc gaggcggctg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcg TTACGTCGTT GTTGGTGATG GCGCAAGGT TTTGCGCGAC
```

244

501 GGTAGAACCT ACCTGCCCCG TGCCTAAAAT GAGGATTTTC ACGGTATGGG  
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCASt CCGC.r.sGC gCGcCTGTAT  
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC  
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG  
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTGTTGTT  
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG  
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG  
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC  
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TGCGCCGTTG CCGAAAACGG  
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG  
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC  
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG  
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep

1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT  
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC  
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG  
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTGTTGTT  
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG  
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG  
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC  
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TGCGCCGTTG CCGAAAACGG  
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG  
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC  
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG  
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE\*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTI	RTRSSAKRKT	CNAPGQSIRP	ASCSVTSCSG	LMVSVMPNME	
a046	MSAMLRPTSSPPRRACMMTI	RTRSSAKRKT	CNAPGQSIRP	ASCSVTSCSG	LMVSVMPNME	

245

	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKTCNAPGQSIRPASCSTSCSGLMVSVMPNME					
g046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKTCNAPGQSIRPASCSTSCSGLMVSVMPNME					
	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

```

1  ATGGTCATCA TACAGGCGcg gcGCGGCGGG CTGCTTGTCG GACGCAGCAT
51  TGCCGACATC GCCCAAGATT TGCCGACGG GCGCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT GTTTGCCGCC GCCGCGGAAA ACATCGGGGC
201 GGTATACCC gaATTGCGCC CCAAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGCGCG CGGCAACATc tgctACCGCC TCGCCAAGCA GCTCGAACAC

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246

```

301 GCATAcaacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAAC ctcgAcaaCA CCCTCGTCCT GCAAGGTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTAtg tCCGCCCTTt TGGCGAAAAA
501 CCTcggcgCG AAGCgcgtca tcggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCCGCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGAGAAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

**g047.pep**

```

1 MVIIQARRGG LLVGRSIADI AQDLDPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLDDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

**m047.seq**

```

1 ATGGTCATCA TACAGGCGcG C..syGCCGA sTGCTTGTCG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCCTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTCATACCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGCGCGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATAACAGT yAAAATCATC GAATGCCGGC CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTTCG
401 CAACCGACGA AACCTTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GGCGAaAAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCCTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGGCGACAT
651 CGTTGCCGTC CACCCCATCC GGCGCGGCAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAG
751 GGCATCAAAAT GGCCCGAAGG CTGCCACATT GCCGCCGTCG TCCGCGCCGG
801 AACCAGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTT GTCTCGCGCC GGCGCATCCT GAACGAACTG
901 GAAAAACTCA TCCAGGTCAA AATGGGCTTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

**m047.pep**

```

1 MVIIQARXXG XLVGRSIADI AQDLDPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV LQGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE I EVVAHGDKK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRLNEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

**a047.seq**

```

1 ATGGTCATCA TACAGGCGCG GCGCGCGGA CTGCTTGTCG GACGCAGCAT

```

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```

51  TGCCGACATC  GCCAAGATT  TGCCCGACGG  GGCCGACTGC  CAAATCTGCG
101 CCGTTTACCG  CAACAACCGC  CTCATCGTCC  CCGCGCCGCA  AACCCTCATC
151 ATCGAAGGCG  ACGAAATCCT  ATTTGCGGCC  GCCGCCGAAA  ACATCGGCGC
201 GGTCATACCC  GAATTGCGCC  CCAAAGAAAC  CAGCACCCGC  CGCATCATGA
251 TTGCCGGCGG  CGGCAACATC  GGCTACCGTC  TCGCCAAGCA  GCTCGAACAC
301 GCATACAACG  TCAAATCAT  CGAATGCCGG  CCGCGCCGTG  CCGAATGGAT
351 AGCCGAAAAC  CTCGACAACA  CCCTCGTCCT  GCAAGGTTTC  GCAACCGACG
401 AAACCTTGCT  CGACAACGAA  TACATCGACG  AAATCGACGT  ATTCTGCGCC
451 CTGACCAACG  ACGACGAAAG  CAACATTATG  TCCGCCCTTT  TGGCGAAAAA
501 CCTCGGCGCG  AAGCGCGTCA  TCGGCATCGT  CAACCGCTCA  AGCTACGTCG
551 ATTTGCTCGA  AGGCAACAAA  ATCGACATCG  TCGTCTCCCC  CCACCTCATC
601 ACCATCGGCT  CGATACTCGC  CCACATCCGG  CGCGGCGACA  TCGTTGCCGT
651 CCACCCCATC  CGGCGCGGCA  CGGCGGAAGC  CATCGAAGTC  GTCGCACACG
701 GCGACAAAAA  AACTTCGCGC  ATCATCGGCA  GGCGCATCAG  CGGCATCAAA
751 TGGCCCGAAG  GCTGCCACAT  TGCCGCCGTC  GTCCGCGCCG  GAACCGGCGA
801 AACCATTATG  GGACACCATA  CCGAAACCGT  CATCCAAGAC  GGCGACCACA
851 TCATCTTTT  CGTCTCGCGC  CGGCGCATCC  TGAACGAACT  GGAAAAACTC
901 ATCCAAGTCA  AAATGGGCTT  TTTCGATAA

```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```

a047.pep
1  MVIIQARRGG  LLVGRSIADI  AQDLPDGADC  QICAVYRNNR  LIVPAPQTVI
51  IEGDEILFAA  AAENIGAVIP  ELRPKETSTR  RIMIAGGGNI  GYRLAKQLEH
101 AYNVKIIECR  PRRAEWIAEN  LDNTLVLQGS  ATDETLDDNE  YIDEIDVFCA
151 LTNDDESIM  SALLAKNLGA  KRVIGIVNRS  SYVDLLEGNK  IDIVVSPHLI
201 TIGSLAHIR  RGDIVAVHPI  RRGTAEAIEV  VAHGDKKTS  IIGRRISGIK
251 WPEGCHIAAV  VRAGTGETIM  GHHTETVIQD  GDHIIFFVSR  RRILNELEKL
301 IQVKMGFFG*

```

m047/a047 96.5% identity over a 312 aa overlap

```

m047.pep      10      20      30      40      50      60
MVIIQARXGXLVGRSIADIAQDLPDGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
||||| | |||||||
a047           10      20      30      40      50      60
MVIIQARRGGLLVGRSIADIAQDLPDGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
||||| | |||||||

m047.pep      70      80      90     100     110     120
AAENIGAVIPELRPKETQRNQPXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
||||| | : ||| |||||||
a047           70      80      90     100     110
AAENIGAVIPELRPKETSTR---IMIAGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
||||| | ||| |||

m047.pep     130     140     150     160     170     180
AENLDNTLVLQGSATDETLDDNEYIDEIDVFCAITNDDESIMSAALLAKNLGAKRVIGIV
||||| | |||||||
a047         120     130     140     150     160     170
AENLDNTLVLQGSATDETLDDNEYIDEIDVFCAITNDDESIMSAALLAKNLGAKRVIGIV
||||| | |||||||

m047.pep     190     200     210     220     230     240
NRSSYVDLLEGNKIDIVVSPHLITIGSLAHIRRGDIVAVHFIRRGTAEAIEVVAHGDKK
||||| | |||||||
a047         180     190     200     210     220     230
NRSSYVDLLEGNKIDIVVSPHLITIGSLAHIRRGDIVAVHFIRRGTAEAIEVVAHGDKK
||||| | |||||||

m047.pep     250     260     270     280     290     300
TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRLNEL
||||| | |||||||
a047         240     250     260     270     280     290
TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRLNEL
||||| | |||||||

m047.pep      310
EKLIQVKMGFFGX
|||||

```



a047            EKLIQVKMGFFGX  
                 300            310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLVPAPQTVIIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNPXXIMIXGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
	: :	
g047	AAENIGAVIPELRPKETSTR---IMAGGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	300
g047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	297
m047.pep	EKLIQVKMGFFGX    313	
g047	EKLIQVKMGFFGX    310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

```

1  ATGCTCGACA AAGGCGA3GA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTc ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTTACCG CCAAATGCTC
151 AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201 cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGGC ATACCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCGA AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351 TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

```

1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  KQTGLLMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAV YEFVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

```

1  ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC GGCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG

```

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```

101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTCACCCG CCAAATGCTC
151 GAACAAACCG ACCTCTTGGG CATGATCGGC AAATCCGAGC GCGGCGTGGC
201 CACCTGCGAA GCCATCGCCG ACAACAAAGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGGC GTATCTCGTG GCAAAGCCA TCAATCTTC CAAAGTCTTG
301 GCGTTCCCCG AATTGGGCAT GGAAGCCATT TACGAATTG AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCCG TAGATAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAATCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 202; ORF 048>:

```

m048.pep
1 MLNKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51 EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 203>:

```

a048.seq
1 ATGCTCGACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCTGTAT
51 TTAACGTCG GCGCCCGTCG ATCCGCTCGG CGACGAAATC GTCGGCCCGAG
101 CAGGTCCGAC CACCGCCACC CGCATGGACA AATTCACCCG CCAAATGCTC
151 GAACAAACCG ACCTCTTGGG CATGATCGGC AAATCCGAGC GCGGCGCGGC
201 CACCTGCGAA GCCATCGCCG ACAACAAAGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGGC GTATCTCGTG GCAAAGCCA TCAATCTTC CAAAGTCTTG
301 GCGTTCCCCG AATTGGGCAT GGAAGCCATT TACGAATTG AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCCG TAGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCC CCAATGGCAG GCGAAAATCG GCATCATCCC CGTCAAATCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 204; ORF 048.a>:

```

a048.pep
1 MLDKGEELPV DFTNRLIYYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
51 EQTDLLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFVKDMPV TVAVDSKGES IHATAPQWQ AKIGIIPVKS
151 *

```

m048/a048 96.0% identity over a 150 aa overlap

m048.pep	10	20	30	40	50	60
	MLNKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
a048	MLDKGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	10	20	30	40	50	60
m048.pep	70	80	90	100	110	120
	KSERGVATCEAIADNKAVYLMAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVKDMPV					
a048	KSERGAATCEAIADNKAVYLMAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVKDMPV					
	70	80	90	100	110	120
m048.pep	130	140	150			
	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
a048	TVAVDSKGESIHATAPQWQAKIGIIPVKSX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 209>:

a049.seq

```

1  ATGCGGGCGC AGGCGTTTGA TCAGCCGTTT GGTGAGCTCC TGTTCGGACA
51  GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTCAG AATATTGATT
101 TGGACGGGCA TCAACGCTTC TTCCGCACCG CCTTCGCCGT TTTCCGCAAC
151 CCCGTCTGCC GCCGTACCCG ATTCTGCCGC ATCGGCGTTT TCCCCGCTT
201 CAATCTGTCC GGTTCAAAT TCGGCACTGT CTTTTTGGC ATCAAACCGG
251 ATTCTCCGCC GCGATTGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTCTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTTGTGTT CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT

```

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

```

a049.pep
1  MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFVFRN
51  PVCRRTRFCR IGVFFAFNLS GFKFGTVFFG IKPDSPPRFD VFFRNRLQ
101 SLRVEPVFLK DHRVGFDFL AAIGNGGIVF LLPFFQIRL

```

m049/a049 90.6% identity over a 139 aa overlap

```

m049.pep      10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRF FRIVFPVFRNRRLIRAGFCL
|||||
a049           10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFVFRNPVCRRTRFCR
|||||

m049.pep      70      80      90     100     110     120
VGVPFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
:|||||
a049           70      80      90     100     110     120
IGVFFAFNLSGFKFGTVFFGIKPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
|||||

m049.pep      130     139
AAIGNGGIVF LLPFFQIRL
|||||
a049           130
AAIGNGGIVF LLPFFQIRL
|||||

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

```

m049/g049
m049.pep      10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRF FRIVFPVFRNRRLIRAGFCL
|||||
g049           10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRL FRTAFVFRNPVCRRTGFCR
|||||

m049.pep      70      80      90     100     110     120
VGVPFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
:|||||
g049           70      80      90     100     110     120
IGVFFALNLCGFKFGTVFFGIEPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
|||||

m049.pep      130     139
AAIGNGGIVF LLPFFQIRL
|||||
g049           130     140
AAIGNGAVVF LLPFLQIRLX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

```
g050.seq
1  atgggCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGg
51  cagccccGAA AAAGccgtgt TGATGGcaaA AGAATCCCTG ATGAGCCACA
101 TCGAcatCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGgtcc
351 TGTCGAactc acgccGCcg gtgtCGAAGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

```
g050.pep
1  MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

```
m050.seq
1  ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGCTATCG GCATCGGCGG
51  C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCTGCGCCT CGAACTCTTT GAAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA TGGCCCGATT TGA
```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

```
m050.pep
1  MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

```
a050.seq
1  ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  TACGCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCTGCGCCT CGAACTCTTT GAAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA CTGGCCC
```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

```
a050.pep
1  MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP
```

m050/a050 97.7% identity over a 129 aa overlap

```

10      20      30      40      50      60
m050.pep  MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
          |||||
a050      MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
```

253

	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPV					
a050	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPV					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMKESLSMHSIDIQELQEKASGAELSTTEALRLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMKESLSMHSIDIQELQEKASGAELSTTEALRLELF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPV					
g050	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPV					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACCAACGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGAAGGCAA CACCCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGCGCTCTG AAAACAAATC CAAACTCGCT ATGCTCAACC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGC ATCGGCATCG GCGGCAcgc CGAAAAAGCC
601 GTGTTGATGG cgaAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GGAGGAAAAA GCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCGTCGAAC TTTGAAAAG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GTCTGTGCGA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCCG ACAACGGCAA
951 ACGCGTCGAT GTCGATAAGC TGACCAAGA AGAAGTGGA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCGATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGGCGAGG AGTTGCCCGT
1101 CGATTTCACC AACCCGCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCC
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAATGCT CAAACAAACC GGCTCTTGG GCATGATCGG

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1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGACCT CATGGCAGTC GGCGGCGCGG CATACCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCG GAATTGGGTA TGGAAAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCGT AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGC GCAAATGGCA GGCAGAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDANTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVGMDVQWDADMSV EKMVNEGVR
101 AYTWEENTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSSENKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELOEK AASGAELSTT EALRLELF EK VNALGIGAQG
251 LGGLTTVLVD KILDYPHTAA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVED*PDLT YSPDNGKRV DKLTKEEVA SWKTGVDLLL NGKILTGRDA
351 AHKRLVNMLD KGEELPVDF NRIYYVGPV DPVGDEVVGP AGPTTATRMD
401 KFTROMLKQT GLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAVYEF EVKMPVTV VDSKGESIHA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11 QSIDAFQFISYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
      Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53 QAFHDASFMLRPAHQKQVAAIHLHDPASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71 IATVFLKVGMDVQWDADMSVEKMVNEGVRAYTWEGNTLRASVLADPAGKRQNTKDNTPA 130
      A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAILVGKKGQRV-WTGGGD-EETLSKGVYNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCAAKGGSENKSL-----AMLNPSDNIVDWVLKTIPTMGAGWCP 185
      I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGDYKFLCVAKGGGSANKTYLYQETKALLTPG-KLKNFLVERMRLGTAACP 225

```

```

Query: 186 PXXXXXXXXXXTPKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLELFKVNXXX 245
      P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGTS AETNLKTVKLASAHY-YDELPTEGNEHGQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXXTTVLDVKILDYPHTAASKPIAMFNCAATRHVEFELDGS-----PVELTPP 301
      D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIIEKLEHNPG 343

```

```

Query: 302 RVEDXPDLTYSPDNGKRVVDKLTK---EVASWKITGDVLLNGKILTGRDAHKRLVNM 358
      + +VD+++ KE +-+ + L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRLSLTGTIIIVGRDIAHAKLKL 403

```

```

Query: 359 LDKGEELPVDFNRLIYXXXXXXXXXXXXXXXXXXTTATRMDKFTROMLKCTGLLGMIGK 418
      +D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSMIMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVAVG--AAYLVAKAIKSSKVLAFPGLMEAVYEFVVKMPV 477
      R +A + YL ++GG AA L ++IK + +A+PELCMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSIGGPAAVLAQQSIKHLECVAYPELMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
      + VD KG
Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGCGA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACAACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

```

```
301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCGGTCC TCGCCGATCC
351 GGCCGGGCAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCATA
401 TGAGCATCGT GCCGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAATC CAACTCGCC ATGCTCAATC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGCTGATGG CAAAAGAGTC CCTGATGAGC CACATCGACA TTCAAGAATT
651 CCAGGAAAG GCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTTGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCTGA ACTCACGCGG
901 CCGCGCGTCG AAGACTGGCC CGATTGACT TACAGCCCGG ACAACGGCAA
951 ACGCGTCGAT TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCGATGCC
1051 GCACACARAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCC
1151 GCGATTGAAT CGTCGGTCCG GCAGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTGCGA AGCCATCGCC GACAACAAAG
1301 CCGGTACCT CATGGCAGTC GCGGCGCGG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCG GAATTGGGCA TGGAAAGCCAT
1401 TTACGAATT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCAGGCC ACCGCCCGC GCAAATGGCA GCGAAAAATC
1501 GGCATCATCC CCGTCGAATC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```
1  MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVG M NVQWDADMSV EEMVNEGVR
101 AYTWEGLTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSSENKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQG
251 LGGLTTVLVD KILDYPTHA SKPIAMIPNC AATRHVEFEL DGSGPVELTP
301 PRVEDWPLDT YSPDNKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVMDLN KGEELPVDET NRLIYYVGPV DPVGDEVVGP AGPTTATMD
401 KFTRQMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKMPVTVA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*
```

m050-1/g050-1 98.2% identity in 507 aa overlap

	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSIDAFQFISYYH	PKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE				
g050-1	MTVIKQEDFIQSIDAFQFISYYH	PKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE				
	70	80	90	100	110	120
m050-1.pep	NNRPICQDTGIATVFLKVG	MNVQWDADMSVEEMVNEGVR	RAYTWEGNTLRASVLADPAGK			
g050-1	NNRPICQDTGIATVFLKVG	MDVQWDADMSVEKMNNEGVR	RAYTWEGNTLRASVLADPAGK			
	130	140	150	160	170	180
m050-1.pep	RQNTKDNTPAVIHMSIVPGG	KVEVTCAAKGGGSENKSLAMLNPSDNIVDWLKTIP	TMG			
g050-1	RQNTKDNTPAVIHMSIVPGG	KVEVTCAAKGGGSENKSLAMLNPSDNIVDWLKTIP	TMG			
	190	200	210	220	230	240
m050-1.pep	AGWCPPGILGIGIGGTPEKAV	LMKESLSHDIQELQEKAA	SGAELSTTEALRLELFEK			
g050-1	AGWCPPGILGIGIGGTPEKAV	LMKESLSHDIQELQEKAA	SGAELSTTEALRLELFEK			
	250	260	270	280	290	300
m050-1.pep	VNALGIGAQGLGGLTTVL	DKILDYPTHAASKPIAMIPNCA	ATRHVEFELDGSGPVELTP			
g050-1	VNALGIGAQGLGGLTTVL	DKILDYPTHAASKPIAMIPNCA	ATRHVEFELDGSGPVELTP			
	250	260	270	280	290	300



256

```

      310      320      330      340      350      360
m050-1.pep PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLV DMLN
           |||||
g050-1      PRVEDXPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLV NMLD
           310      320      330      340      350      360

      370      380      390      400      410      420
m050-1.pep KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE
           |||||
g050-1      KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLKQTGLLGMIGKSE
           370      380      390      400      410      420

      430      440      450      460      470      480
m050-1.pep RGVATCEAIADNKAVYLMVSGAAYLVAKAIKSSKVLAFPELGMEAIYEFVKDMPVTVA
           |||||
g050-1      RGAATCEAIADNKAVYLMVSGAAYLVAKAIKSSKVLAFPELGMEAVYEFVKDMPVTVA
           430      440      450      460      470      480

      490      500
m050-1.pep VDSKGESIHATAPRKWQAKIGIIPVESX
           |||||
g050-1      VDSKGESIHATAPRKWQAKIGIIPVESX
           490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

```

a050-1.seq
1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCCTT
51  CCAATTCATC AGCTACTACC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AACCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGCAT GTGTGCCGAA AACCAACGCC CCATCTGCCA
201 AGATACCGGT ATCGCGACCG TGTTTTGAAG AGTCGGTATG GATGTGCAAT
251 GGGATGCAGA CATGAGCGTC GAAGAGATGG TTAACGAAGG CGTGCGCCGC
301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCCGTTC TCGCCGACCC
351 CGCCGGCAAA CGCCAAAATA CCAAGACAA CACGCCGCC GTCATCCATA
401 TGAGCATCGT GCCGGGCGAC AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGCGTCTG AAAACAAATC CAAACTCGCC ATGCTCAACC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATTC GACCATGGG CGGGGCTGST
551 GTCCTCCGCG CATCTTGGGC ATCGGCATCG GCGGTACGCC CGAAAAGGCC
601 GTGTTGATGG GAAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCACGCGC TAGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCGCAC
801 CCACGCCGCC TCAAACCGA TTGCCATGAT TCCGAATGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCGA ACTCAGCCCG
901 CCGCGGTCG AAGACTGGCC CGATTTGACT TACAGCCCCG ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGCCA AGCTGGAAAA
1001 CGCGCGAGCT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCGAC AAAGGCCAAG AATTGCCCGT
1101 CGATTTTACC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGACGAAAT CGTCGGCCCA GCAGGTCCGA CCACCGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAAG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCC GAATTGGGCA TGGAAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGCG CCCAATGGCA GGGCAAAATC
1501 GGCATCATCC CCGTCAAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

```

a050-1.pep
1  MTVIKOEDEFI OSICDAFOFI SYHHPKDYID ALYKAWOKEE NPRAKDAMTO
51  ILVNSRMCAE NRPICQDTG IATVFLKVGM DVQWDADMSV EENVNEGVR
101 AYTWEGNTLR ASVLADPAGK RONTKDNTPA VIHMSIVPGD KVEVTCNAKG
151 GGSSENKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IIGGTPPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQQ
251 LGGLTTVLVDV KILDYPTHAA SKPIAMTPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGRRVD VDKLTKEEVA SWKTGDVLLN NGKILTGRDA
351 AHKRLVDNLD KGEELPVDFN NRIYYVGPV DPVGDEIVGP AGPTTATRMD
401 KFTROMLEQT DLLCMICKSE RCAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKDMPVTVA VDSKGESIHA TAPPQWQAKI
501 GIIPVKS*

```

a050-1/m050-1 98.4% identity in 507 aa overlap

```

      10      20      30      40      50      60
a050-1.pep MTVIKQEDFIQSICDAFOFISYYHPKDYICALYKAWQKEENPAAKDAMTQILVNSRMCAE
          |||
m050-1      MTVIKQEDFIQSICDAFOFISYYHPKDYICALYKAWQKEENPAAKDAMTQILVNSRMCAE
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
a050-1.pep NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAAYTWEGNTRASVLADPAGK
          |||
m050-1      NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAAYTWEGNTRASVLADPAGK
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
a050-1.pep RQNTKDNTPAVIHMSIVPGDKVEVTCAARGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
          |||
m050-1      RQNTKDNTPAVIHMSIVPGDKVEVTCAARGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
a050-1.pep AGWCPPGILGIGIGGTPEKAVLMAKESLMSHIDIQELQEKAAAGELSTTEALRLELFK
          |||
m050-1      AGWCPPGILGIGIGGTPEKAVLMAKESLMSHIDIQELQEKAAAGELSTTEALRLELFK
          |||
      190     200     210     220     230     240

      250     260     270     280     290     300
a050-1.pep VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP
          |||
m050-1      VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP
          |||
      250     260     270     280     290     300

      310     320     330     340     350     360
a050-1.pep PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD
          |||
m050-1      PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN
          |||
      310     320     330     340     350     360

      370     380     390     400     410     420
a050-1.pep KGEELPVDFTNRLIYYVGPVDPVGVDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE
          |||
m050-1      KGEELPVDFTNRLIYYVGPVDPVGVDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE
          |||
      370     380     390     400     410     420

      430     440     450     460     470     480
a050-1.pep RGAATCEAIADNKAVYLMVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA
          |||
m050-1      RGVATCEAIADNKAVYLMVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA
          |||
      430     440     450     460     470     480

      490     500
a050-1.pep VDSKGESIHATAPPQWQAKIGIIPVKSX
          |||
m050-1      VDSKGESIHATAPRKWQAKIGIIPVESX
          |||
      490     500

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGCGGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAACAGC AGTTTGTTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
251 TGCCGAATTT GGTAAACGAT TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 224; ORF 052.ng&gt;:

g052.pep

258

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP  
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN  
 101 RLRLETTWSP ACRKVKNAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

m052.seq  
 1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG  
 51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC  
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC  
 151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC  
 201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA  
 251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC  
 301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA  
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

m052.pep  
 1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP  
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN  
 101 RLRLETTWSP ACRKVKNAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

a052.seq  
 1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG  
 51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC  
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC  
 151 AAGGGATTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC  
 201 GGCGGCTTTC CATTGTTTA TATCAGTCGG CGACACGTGA CTCACTTCGA  
 251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC  
 301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA  
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

a052.pep  
 1 MALVAEETEI SAPCFKG\*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP  
 51 KGLDGVSKNS SLVLALTAAF HSFISVGD\* LTSMPLVTM LLIKPTVVPN  
 101 RLRLEITWSP ACKKVKNAA\*

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTAAFHSFISVGDXTLSMPNLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					

259

```

g052      MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANSKASKSATSPKGLDGVSKNS
           10      20      30      40      50      60

           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDTWLTSMPLATMLLIKPTVVPNRLRLEITWSPACKVKVNAAX
           |||||
g052      SLVLALTAAFHSFISVGDTRLTPMPLVTMLLIKPTVVPNRLRLETTWSPACRKVKVNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGatacCGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGCG TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCTCCGCC TCGGATGGT CGGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPIAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51  SPGRIPAAFS SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101 ATSKPMTMPP PFCCLRISSA CWWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101 TCAATCGGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CGGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201 TGTCCACGGG TGGTAATGGT TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAACCT TCCACGCCGC TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCGCGGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51  RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASXS
101 ATSKPMTMPP PFCCLRISAA XGWSNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTCCG GCACTTCAA GCGGATGACG ATGCCGCCGC CSTTTTGCTG
351 TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMYSKIRVS DGICGVFPPM PSEXNRQRAS ACFKSSIKSP TYSKPTDRRT
51  NPGRMILAASF SSGCILPCVV VHGWVVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEKRNQASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCLRI				
a073	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPSTTFHAAAWSATSKPMTMPPPFCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNPNVX				
a073	SSAXGWSGNPNVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
g073	MCMPIAIRVSDGICRIFPPMPSETRNQASACFKSSIKSPTYSKPTDRRTSPGRIPAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCLRI				
g073	SSGCILPCVVVHGLVMVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNPNVX				
g073	SSACGWSGNPNVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCCGTTTCGG GCAACGCTGC GTTTGCCTGT
151 GCGCCCAAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGCGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTTAGAGA CCGCTGCCG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAA ATTACAAAT
351 CCCCCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTC ATAGCTGTCA
401 TATTACCG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFILLT MENTKSAAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLRQ VLINFMIFSF TKFLKKCVCG LCEGFRDRLP
101 GLNLIFFFV ESENYKFPAY LFQCRKSVF IAVIFTG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 237>:

```
m075.seq
1  ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCGAAAATG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CCGCTTCCAA AGCGTTTTTT GCGGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTATGAT ATTTTCCTTC AAAAAAGTGT
251 TGGCGGTAAT GGATGGAGCG TTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TCGGTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 238; ORF 075>:

```
m075.pep
1  MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLRO VLINFMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

```
m075/g075

          10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          |||||||
g075       MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAAVT
          10      20      30      40      50      60

          70      80      90      100     110
m075.pep  TASFAPYLROVLINFMIFSF---KKCLAVMDGAFRRPPNIRKSVFQKSEYDKFVLVAD
          |||||||
g075       TASFAPYLROVLINFMIFSFTKFLKKVCGLCEGFRDRLPGLNLIFFVSESENYKFPAY
          70      80      90      100     110     120

          120     130
m075.pep  FFQTCVNRFFEVEIIGIGDX
          :|| :| :| :|
g075       LFQCRAKSVFIIVFTGX
          130
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 239>:

```
a075.seq
1  ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAAGA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CCGCTTCCAA AGCGTTTTTT GCTGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTATGAT ATTTTCCTTC AAAAAAGTGT
251 TGGCGGTAAT GGATGGAGCG TTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TCGGTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 240; ORF 075.a>:

```
a075.pep
1  MPSYFITLLT MEKTKSAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLRO VLINFMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

m075/a075 98.5% identity over a 136 aa overlap

```

      10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQFASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a075      MPSYFITLLTMEKTKSAAKTPTTIQFASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
      10      20      30      40      50      60

      70      80      90     100     110     120
m075.pep  TASFAPYLRLQVLINFMIFSEKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT
          |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a075      TASFAPYLRLQVLINFMIFSEKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT
      70      80      90     100     110     120

      130
m075.pep  CVNRFFEVEIIGIGDX
          |||:||||| |||||
a075      CVNRFFEVEIIGIGDX
      130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

```

g080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAAGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA TACGGTTGAG
301 GTCGTCTCTGA CCGAGCGCAA GCCGGTTCGA CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAA TGTGCTTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACgaGA TGAAACGCCT CCgGCTTTT
601 ACcgAAGCGT GGCAGCATCT gttgcGTAAG AATAAAAATC GGTTATCCTA
651 TGTGGATATG Aggtataagg acggatttTC agtcccccat gctCCCGACG
701 GTTTACCCGA AAAAGAAATcc gAAGAAATatt gggaaacaggt ttgggacata
751 ttacggcctg gcgtcggaaa cggttcgacg caaatttcaa tcagttataA
801 GGGCAGacga acaatggaac AGcagtaa

```

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

```

g080.pep
1  MWDNAEAMER LTRWLLVMMa MLLAASGLVW FYNsNHLpVK QVSLKGNLVY
51  SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYpWIASVM VRRRFpDTVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RpgMPVFRGA EGTSaEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSAWNVVL DNGITVRLGR ENEMKRLRLP
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVPH APDGLPBKES EEYWEQVWDI
251 LRPgVNGGST QISISYKGRR TMEQQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

```

m080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
301 GTCGTCTCTGA CCGAGCGCAA GCCGGTTCGA CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTGCTTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTT

```

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAAATC GGTATCCTA  
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG  
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep  
 1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNHNLVPVK QVSLKGNLVY  
 51 SDKKTGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE  
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA EGTSAEMLRR  
 151 YDEFSTVLAK OGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF  
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES RE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng)

from *N. gonorrhoeae*:

m080/g080

	10	20	30	40	50	60
m080.pep	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLVPVKQVSLKGNLVYSDKKTGSLA					
080	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLVPVKQVSLKGNLVYSDKKTGSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKOGLGIKEMTYTARSAWIVVL					
080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKOGLGIKEMTYTARSANNVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGRENEMKRLRLFTEAWQHLLRK NKNRLSYVDMRYKDGFSVRYASDGLPEKES					
080	DNGITVRLGRENEMKRLRLFTEAWQHLLRK NKNRLSYVDMRYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
	m080.pep EEX					
080	EEYWEQVWDILRPGVNGSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq

1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT  
 51 CATGATGGCG ATCCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT  
 101 CGAATCATCT GCCCGTCAAG CAGGTGTGCG TGAAGGGCAA CTTAGTTTAT  
 151 TCCGATAAGA AAGCATTGGG CAGTTTGCG AAAGAATACA TCCATGGGAA  
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC  
 251 CGTGGATTGC GTCGTCATG GTGCGCGGCC GTTTCCCGA CACGGTTGAG  
 301 GTCGTCCTGA CCGAGCGCAA GCCGGTCCGG CGTTGGGGCG ACCATGCCTT  
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTGGAC AGACCCGGAA  
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT  
 451 TATGACGAAT TTTGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA  
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTGTTTTG GACAACGGCA



264

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT  
 601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAATC GGTTATCCTA  
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCACG  
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYN SNHLPVK QVSLKGNLVY  
 51 SDKKALGSLA KEYIHGNILR TJINGAQEAY RRYPWIASVM VRRRFEDTVE  
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA ESTSAEMLRR  
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF  
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY APDGLPEKES EE\*

m080/a080 99.2% identity over a 242 aa overlap

m080.pep	10	20	30	40	50	60
	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKTLGSLA					
a080	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVVLTERKPVARWGDHALVDG					
a080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
a080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRENEMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
a080	DNGITVRLGRENEMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

1 ATGAAACCAC TGGACCTAAA TTCATCTGCG CAAGCCCTCA AGCTTCCGAT  
 51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA  
 101 TTCGGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG  
 151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GCGCGGCGCG CGGTGTGGT  
 201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA  
 251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC  
 301 CCGTTTGTGT TCGGCATTAC CGGTTGCGGC GGCAAGACGA CGGTGAAGGA  
 351 GATGCTGGCT GCGGTATTGC GCGCCGTTT CGGCGATGAT GCCGTTTCGG  
 401 CGACGCGAGG CAACTTCAAC AACCACatcg gaTTGCCGCT GACTTTATTG  
 451 AAATtaaAcg aAAAAACCCG CTATGCCGTG ATTGAAATGG GCATGAACCA  
 501 TTTTGGcgaa ctggcggtTt taacgcaaaT CGCCAAACCC GATGCCGCTT  
 551 TGGtcaACAA CGCCCTGCGC GCCCATGTGCG GATGCGGTTt cgacggagtg  
 601 GGCGATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTCAGA  
 651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA  
 701 CGGCAACGTT TAATTTGAAT ACGTGCACTT TCGGCGTCTGA TAGCGGCGAT  
 751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT

265

```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TCGGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG CATTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGTTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTGTTAGACC ACGATTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGAtggAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

```

g081.pep
1 MKPLDLNFIC QALKLMPSE NKPVSRIVD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTQIAKP DAALVNNALR AHVGCDFDGV
201 GDIKAKSEI YAGLCSDGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNVHNA AALALALAAG
301 LSLNDVAEGL QGFSNIKRL NVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMLBELGED EAAAMHAEVG AYARDQIEA AYFVGDNSE
401 AAEKFGADGL WFAAKDELIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

```

m081.beq
1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 FCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTTGTGGT
201 TCGCGCGGAA GATTGTGCTG CAATGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCGCGGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AAGTTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGGCGAA CTGGCGGTTT TAACGCAMAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCT GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTTACA
651 CGGCATTGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGCGGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTGTATTT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCGGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TCGGAACCCG GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCG TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCG CGACCAAGGC ATCGAAGCGG CTATTTTGTG CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCGCCGC
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTGCCG GAACGCCCCA
1301 CCGTGTGGT GAAAGGTTTG CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

```

m081.pep
1 MKPLDLNFIC QALKLMPSE SKPVSRIVD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTXIAKP NAALVNNAMR AHVGCDFDGV

```

```

201  GDIKAKSEI YQGLCSGIA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251  VHAENIVLKP LSCEFDLVCG DERAADVLPV PGRHNVHNA A A A A L A L A A G
301  LSLNDVAEGL KGFSNIKGRL NVKSGIKGAT LIDDTYNANP DSMKAAIDVL
351  ARMPAPRIFV MGDMGELGEL GEDEAAAMHA EVGAYARDQG IEAAYFVGDN
401  SVEAAEKFGA DGLWFAAKDP LIQVLRHDLR ERATVLVKGS RFMQMEEVVE
451  ALEDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng) from *N. gonorrhoeae*:

m081/g081

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSRDIRAGDVFFALAGERFDAHDFVEDVLAA					
g081	MKPLDLNFICQALKLPMPSENKPVSRIVTDSRDIREGDVFFALAGGRFDAHDFVGGVLSA					
	10	20	30	40	50	60
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
g081	GAAAVVVSREDCAALGGALKVDDTLAALQTLAKAWRDNVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTXIAKP					
g081	AVLRRRFGDDAVSATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTQIAKP					
	130	140	150	160	170	180
m081.pep	NAALVNNAMRAIIVGCGFDGVGDIKAKSEIYQGLCSGIALIPQEDANMAVFKTATLNLN					
g081	DAALVNNALRAHVGCGFDGVGDIKAKSEIYAGLCSDGMALIPQEDANMAVFKTATFNLN					
	190	200	210	220	230	240
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVVLVPGRHNVHNA A A A A L A L A A G					
g081	TCTFGVDSGDVRAENIVLKPLSCEFDLVCGDERTAVVLVPGRHNVHNA A A A A L A L A A G					
	250	260	270	280	290	300
m081.pep	LSLNDVAEGLKGFSNIKGRLNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
g081	LSLNDVAEGLQGFSNIKGRLNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
m081.pep	MGDMGELGELGEDEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
g081	MGDMGELGE--DEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	420
m081.pep	LIQVLRHDLPERATVLVKGS RFMQMEEVVEALEDKX					
g081	LIQVLSHDLPERATVLVKGS RFMQMEEVVEALEDKX					
	430	440	450			
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

## a081.seq

```

1  ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGCGG CGGTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGGT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGCTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTCAGA
651 CGGCATGGCG CTGATTCTCT AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGCG CAGCCGTGGT TCTGCCCGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCTT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCCG CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGGTTTG TGGTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTTTGCGCC ACGATTGCCC CGAACGCGCC ACCGTGTTGG
1301 TGAAGGTTG GCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

## a081.pep

```

1  MKPLDLNFC QALKLMPSE SKFVSRIVD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLA GAAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNAMR AHVCGGFDGV
201 GDIKAKSEI YQGLCSOGMA LIPQEDANMA VEKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNA AAAAAISLAA
301 LSLNDVAEGL KGFNKNIGRL NVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMLGELGD EAAAMHAEVG AYARDQIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFCQALKLMPSESKFVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLA					
a081	MKPLDLNFCQALKLMPSESKFVSRIVTDSDIRAGDVFFALAGGRFDAHDFVEDVLA					
	10	20	30	40	50	60
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCVAMDGALKVDDTLTALQMLAKAWRENVNPFVFCITGSGCKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTQIAKP					
a081	AVLRRRFGDNVAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTQIAKP					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVCGGFDGVDIAKAKSEIYQGLCSDGIALIPQEDANMAVFKTATLNLN					
a081	DAALVNNAMRAHVCGGFDGVDIAKAKSEIYQGLCSDGMALIPQEDANMAVFKTATLNLN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVVLVPVGRHNVHNAALALALAAG					
a081	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGNECAAVVLVPVGRHNVHNAALALALAAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFSENIKGRINVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	LSLNDVAEGLKGFSENIKGRINVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEVGAAYARDQGIEAAYFVGDNVSEAAEKFGADGLWFAAKDP					
a081	MGDMGELGE---DEAAAMHAEVGAAYARDQGIEAAYFVGDNVSEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFMQEEVVEALEDKX					
a081	LIQVLRHDLPERATVLVKGSRFMQEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

g082.seq

```

1  aTGTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTCACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGGT TCACATTATC GCGCCACGCC
151 TTCGCCAACG TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCGCCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTGTGTTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTGCTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTAGCCGAT TTGCCTTTC CCGCATACCA
601 CGGCGCGGG TCGTCGGACT GTCTGTCGAT AAAGGCAAGG TTATTGCCIT
651 CGCCCGGCAC ATCGGGGACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAACG CCGAATCCG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

g082.pep

```

1  MWLLKLPAVA ETASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTA AAPADNTPPT KSCASNRPFA
101 NAKNTSPSRI SRLSVTMRDT GLFSDGIGSL RAWQMKFRSS GFIFAFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI PSRPAFSRIP
201 RRGVVGLSVD KGKVIARH IGDIPKIIA VIGQLVGFD TPTAES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

m082.seq

```

1  ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATTTC CTTCACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGAT TCACATTTC ACGCCACGCC
151 TTTGCCAGCG TTTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```

```

201 ATCCATTGCA GCACAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTTGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTAATTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGsATTT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAAC TG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
1  MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTFSRHA
51  FASVCNAASV SSTFNAPSIA AQSSRETTTA AAPAANTSST KSCASNRSPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI FSRFAFSRIP
201 RRGVVQSVD KGKVIAPALH IGNIPPKIIA VIGQLVGFD T RPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng)

from *N. gonorrhoeae*:

```

m082/g082
      10      20      30      40      50      60
m082.pep MXLLKLPAVANTASSPKRRRNTAASISFTVLPPEPVMPNTNGFTFSRHAFAVCNAASV
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      MWLLKLPAVAETASSPKRRRNTAASISFTVLPPEPVMPNTNGFTLSRHAFANVCNAASV
      10      20      30      40      50      60

      70      80      90      100     110     120
m082.pep SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSPANAKNTSPARMSRLSVTMRDT
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      SSTFNAPPKAAQSSRETTTAAAPADNTPTTKSCASNRPPANAKNTSPSRISRLSVTMRDT
      70      80      90      100     110     120

      130     140     150     160     170     180
m082.pep GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF
      130     140     150     160     170     180

      190     200     210     220     230     240
m082.pep FLYVSFFRRIFSRFAFSRIPRRGVVQSVDKGKVIAPALHIGNIPPKIIAIVIGQLVGFD
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGKVIAPARHIGDIPPKIIAIVIGQLVGFD
      190     200     210     220     230     240

m082.pep RPTAESAX
      | | | | | |
g082      RPTAESAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

```

a082.seq
1  ATGTGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAACATTTC CTTCACCGTC GTCTTGCCGC

```

270

```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTGCAACGC GGTAAACGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTTT CAGACGGCAT CGGAAGCTT AGGGCTTGCG
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTA AACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAAC TG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

a082.pep

```

1 MWLLKLPVA KTALSPKRRR NTAANISFTV VLPPEPVI PN TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA APAANTSST KSCASNRP
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSSHSAF FLYVSFFRRI FSRAFSRIP
201 RRGVVGQSDV KGKVIAFALH IGNIPPKIIA VIGQLVGFD TPTAESAX*

```

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLP	AVANTASS	PKRRRNTA	ASISFTV	VLPPEP	VMPTNG
a082	MWLLKLP	AVAKTALS	PKRRRNTA	ANISFTV	VLPPEP	VIPTNG
	70	80	90	100	110	120
m082.pep	SSTFNAPS	IAAQSSRE	TTTAAAPA	ANTSSTK	KSCASN	RSPANAK
a082	SSTFNAPS	IAATQSSRE	TTTAAAPA	ANTSSTK	KSCASN	RPPANAK
	130	140	150	160	170	180
m082.pep	GLLSDGIG	SLRAWQMK	FRSSGFIF	TFVNIRA	ADTSVAAD	FFIACFA
a082	GLLSDGIG	SLRAWQMK	FRSSGFIF	TFVNIRA	ADTSVAAD	FFIACFA
	190	200	210	220	230	240
m082.pep	FLYVSFFR	RIFSRFA	FSRIPRR	GVVGQSD	KGKVIA	FALHIGN
a082	FLYVSFFR	RIFSRFA	FSRIPRR	GVVGQSD	KGKVIA	FALHIGN
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

g084.seq

```

1 ATGAAaCaAT CCGcccgaaT aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgcG gccatCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTG TGCCGTGGGC
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTCG
301 ATATTGGAAA GCAATCCTGC CGAGGCGCGT GAATTGTGCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG

```

271

```

401 TTTGGAAATA TTGTGTATCT GTGGGGGTAT TTGCTGACGT AAAAAACTAT
451 AAACGTCGCA GCAAAATATG GCTGACCATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGAGAAAA TCGccggcgca taaAGATTGG CGAGaacctg
551 atgccggcct gttgttgaat ATTTTcgacc tgtattaCga cttggctttc
601 cgcgccggca CAATATGCCG CCAAGCGCGC CCACattttg gaagCagcaa
651 aaaaagcgtC AACATGGCAt atccgccaac ttgcgcccaa gTataa

```

This corresponds to the amino acid sequence <SEQ ID 260; ORF 084.ng>:

g084.pep

```

1 MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51 ALASVVFLLL LARGFPRVSS VLLLIYVGTI ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MEKIAGDKDW REPDAGLLLN IFDLYYDLAF
201 RAGTICRQAR PHFGSSKKS SV NMAYPPTCAQ V*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

```

1 ATGAAACAAT CCGCCcGAAT AAAA .ATATG AATCAGACAT TACTTTATAC
51 ATTGGGCATT TCGCGCTTT TAACCTTInn nnnnnnnnnnn nnnnnnnnnnn
101 ILESNPAAER EFVGNLPGSL GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCGCT CTTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGCGCGCT GAATTTGTCG GCAATCTTCC
351 CGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG
401 TTTGGAAATA TTGTGTATCG GGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTGG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTGGCT.TC
601 CGCGCCGCA CAATATGCCG CCAAGCGCGC CCACATTTC GAAGCAGCAA
651 AAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084.pep

```

1 MKQSARIKMN NQTLTYTLGI CALLTFXXXX XXXXXHPEY EYGYRYSAVG
51 ALASVVFLLL LARGFPRVSS VLLLIYVGTI ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLLN IFDLYYDLAX
201 RAGTICRQAR PHFGSSKKS SV NMAYPSCCAQ V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

	10	20	30	40	50
m084.pep	MKQSARIKMNQTLTYTLGICALLTF-----YHPEY EYGYRYSAVGALASVVFLLL				
	:         :  :				
g084	MKQSARIKMNQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVGALASVVFLLL				
	10	20	30	40	50
	60	70	80	90	100
m084.pep	LARGFPRVSSVLLIYVGTI ALYLPVGWLY GAPSYQIVGS ILESNPAEAR EFVGNLPGSL				
g084	LARGFPRVSSVLLIYVGTI ALYLPVGWLY GAPSYQIVGS ILESNPAEAR EFVGNLPGSL				
	70	80	90	100	110
	120	130	140	150	160
m084.pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAV MDKIASDKDL				
g084	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAV MEKIAGDKDW				
	130	140	150	160	170
					180



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	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYYDLAFRAGTICRQARPHFGSSKKSVMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGCGCGCTTT TAGCCCTTTG TTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGTCGCG CTGGCTGTAT GGTGCGCCGT CTATCAGAT AGTCGGTTCG
301 ATATTGGAAG GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGGTCGCTT TATTTGTGC AGGCATTATT TTCATTTT GGCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGSGTAT TTGCTGACGT AAAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGLWY GAPSYQIVGS
101 ILESNPAEAR EFGNLPGLS YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKMNQTLTYTLGICALLTFXXXXXXHYHPEYGYRYSAVGALASVVFLLL					
a084	MKQSARIKMNQTLKNTLGI CALLAFCFGA AIASGYHLEYEYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGLWYGAPSYQIVGSI L ESNPAEAREFVGNLPGLS					
a084	LARGFPRVSSVLLIYVGTALYLPVGLWYGAPSYQIVGSI L ESNPAEAREFVGNLPGLS					
	70	80	90	100	110	120
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYYDLASXAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGAC3CGT TGAAAGATAA

```

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```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCGCCGCA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTCAGA CGGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACC GTT
251 CGGAAGTGTT taTCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

**g085.pep**

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGCL NLTDCVTLEE
51 AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

**m085.seq**

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCTG CGCGATGCAC TGGTAGGCAA
51 GGCAAAAGGC GTGTTCTGA TGGTGTCGA TCGCGCCGCA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCGGTTTCAGA CGGCATATGC CCAAGCCGAA GCAGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGGAGCT TTGATATGTT CAAAGGCTAC GCGCACC GTT
251 CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

**m085.pep**

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGCL NMTDCATLGE
51 AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

**m085/g085**

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQA E					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGCLNLTDCVTLEEAVQTAYAQA E					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

**a085.seq**

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGC TTGCCGGCAA
51 GGCAAAAGGC GTGTTCTGA TCGGTGTCGA TCGCGCCGCA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTCAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACC GTT
251 CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

**a085.pep**

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51 AVQKAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

**m085/a085** 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQA E					

```

g086.seq
1  ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATT TATCGGCTTC
51  TGTGTATTTG GCATCGAAGG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GGCAGCGGGG GTTCGTCTGT GCGGCGCTTA TAGCGAGCGG TTTTTATATG
151 TTCTTTTGCA GGATGAGGAC ATGGCGGCGG CTGTGCGCGT GGATTTTTTG
201 CTTATCCGGC CTGTTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAAATT CAGCCGACCC
301 GAGCTGTTCa AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTACCGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAGA TTTGGGTTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAAACCTG ATTATGTCCG CCACCAATCC CAGGCCACGT
451 CGTGAACATa TAGAAATGTA CGgcCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTCG
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTTCGGTGG
601 GGATTGCCGT GGAAATATTT TTTTGTCCCT GTAGGACGCG TCTTTGGTGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CCGGATAGTG
701 CATTTTTGGA CCCGTGGAaA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGTTTCGGTA TGGGTTTGGG
801 TGCGAGTTTG AGCAAAACGG GCTTCTGCCG GGAAGCGCAT ACCGATTTTA
851 TTTTGTGCCaT CATCGCTGAA GAATTCGGGT TCTTCGGGAT GTGCGTGCTG
901 ATAATTCTGT ATCGCTGGCT GGTTGTGCGG CGGTTTTCCA TCGCGAAGCA
951 GTCGCGCGAT TTGGGtttgA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CCGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGctgCcg tTGATGCTCT ATGGcggTTC
1101 GTCAGCTCTT TCACTGCTaT TCAGCATGAT GCTGCTGTTG CGTATCGATT
1151 ATGAAAACCG CCAAAAATG CGCGGTTACC GGGTGGAGTA AA

```

g086.pep

1	MVVLMTAFGL	LMIYSASVYL	ASKEGGDQFF	YLTRQAGFVV	AGLIASGFLW
51	FLCRMRTWR	LVPWIFALSG	LLLVAVLIAG	REINGATRWI	PLGPLNFQPT
101	ELFLAVILY	LKSLVITREE	VLVSMESLWG	QSIWRGTANL	IMSTANLQAT
151	RETLEMYGRF	RAIILPIMLV	AFGLVLIMVQ	PDFGSFVVIT	VITVGMFLFA
201	GLPWKYFFVL	VGSVLGGMVL	MITAAPYRVQ	RVVAFLDPWK	DPQAGAGYQLT
251	HSLMAIGRGE	WFGMGLGASL	SKRGFLPEAH	TDPFIAITAE	EFGFFGMCVL
301	IFCYGWLVRV	AFSIGKQSRD	LGLTFNAYIA	SGIGIATIGQ	SFFNGVGNIG
351	ALPTKGLTLP	LMSYGGSSVF	PMLISMMLLL	RIDYENRQKM	RGYRVE*

```
m086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTGT GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTCCCGT GGATTTATGC
201 CCTATCCGGT CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGAGc
301 GAGCTGTTCa AGcTGCGGcT CATCCTTTAT TTGGCAAGCC TGtTCACGCG
351 CCGTGAAGAA GTGTTGcGCA GCATGGAAG TTTGGGTTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CTGTGAaACAT TAGAAATGTA CGCGCGTWTc CGGGCGATCA TCCTGCCGAT
501 TAGCTCGGTG GCGTTTCGTT TGGTGCTGAT AATGGTACAG CCGGATTTTCG
```

```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCGTCTCTG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CCGGTAGTGG
701 CATTTTTGGA CCCGTGGAAA GACCCGAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGGGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTGGGAT CGGkrTCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCyGCCG Tg.AtGTCCw ATGGCGGTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

```

m086.pep
1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTTREE VLRSMESLWQ QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGWLVR AFSIGKQSRD LGLTFNAYIA SGIGIWIQXQ SFFNIGVNI
351 ALPXKGLTXP XMSXGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng) from *N. gonorrhoeae*:

```

m086/g086
      10      20      30      40      50      60
m086.pep  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR
          |||
g086      MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR
          |||
      10      20      30      40      50      60
m086.pep  LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTREE
          |||
g086      LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTREE
          |||
      70      80      90      100     110     120
m086.pep  VLRSMESLWQ QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILPIMLV AFGLVLIMVQ
          |||
g086      VLRSMESLWQ QSIWRGTANL IMSATNPQAR RETLEMYGRF RAILPIMLV AFGLVLIMVQ
          |||
      130     140     150     160     170     180
m086.pep  PDFGSFVVIT VIAVGMLFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK
          |||
g086      PDFGSFVVIT VITVGMFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK
          |||
      190     200     210     220     230     240
m086.pep  DPQAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
g086      DPQAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
      250     260     270     280     290     300
m086.pep  DPQAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
g086      DPQAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
      310     320     330     340     350     360

```

```
m086.pep      IFCYGWLVVRAFSICKQSRDLGLTFNAYIASGGIGIWIGXQSFFNIGVNI310GALPXXKGLTXP360  
              |||  
g086          IFCYGWLVVRAFSICKQSRDLGLTFNAYIASGGIGIWIGIQSFFNIGVNI310GALPTKGLTLP360  
              |||  
  
              370      380      390  
m086.pep      XMSXGGSSVFFMLISMMLLXRIDYENRRKMGRGYRVEX  
              |||  
g086          LMSYGGSSVFFMLISMMLLRIDYENRQKMGRGYRVEX  
              |||
```

a086, seq

1	ATGGTGGTGC	TGATGACGGC	GTTACGCTG	CTGATGATTT	ATTCGGCTTC
51	TGTGTATTTG	GCATCAAAAG	AAGGCGCGCA	TCAGTTTTTC	TAATTTGACCA
101	GACAGCGGGG	GTTCTGCTGT	GCCGGCTTGA	TAGCAGAGCG	TTTGGTTATGG
151	TTTCTTTTGA	GGATGAGGAC	ATGCGCGCGG	TGTTG GCCGT	GGATTTTTTGC
201	CCTATCCGGC	CTGTTGCTGG	TAGTCGTATT	GATTGCCGGG	CGCGAAATCA
251	ATGGCGCGAC	CCGTTGGATA	CCTTTGGGTC	CGTTGAATTT	CCAGCCGACG
301	GAGCTGTTCA	AGCTGGCGGT	CATCCTTTAT	TGGGCAAGCC	TGTTTCAACGC
351	CCGTGAAGAA	TGTTTGCBCA	GCATGGGAAG	TTTGGTTGG	GAGTCCATTT
401	GGCGGGGGAC	GGCCAATCTG	ATCATGTCCG	CCACCAATCC	GCAGGCACGT
451	CGTGAACAT	TAGAAATGTA	CGGCCGTTTC	CGGGCGATCA	TCCTGCCGAT
501	TATGCTGGTG	CGGTTCCGTT	TGGTGCTGAT	AATGGTACAG	CCGGATTTTC
551	GTTCTGTTGT	CGCTATTACC	GTCATTCGCC	TTGGAATGCT	GTTTTTGGCA
601	GGATTGCCGT	GGAATAATTT	TTTCGTCCTG	GTAGGCAGCG	TCTTTGGGCG
651	GATGCTGCTG	ATGATATACC	CCGCTCCCTA	CCGTTGTCAG	CGGGTAGTGG
701	CATTTTTTGA	CCCGTGGAAA	GACCCGACAG	GTCCCGGCTA	CCAGCTTTACC
751	CACCTCTCTA	TGGCAATCGG	GC CGGAGAG	TGGTTCTGGTA	TGGGTTTTGGG
801	TGCGAGTTTG	AGCAAACGCG	GCTTTCTGCC	GGAAGCGCAT	ACCGATTTTA
851	TTTTTGCCAT	CATCGCCGAA	GAATTCGGTT	TCTTTCGGTAT	GTCGCTGCTG
901	ATATTTCTGT	ACGGCTGGCT	GGTGGTGCGG	CGCTTTTCCA	TCGGCAAGCA
951	GTCCGCGCAT	TTGGGTTTGA	CTTTCAACGC	CTATATCGCT	TCGGGTATCG
1001	GCATTTGGAT	CGGTATCCAA	AGTTTCTTCA	ATATCGGTGT	GAACATCGGT
1051	GCTTTGTCGA	CCAAGGPTCT	GACGCTGCCG	TTGATGTCTC	ATGGCGGTTT
1101	GTCAGCTCTT	TTCATGCTGA	TACGCATGAT	GCTGCTGTTG	CGTATAGATT
1151	ATGAAAACCG	CCGGAAAAATG	CGCGGTTACC	GGGTGGAGTA	A

a086.pgp

1	MVVLMTAFSL	LMIYSASVYL	ASKEGGDQFF	YLTRQAGFVV	AGLIASGLLW
51	FLCRMRTWR	LVPWTFALSG	LLLVLMVLIAG	REINGATRWI	PLGPLNFQPT
101	ELFKLAVILY	LASLFTREE	VLRSMSLJG	QSIWRGTANL	IMSATNPQAR
151	RETLEMYGRF	RAIILPIMLV	AFGLVLIMVQ	PDFGSFVUIT	VIAVGLMFLA
201	GLPWKYFFVL	VGSVLGGMVL	MITAAPYRVO	RVVAFDPWK	DPQAGYQLT
251	HSLMALTGRG	WFGMGLGASL	SKRGFLPEAH	TDPIFAITAE	EPGFFGMCVL
301	IFCYGWLVR	AFSIGKQSRD	LGLTFNAYIA	SGIGIWIGIQ	SFFNIGVNI
351	ALPTKGLTLP	LMSYGGSSVF	FMLSIMMLLL	RIDYENRRKM	RGYRVE*

	10	20	30	40	50	60
m086.pep	MVVLTAFSLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
a086	MVVLTAFSLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYASLFTTRREE					
a086	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYASLFTTRREE					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLQWQSIWRGTANLIMSATNPQXRRETLEMYGRXRAILPIMLVAFGLVLIMVQ					
a086	VLRSMESLQWQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
a086	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m086.pep	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIGALPKXGLTXP					
a086	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIGALPTKGLTLP					
	310	320	330	340	350	360
	370	380	390			
m086.pep	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX					
a086	LMSYGGSSVFFMLISMMLLLRIDYENRRKMRGYRVEX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

```

g087.seq
1  ATGGGCGGTA  AAACCTTTAT  GCTGATGGCG  GGCGGAACGG  GCGGACACAT
51  TTTCCAGCT  CTGGCTGTGG  CGGATTCATT  GCGCGTGCGC  GGTCAATCAT
101 TAATTGGCT  GGGCAGCAAG  GATTCGATGG  AAGAGCGCAT  CGTGCCGCAA
151 TACGGCATA  GCTTGGAAC  GCTGGCGATT  AAAGGAATAC  GCGGCAACGG
201 CATCAAACG  AAGCTGATGC  TTCCGTTTAC  TCTGTACAAA  ACCGTCCGCG
251 AAGCGCAGC  GATTATCCGC  AAACACCGTG  TCGAGTGCGT  CATCGGCTTC
301 GCGCGTTTIG  TTACCTTTCC  CGGCGGTCTG  GCGGCGAAAC  TCTTGGGCGT
351 GCCGATTGTG  ATTCACGAGC  AAAACGCCGT  GGCAGGCTTG  TCCAACGCC
401 AccTGTCGCG  ctGGGCGAAA  CGGGTGTGTG  ACGCTTTTCC  GAAAGCGTTC
451 AGCCACGAAC  GCGGTTTGGT  CGGCAACCCC  GTCCGCGCCG  ATATTAGCAA
501 CCTGCCCGTG  CCGCCGAAC  GCTTCCAAGG  GCGCGAAGGC  CGTCTGAAAA
551 TTTTGGTGGT  CGGCGGCAGT  TTGGGTGCGG  ACGTTTTGAA  CAAAACCGTA
601 CCGCAGGCGT  TGGCACTGCT  GCCTGAAGAG  GTGCGCCCGC  AGATGTACCA
651 CCAGTCGGGG  CGTAACAAGC  TGGGCAATCT  TCAGGCGGAT  TATGACGCGT
701 TGGGCGTGAA  AGCGGAATGC  GTGGAATTTA  TTACCGACAT  GGTGTCCGCC
751 TACCGTGATG  CCGATTGGT  GATTGCGCGT  GCCGGCGCGC  TGACGATTGC
801 CGAGTTGACG  GCGGCGGGG  TGGGCGCGTT  GTTAGTGCCG  TATCCTCAGC
851 CCGTTGATGA  CCATCAAACC  GCCAACGCGC  GTTCATGGT  GCAGGCAGAA
901 GCGGGGCTGC  TGTGCGCGCA  AACCCAGTTG  ACGGCGGAAA  AACTCGCCGA
951 AATCCTCGGC  AGCCTCAACC  GCGAAAAATG  CCTCAAATGG  GCGGAAAACG
1001 CCCGTACGTT  GGCATTGCCG  CACAGCGCGG  ATGACGTTGC  CGAAGCCGCG
1051 ATTGCGTGTG  CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

```

g087.pep
1  MGGKTFMLMA  GGTGGHIFPA  LAVADSLRVR  GHVVIWLGSK  DSMEERIVPQ
51  YGIRLETLAI  KGIRNGIKR  KLMLPFTLYK  TVREAQRIIR  KHRVBCVIGF
101 GGFVTFPGGL  AAKLLGVPIV  IHEQNAVAGL  SNRHLSRWAK  RVLYAFPKAF
151 SHEGGLVGNP  VRADISNLPV  PAERFQGREG  RLKILVVGGS  LGADVLNKTV

```

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201 FQALALLPEE VRPQMYHQSG RNKLGNIQAD YDALGVKAEC VEFITDMVSA  
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE  
 301 AGLLLPQTQL TAEKLAELIG SLNREKCLKW AENARTLALP HSADDDVAEAA  
 351 IACAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq  
 1 ATGGGCGGTA AAACCTTTAT GCTGAWkkCG GCGGGAACGG GCGGACATAT  
 51 TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG  
 101 TGATTGGCT GGCAGCAAG GATTCGATGG AAGAGCCTAT CGTGCCGCAA  
 151 TACGGCATA GCTTGGAAAC GCTGGCGATT AAAGGCCTGC GCGCCAACGG  
 201 CATCAAACGC AAACCTGATG TGCCGGTTAC TTTGTATCAA ACCGTCCGCG  
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC  
 301 GCGCGGCTTC TTACCTTCCC CGGCGGTTTG GCGGCGAAGC TATTAGCGT  
 351 GCGGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC  
 401 ACCTGTCGCG CTGGGCGAAG CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC  
 451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCGCGCGCG ATATTAGCAA  
 501 CTTGCCCGTG CTGCGGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA  
 551 TTTTGGTGGT CGGCGGCAGT TTGGGCGCGG ACGTTTGTAA CAAAACCGTA  
 601 CCGCATGCAT TGGCTTTGCT GCCCGACAAT GCGCGTCCGC ATATGTACCA  
 651 CCAATCGGGA CGGGGCAAGC TGGGCATCTT GCAGGCGnnn nnnnnnnnnn  
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CGGTTGACGA  
 801 TCACCAAACC GCCAACGCGC GTTTTATGCT GCAGGCGGAG GCGGGATTGC  
 851 TGTGCGCGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC  
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT  
 951 GGCAGTGCCG CACAGTGCGG ACGACGTGGC GGAAGCCGCG ATTGCGTGTG  
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep  
 1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVHVLGSK DSMEERIVPQ  
 51 YGIRLETLAI KGVNGNIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF  
 101 GGFVTFPGGL AAKLLXVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF  
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKT  
 201 PHALALLPDN ARPHMYHQSG RGKLGILQAX XXXXXXXXXXX XXXXXXXXXX  
 251 XAGLGALLVP YPHAVDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAELIG  
 301 GLNREKCLKW AENARTLALP HSADDDVAEAA IACAA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQYGIRLETLAI					
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVGRHHVHVLGSKDSMEERIVPQYGIRLETLAI					
	10 20 30 40 50 60					
	70	80	90	100	110	120
m087.pep	KGVNGNIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
	:					
g087	KGIRNGNIKRKLMLPFTLYKTVEAQRIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70 80 90 100 110 120					
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
g087	IHEQNAVAGLSNRHLSRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130 140 150 160 170 180					

279

	190	200	210	220	229	
m087.pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQA-----					
	:     : : : : : : :					
g087	RLKILVVGGSLGADVLNKTVPQALALLPEEVPRQMYHQSGRNKLGNLQADYDALGVKAEC					
	190	200	210	220	230	240
			230	240	250	
m087.pep	-----AGLGALLVPYPHAVDDHQTANARFMVQAE					
	: : : : : : :					
g087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHOTANARFMVQAE					
	250	260	270	280	290	300
	260	270	280	290	300	310
m087.pep	AGLLLPQTQLTAEKLAELGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	: : : : : : :					
g087	AGLLLPQTQLTAEKLAELGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACATAT
51  TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTCCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGACATCC TGCTCGAAAC GCTGGCGATT AAAGCGGTGC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TGCCGTTTAC TTTGTATCAA ACTGTCCGCG
251 AAGCGCAGCA GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
301 GCGGCGTTCG TTACCTTTCC CGGCGGTTTG GCGGCGAAGT TATTAGGCGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGTTTG TCCAACCGCC
401 ACCTGTCGCG CTGGGCGAAG CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCACT TTGGGCGCGG ACGTTTGA CAAAACCGTA
601 CCGCAGGCAT TGGCTTTGCT GCCGACAAT GCGCGTCCGC AGATGTACCA
651 CCAATCGGGA CGGGGCAAGC TGGGCAGCTT GCAGGCGGAT TACGACGCGC
701 TGGGCGTGCA AGCGGAATGC GTGGAATTTA TTACCGATAT GGTGTCCGCC
751 TACCGCGATG CCGATTGGT GATTTGCCGT GCCGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG
901 GCGGGATTGC TGTGTCGCGA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 GATTCTCGGC GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG
1001 CCCGTACGTT GGCACGTCCG CACAGTGCGG ACGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRAR GHVIVLWLSK DSMEERIVPQ
51  YDILLETLAI KGVRGNGIKR KLMLPFTLYQ TVREAQQIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEONAVAGL SNRHLSRWAK RVLVAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQGREG RLKILVVGGS LGADVLNKTVP
201 PQALALLPDN ARPQMYHQS R3KLGSQAD YDALGVQAE VEFITDMVSA
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
301 AGLLLPQTQL TAEKLAELG GLNREKCLKW AENARTLALP HSADDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIVLWLSKDSMEERIVPQYGRILETLAI					
	: : : : : : :					
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVIVLWLSKDSMEERIVPQYDILLETLAI					
	10	20	30	40	50	60



280

	70	80	90	100	110	120
m087.pep	KGVNRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVNRNGIKRKLMLPFTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
m087.pep	130	140	150	160	170	180
	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180
m087.pep	190	200	210	220	230	240
	RLKILVVGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAEC					
	190	200	210	220	230	240
m087.pep		250	260	270	280	
	XX-----	XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE				
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
m087.pep	290	300	310	320	330	
	AGLLLPQTQLTAEKLAELGGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAELGGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

g088.seq

```

1  ATGTTTATAT GGCTCGCACA TTTCAGCAAC TGGTTAACCG GTCTGAATAT
51  TTTTCAATAC ACCACATTCC GCGCCGTTAT GCGCGCGTTG ACCGCTTGG
101 CGTTTTCCTT GATGTTCCGC CCGTGGACGA TACGCAGGCT GACCGCGCTC
151 AAATGCGGGC AGGCAGTGGC TACCGACGGC CCGCAAACCC ACCTCGTCAA
201 AAACGCGACG CCGACGATGG GCGGTTGCTT GATTCTGACC GCCATTACCG
251 TGTCCACCCT GTTGTGGGGC AACTGGGCGA ACCCGTATAT CTGGATTCTC
301 TTGGGCGTAC TGCTTGCCAC CCGTGGGCTC GGTTTTACG ACGACTGGCG
351 CAAAGTCGTT TATAAAGACC CCAACGGCGT GTCCGCCAAA TTCAAATGG
401 TGTGGCAGTC AAGCGTTGCC GTTatcgccG GTttggcaTT GTTTTACctt
451 GCcgcaAATT CCGCCAACAA TATTTTGATT GTCCGtthtT TCAAACAAT
501 CGCCCTGCCG CTGGGCGTGG TCGGCTTttt gGtggtgtTCT TACCTGACCA
551 TCGTCGGCAC ATCCAACGCC GTCAACCTCA CcgaCGGCTT GGACGGCCTT
601 GCCGCcttcc cgttcgtcct cgttgccgcC GGGCTCGCCA ttttcgctTA
651 CGTCAGCGGA CACTACCAAT TTTCCTCAATA CCTCCAGCTT CCCTATGTCTG
701 CCGGCGCGAA CGAAGTCGCT ATATTCTGCA CCGCATGTG CCGCGCGTGC
751 CTCGGATTTT TGTGGTTCAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTCGCGCGC CTGGCATTGG GTGCGCGCTC CGGTaccGtt gCCGTcaTcg
851 tCCGCCAAGA ATTTGTcttc gtcattatGG GCGGTCTGTT cgtcgtagaa
901 gccgtgTCCG TTATGCTTca tgteggCTGG TACAAGAAAA Ccaaaaaacg
951 CATCTTcCTg acgGcaccga ttcacacca ttaCCAactt cgtcgCTGga
1001 aagaaaaagca agtcgtcgtc CGTTtCTGGA TTAtTaccat cgtcggtggt
1051 tTgatagggtt tGagtacctt caAAattcgc ggaaactatg ccgTCCGAAC
1101 ACCTTCAGA CGGCATTGA ACGCGCAATA A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

g088.pep

```

1  MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMFG FWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSLILT AITVSTLLWG NWANPYIWIL
101 LGVLLATGAL GFYDDWRKVV YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL

```

281

201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC  
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE  
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV  
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

m088.seq

1 ATGTTTAT GGCTCGCACA TTTCAGCAnC TGGTTAACCG GTCTGAATnn  
 51 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 101 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 251 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 301 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 501 nnnnnnnnnn nnnGGCGTGG TCGGCTTTT GGTGTGTCT TACCTGACCA  
 551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT  
 601 GCGACCTTCC CCGTCGTCCT CGTTGCCGCC GGCCTCGCCA TCTTCGCCTA  
 651 TGCCAGCGGC CACTACAAT TTGCCAATA CCGCAATTA CCTTACGTG  
 701 CCGCGCAAAA CGAAGTGGTG ATTTCTGTA CCGCCATGTG CGGCGCGTGC  
 751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA  
 801 TGTCGGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGTC GCCGTTATCG  
 851 TCCGCCAAGA GTTTGTCCTC GTCATTATGG GCGGATTATT TGTCGTAGAA  
 901 GCCGATCCG TTATGCTTCA GGTGGCTGG TATAAGAAAA CCAAAAAACG  
 951 CATCTTCTG ATGCGGCCCA TCCATACCA CTACGAACAA AAAGGCTGGA  
 1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGA TTATTACCAT CGTCTGGTG  
 1051 TTGATCGGTT TGAGTACCCT CAAAATCCGC TGAACCTATG CCGTCTGAAC  
 1101 ATCTTTCAGA CGGCATTGA ACGCCAATA A

1 MFLWLAHFSN WLTGLNIFOY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL  
 51 KCGQAVRTDG POTHVKNGT PTMGSLILT AITVSTLLWG NWANPYIWL  
 101 LGVLLATGAL GFYDDWRKVY YKDPNGVSAK FKMVWQSSVA VIAGLALFYL  
 151 AANSANNILI VPFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL  
 201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC  
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE  
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV  
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ\*

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

m088.pep

1 MFLWLAHFSX WLTGLNXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX  
 51 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX  
 101 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX  
 151 XXXXXXXXXX XXXXXXXXXX XGVVGFLVLS YLTIVGTSNA VNLTDGLDGL  
 201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFCTAMCGAC  
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE  
 301 AVSVMLQVGW YKKTKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV  
 351 LIGLSTLKIR XTYAVXTSFR RHLNAQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/g088

			10	20	30
m088.pep			GVVGFLVLSYLTIVGTSNAVNLTGDLGDLA		
g088	IAGLALFYLAANSANNILIVPFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGDLA				
	150 160 170 180 190 200				

```

a088.seq
1  ATGTTTTTAT  GGCTCGCACA  TTTCAGCAAC  TGGTTAACCG  GTCTGAATAT
51  TTTTCAATAC  ACCACATTCC  CGCGCGCTCAT  GCGCGCGCTTG  ACCGCGCTTG
101 CGTTTTCCCT  GATGTTTCGG  CCGTGGACGA  TACGACAGGT  GACCGCGCTG
151 AAATGCGGGC  AGGCAGTGCG  TACCGACGGT  CCGCAAACCC  ACCTCGTCAA
201 AAACGGCACG  CCGAGTGGCG  GCGGTTTCGCT  GATTCTGACC  GCCATTACCG
251 TGTCCACCCT  GTTGTGGGGC  AACTGGGCAA  ACCCGTATAT  CTGGATTCTC
301 TTGGCGCTAT  TGCTCGCCAC  GGGCGCACTC  GGTTTTACG  AGCACTGGCG
351 CAAAGTCGTC  TATAAAGACC  CCAACGGCGT  GTCGCGCAA  TTCAAATGCG
401 TGTGGCAGTC  AAGCGTTGCC  ATTATGCGCG  GTTTGGCAT  GTTTTACCTT
451 GCCGCCAATT  CCGCCAACAA  TATTTTGATT  GTCCCGTCT  TCAAAACAA
501 CGCCCTGCGC  CTGGCGCTGG  TCGGCTTTT  GGTGTTGCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAATGCC  GTCACCTCA  CCGACGGCTT  GGACGGCCTT
601 GCGACCTTCC  CCGTCGTCT  CGTTGCCGCC  GGCTCGCCA  TCTTCGCGTA
651 TGCCAGCGGC  CACTCACAAT  TTGCCCAATA  CCTGCAATTA  CCTTACGTTG
701 CGGGCGCAAA  CGAAGTGGTG  ATTTTCTGTA  CCGCATATG  GCGCGCGTGC
751 CTCGGTTTCT  TGTGGTTTAA  CGCCTATCCC  GCGCAAGTCT  TTATGGGCGA
801 TGTGCGTGCA  TTGGCATTGG  GTGCGCGCT  CGGTACCGTC  GCGCTCATCG
851 TCCGCCAAGA  GTTTGTCTTC  GTCATTATGG  CGGGATTATT  TGTCGTAGAA
901 GCGGTATCCG  TTATTGCTTCA  GGTGCGCTGG  TATAAGAAAA  CAAAAAACG
951 CATCTTCTCG  ATGGCGCCCA  TCCATCACCA  CTACGAACAA  AAAGGCTGGA
1001 AAGAAACCCA  AGTCGTCGTC  CGCTTTTGA  TTATTACCAT  CGTCTTGGTG
1051 TTGATTCGGT  TGAGTACCCT  CAAATACCG  TGAACCTATG  CCGTCTGAAC
1101 ACCTTTCAGA  CGGCATTTGA  ACGCGCAATA  A

```

```

a088.pep
1  MFLWLAHFSN WLTGLNIFQY TTFRVMAALT TALAFSLMFG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTKGGSLALT AITVSTQLWG NWANPYIWL
101 LGVLLATGAL GFYDDWRKVV YMDGNSVSAK FKMVWQSSVA I1AGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTNSA VNLTDGLDGL
201 ATFFPVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AV1VRQEFVL V1MGGLFVVE
301 AVSVMLQVWG YKTKTKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV
351 LGLSTLKR *TYAV*TPFR R1LNAQ*

```

```

                150      160      170      180      190      200
m088.pep  XXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFLVLSYLTIVGTSNAVNLTDLGLDGLA
                |||
a088      IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTDLGLDGLA

```

283

	150	160	170	180	190	200
	210	220	230	240	250	260
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088.pep	QVEMGDVGALALGAALGTAVIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVEMGDVGALALGAALGTAVIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088.pep	APIHHHYEQKGWKETQVVVRFWIIITIVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIIITIVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

```

g089.seq
1  ATGCCGCCCA AAATCACGAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCGGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTTT TCCACACGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGGCA GCCATAACGT TGGCGCGGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTTCGT AGAAATCAAA TCTTCATTGC CTTGTTTAA ACAGCCCGTC
301 CCGCGTTCCA ACCAAAAATC GGCTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAAATCT CGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

```

g089.pep
1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKTCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

```

m089.seq
1  ATGCCGCCCA AAATCACKaw GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTTT TCCACGCGGT GCGGCAGGCC TTGGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwa
251 TGTCTTTCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

```

m089.pep
1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSI NTTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng)

from *N. gonorrhoeae*:

m089/g089

284

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	:       :       :       :       :					
g089	MPPKITKSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGKPKWVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPNGMSCVTIKSSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	:       :       :       :       :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSSLPCFKQPVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	:     :       :       :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

```

1  ATGCCGCTA AAATCACGAA GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCGGTCGCA CCGACGTTTCG TGCCTTTGCT GTCGTCGATG AACACCACGC
101 CATT TTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGAAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGGC AAACCGACGG CTTGCACAA
201 GGCAACGGCA GCCATCACGT TAGTGGCGTT GTGCAAGCCT TGCAGCGGAA
251 TATCTTTCGT GGCAATCAA TCTTCATTGC CTTGTTTCAG GCGACCTGTC
301 TCACGTTCGA ACCAAAATC GGCTTCGTAT TCCAACGAAA ACCATTTCAC
351 CTCGCGCCCG GCGCGCTTCA TCGCACGACA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC ACCGTCGCCA CGGAAAATCT TGGCTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

```

1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGRP*KV
51  LTCSSNASRG KPTASHKATA AITLVALCKP CSGISCVAIK SSLPCFRRPV
101 SRSNQKSASY SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	:       :       :       :       :					
a089	MPPKITKSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPKWVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPNGMSCVTIKSSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	:       :       :       :       :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSSLPCFRRPVSRNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	:       :       :       :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

```

1  ATGCGCGTAG TCGAGCAAAT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA

```

q090 . pep

1 MRVVEQIVVA VEMVFGNVHH RRRSRAQAFG VFQLEAGKLP HPHVRLFAFA  
51 LQFCLQDGR TDIARN DGIQP ALDAE IADQA GYRGFAVAAG NRNHLVAAAV  
101 HNVROOLDVA XHAXRRFA\*

m090.seq

1	ATGCGCATAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA
51	TGTTCAAGC	CGTCGCGCGA	GTCGAGCGCA	GGCTTTCG	GTTTTCCAGT
101	TGGAAGCTGG	AAAGCTCCAA	CACCCACAGC	TCCGCTTTT	TGCCTTCGCG
151	TCTGCCATTCC	GCCTCCAAAA	CCGCGTGC	GATATTGCC	GGCATAACGG
201	TATCCAGCCC	GCACTTGATA	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG
251	GTTTTGCCGT	TGCTGCGCGT	AATCGCAATT	ACCTTGTCGT	CCGCGCGGTT
301	CACAATGTCC	GCCAGCAATT	CGATGTGC	CAACACGCGT	.CCGCGGTTT
351	TGCTGTGA				

m090 . pep

1 MRIVEQVVVA VEMVFGNVQH RRRSRQAFG VFQLEAGKLQ HPHVRLPAPA  
51 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRRNYLVVPAV  
101 HNVROQEDVA OHAXRRFA\*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 090 shows 83.9% identity over a 118 aa overlap with a predicted ORF (ORF 090.ng) from *N. gonorrhoeae*:

m090/q090

	10	20	30	40	50	60
m090.pep	MRIVEQVVVAVEMVFGNVQHRRRSRTQA	FGVFQLEAGKLQHPHVLFAFALP	FRLQN	RRA		
	::   :		:   :			:: :
g090	MRVVEQIVVAVEMVFGNVHHRRRSRAQA	FGVFQLEAGKLPHPHVLFAFALQ	FCLQDGR	T		
	10	20	30	40	50	60
	70	80	90	100	110	119
m090.pep	DIARNNGIQPALDTEIADQARYRGFAVAAGNRNYLV	PVAVHNVRQQPDVAQHAXRRRFAX				
	: :	:	:	:	:	:
g090	DIARNNGIQPALDAEIDQAGYRGFAVAAGNRNHLVAAAVHNVRQQLDVAXHAXRRRFAX					
	70	80	90	100	110	

a090.seq

1	ATGCGCGTAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA
51	TGTTACGAC	TGTCGCCGCA	GTCGGCGCGA	GGCTTTCG	GTTCCTCAGT
101	TGGAACCTGG	AAAGCTCCAA	CACCCACACG	TCCGCTTTT	TGCCTTCGCG
151	CTGCAATTCC	GCCTCCAAAA	CGCGCGCGCC	GATATTGCC	CGGATAACGG
201	TATCCAGCCC	ACACTTGATG	CAGAGATAGC	CGACCAAGCT	CGTTACCGTG
251	GTTTTGCGGT	TGCTGCCGGT	AATCGCAATC	ACCTTGTCGC	CGCGCGCGTT
301	CACAATGTCC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	C. CGCGGTTT
351	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

## a090.pep

```

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
51 LQFRLQNRRA DIARDNGIQP TLDAEIAADQA RYRGFAVAAG NRNHLVAAAV
101 HNVRQQFDVA QHAXRRFA*

```

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAFG	VFQLEAGKLQ	HPHVRLFAFALP	FRLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAFG	VFQLETGKLQ	HPHVRLFAFALQ	FRLQNRRA

	70	80	90	100	110	119
m090.pep	DIARDNGIQPALDTEIADQ	ARYRGFAVAAGNRNYL	VVFAVHNVRQQFDVA	QHAXRRFAX		
a090	DIARDNGIQPTLDAEIAADQ	ARYRGFAVAAGNRNHLVAAAVHNVRQQFDVA	QHAXRRFAX			

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

## m090-1.seq

```

1 ATGACGGCGT TTGCATTTC GACGGCATCA CAAAGCCTTA AACGCTTCGA
51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC
151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
201 AGCCGTCCAA ATCGCGGGCG ATTGCGGCG CATCGACACC AATCAAGAAC
251 ACGCCTTTTG CCTTGCCTAC CAGTGCATCG CGCAGGGGCG TGAAGTCTTG
301 CCCTTTACCC ATGCCGCCCA AAATCACGAA GAGCGGATTT TGCAAACCGG
351 CAATCGCGGC GGCAGTCGCG CCGACATTTC TGCCTTTGCT GTCGTCGATA
401 AACACACGCG CGTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC
451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGGCGTT GTGCAGACCT
551 TGCAACGGAA TGTCTTGCCT GACAATCAAA TCTTCATTGC CTTGTTTCAG
601 GCGGCTGTG TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
651 ACCATTTTAC CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
701 TCCGCAATTA AAACCTGCAC GCCGTGCGCA CGGAAATCT TGGCTTTGGT
751 ATGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA
801 TGTTGAGCAC CGTCGCGGCA GTGCGGACGA GGCTTTGCGT GTTTTCCAGT
851 TGGAAAGCTG AAAGCTCCAA CACCCACAGC TCCGCTTTT TGCCTTCGCG
901 CTGCCATTCC GCCTCCAAA CCGCGTGCC GATATTGCCC GCGATAACGG
951 TATCCAGCCC GCACTTGATA CAGAGATAG CGACAGGCT CGTTACCGTG
1001 GTTTTGCCGT TGCTGCGGTT AATCGCAATT ACCTTGTCGT CCCGCGGTT
1051 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT CCGCGGTTTT
1101 GCTTGAACGC CTCAATATCC GCCTGCCGCT CGCTGATGCC GGGACTGAGA
1151 GCCAGAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA
1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCCGGCT
1251 TCAGCTCCGC ATCATACGCA GCAACCTCCG CGCCGTTTTT GCGCAGGTAG
1301 GCAATCATGG AAATACCGT ACCGCCGAGT CCGGCGACGA GGATTTTTTT
1351 GTTTTGAAAA GTCATTTTGG TTTGCTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

## m090-1.pep

```

1 MTAFAFQTAS QSLKRFDKHF RTVRVAFEH KARAGGAEQH NIACFGLGIC
51 RLNGFSQSGA VGHIAAAVQ IAADLRRIDT NQEHAFCLAY QCIAQGREVL
101 PFTAAQNHE ERILQTGNRG GSRADIRAF VVDKHHAVEL ADFHFAVRQA
151 LEGFDVFEQC FARQTDGLTQ SHGSHDVSGV VQTLQRNVL DNQIFIALFQ
201 AACLAFOPEI SFVFQRKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFG
251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNYLVVPAV
351 HNVRQQFDVA QHASAVLLER LNIRLELADA GTESQNIETV VQRIQTARV
401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVF AQVGNHGNTR TAESGDEDFV
451 VLKSHFGLS*

```





This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

```

a091.pep
  1 MEIPVPPSPA TRIFLFWKSF WFVLKQIILS RGCLILLKPL SDGIASCSIT
 51 RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

m091/a091 93.8% identity over a 96 aa overlap

              10      20      30      40      50      60
m091.pep    MEIPVPPSPATRIFLFEKSFWFVLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
              |||||
a091         MEIPVPPSPATRIFLFEKSFWFVLKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA
              10      20      30      40      50      60

              70      80      90      100
m091.pep    VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQIVLGLGYPLR
              |||||
a091         VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQIVLG
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

```

g092.seq
  1 ATGTTTTTIA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGC GC
 51 AAACGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCGGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCTG TGCCTCTACC GCCGTCAAGA AAGAAaatcc
351 CGAAGTtgtc gcTGCCTTGG AGCGGCAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGgcatcgc cattgccggT
451 ACGCACGCA AAACCACGAC CACCAGCCTG ACCGCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACCT AACGCCGAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTCCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGCAAAA
751 GCCTTTTTGT GTGTTGACAG CGAACACGTC CGCGCGATT TGCCTAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAAA AaggCTTGCT CGGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGAAAA acgtTTGGTG
1201 CtcgCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatGc GCTGGTACTG ACCGAAAGTTT
1301 AtgcgcgcgG CGAAGAGCCG GTTGCCGCGC CGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTACT GCGAAAatgt
1401 cgcgcACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Ggcgatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGatttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

```

g092.pep
  1 MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
 51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHTAEHV
101 NGADV VVAST AVKKNPEVV AALEROIPVI PRALMLAELM RFRDGLAIAAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```

```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTGTGCGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGTTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGGCG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATGTCCGCG
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGCAG
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGCGACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GCGTCGGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCCTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGCGGACCCCT TGCCGCCGCA CGCGCGCGCT ATCTGGAATA ACCTTTGGTA
1201 CTCGCCCTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTGGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCCG TGAAGAGCCG ATTGCCGCCG CCGATTCCCG CACTCTTGGC
1351 CCGGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAAACGT TTTGCAGGAC GCGGACATCG
1451 TGTGGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVNTNIHFVG
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

m092/g092

```

10 20 30 40 50 60
m092.pep MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVMSGIA

```

290

	10	20	30	40	50	60
g092	MFFISIRYIFVRKLCWANGQTFKITPLRKTQPERNIMMKNRVSNIHFGVIGGVGMSGIA					
m092.pep	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHATAEHVNGADVVTSTAVKKENPEVV					
g092	EVLHNLGFKVSGSDQARNAATEHLSSLGIQVYPGHATAEHVNGADVVTASTAVKKENPEVV					
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTSLTASILGAAGLDPTFVIGGKL					
g092	AALERQIPVIPRALMLAELMRFRDGIAGTHGKTTTSLTASILGAAGLDPTFVIGGKL					
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
g092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
g092	FIHRMPFYGKAFLCVDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
m092.pep	QMKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEV GASVEAIQKGLLGFEVGVRGFQKYG					
g092	QMKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEV GASVEAIQKGLLGFEVGVRGFQKYG					
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAQPHRYTRTRDLFEDFTK					
g092	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYPEKRLVLAQPHRYTRTRDLFEDFTK					
m092.pep	VLNTVDALVLTEVYAAGEEPIAADSRLARAIRVLGKLEPIYCENVADLPQMLNVLQD					
g092	VLNTVDALVLTEVYAAGEEPVAAADSRLARAIRVLGKLEPIYCENVADLPQMLNVLQD					
m092.pep	GDIVLNMGAGSINRVPAALLALSQIIX					
g092	GDDVLNMGAGSINRVPSALLELSQIIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 313>:

a092.seq

1	ATGTTTTTTT	TTTCAATCCG	CTATATATTT	GTCAGAAAAAC	TATGGCGCGC
51	AAACGGTCAG	CCCTTTAAAA	TACGCGCTTT	ACGATCGAA	AATCCGAGTT
101	AACGCAACAT	TATGATGAAA	TAATCGAGTA	CCAACATCCA	TTTGTCCGT
151	ATCGGCGGCG	TCGGCATGAG	CGGTATCGCC	GAAGTCTTGC	ACAATTGTTGG
201	TTTTAAAGTT	TCGGGTTCCG	ATCAGCGCGC	AAATGCCGCT	ACCGAGCAAT
251	TGGGCAACCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGC	AGAACACGTT

```
301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCCGCGC
551 GCACCAACGC CCGCTTGGGC AAAGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCAATCAGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAAA TGAAATTCAC CGTCCATGTT
901 TGAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CCGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGAACCGCGC CTCTTGTTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CCGCGACCCCT TCCGCGCGCA CGCGCGCGCT ATCCGAAAAA ACGTTTGTA
1201 CTGCGCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCGCGCCG TGAAGAGCCG ATTGCGCGCG CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTGCAGGAC GCGACATCG
1451 TGTGAATAT GGGTGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GAATTGTCGA AACAGATTTG A
```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

**a092 . pep**

```
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIH FVG
51 IGVGMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIATAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKL PNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP TAAADSRLA
451 PAIRVLCKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ELSKQI*
```

**m092/a092** 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092 . pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGI	GGVMSGIA				
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGI	GGVMSGIA				
	70	80	90	100	110	120
m092 . pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAV	KKENPEVV				
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAV	KKENPEVV				
	130	140	150	160	170	180
m092 . pep	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTTSLTASILGAAGLDPT	FVIGGKL				
a092	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTTSLTASILGAAGLDPT	FVIGGKL				
	190	200	210	220	230	240
m092 . pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHS	VEKLHQAFID				
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHS	VEKLHQAFID				

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	190	200	210	220	230	240
m092.pep	250	260	270	280	290	300
	FIHRMPFYGKAFLCIDSEHVRILPKVSKPYATYGLDDTADIYATDIENVGAQMKEFVHV					
a092	FIHRMPFYGKAFLCIDSEHVRILPKVSKPYATYGLDDTADIYATDIENVGAQMKEFVHV					
	250	260	270	280	290	300
m092.pep	310	320	330	340	350	360
	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
	310	320	330	340	350	360
m092.pep	370	380	390	400	410	420
	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLAQPHRYTRTRDLFEDFTK					
	370	380	390	400	410	420
m092.pep	430	440	450	460	470	480
	VLNTVDALVLTVEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLTVEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	430	440	450	460	470	480
m092.pep	490	500				
	GDIVLNMGAGSINRVPAALLALSQKIX					
a092	GDIVLNMGAGSINRVPAALLELSQKIX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

```

g093.seq
1  aTGCAGAATt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgcTGGACA GCgGTACCGC CATTtTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAC TGGGGCATT
251 CCTTACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTACCCGTTC CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTCGATGC CGTCGAAGAA AAATGGGGT
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggta
451 aAAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAaaCA
501 CCTTcagggg cgaAAtcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaaCCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTCGCGG CGCACAGGCA ATCGGTGCGG AAGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

```

g093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTIGE DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVG VV
151 KVKEKGRLKS VYEELKHLOG RNHCRTFYRR RRIFLRPER QRAARHTHP
201 RNRVLRLSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RTGNRCGLR
251 ARRFORYRR OTLSVGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```
1 ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51 ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCtAA GACGGGGCGG TTCAGGGTGC ATTGGAAC TGGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTTCG
351 CGTCCTGCAC GACGACACTG ATTCGATGC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTGCGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G
```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

```
m093.pep
1 MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51 ELKAQGFQTA FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRI FLPRPER QRAARHTHHS
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSR RAGNRCGR LR
251 ARRF PQRYRR QTL SVGNQHP ARYDEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKAQGFQTA					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKERGFQTA					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m093.pep	FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQALGLPVPEFAVLH					
g093	FNILHGTYGEDG AVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQALGLPVPEFAVLY					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m093.pep	DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR					
g093	DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV KVEKGR LKS VYEELKHLQGRNHCRTFYRR					
	130	140	150	160	170	180
	190 200 210 220 230 240					
m093.pep	RRI FLPRPERQRAARH THHSRNRVLR LRSQVQPRRHLSM SFGRFDRSRR KPDARTGGSR					
g093	RRI FLPRPERQRAARH THHSRNRVLR LRSQVQPRRHLSM SFGRFDRSRR KPDARTGGSR					
	190	200	210	220	230	240
	250 260 270					
m093.pep	RAGNRCGR LRARRFPQRYRR QTL SVGNQHP ARYDEPX					
g093	RTGNRCGR LRARRFPQRYRR QTL SVGNQHP ARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

## a093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAC TGGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT EGACAAATAC
301 CGCTGCAAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CSTCTGCAC GACGACACTG ATTTTCGATGC CGTCGAAGAA AAATTGGGCC
401 TSCCGATGTT TGTGAAACCG GCGGCCGAA GACGACGCGT AGGCGTGGA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCTG TGTGAACCG CAAAGGCCTG CCCGCATAC ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTCCGCG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

## a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEAGSSVGTV
151 KVKKGRLKS VYEELKHFOX RNHCRVYRR RRIFLPCVER QRPARHTHP
201 RDRVL*LRSQ VQPQRHLSM SFGSRDSRR KPDARTGGSR RAGNRCGRLR
251 ARRFPQRYRR QTLVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL	MGGFSSEREI	SLDSGTAILN	ALKSKGIDAY	AFDPKETPLS	ELKAQGFQTA
a093	MONFGKVAVL	MGGFSSEREI	SLDSGTAILN	ALKSKGIDAY	AFDPKETPLS	ELKAQGFQTA
	70	80	90	100	110	120
m093.pep	FNILHGTYGD	GAHQGALELL	LGIPYTGSGV	AASAIGMDKY	RCKLIWQALG	LPVPEFAVLH
a093	FNILHGTYGD	GAHQGALELL	LGIPYTGSGV	AASAIGMDKY	RCKLIWQALG	LPVPEFAVLH
	130	140	150	160	170	180
m093.pep	DDTDFDAVEE	KLGLPMFVKP	AAEGSSVGTV	KVKKGRLKS	VYEELKHLQ	RNHCRVYRR
a093	DDTDFDAVEE	KLGLPMFVKP	AAEGSSVGTV	KVKKGRLKS	VYEELKHLQ	RNHCRVYRR
	190	200	210	220	230	240
m093.pep	RRIFLPCVER	QRPARHTHP	RDRVLXLR	SQVQPQRHLS	MSFGSRDSRR	KPDARTGGSR
a093	RRIFLPCVER	QRPARHTHP	RDRVLXLR	SQVQPQRHLS	MSFGSRDSRR	KPDARTGGSR
	250	260	270			
m093.pep	RAGNRCGRLR	ARRFPQRYRR	QTLVGNQHP	PARYDEPX		
a093	RAGNRCGRLR	ARRFPQRYRR	QTLVGNQHP	PARYDRPX		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTAccggc aatggcgatg
151 cCGTCACGGA AGCGCATCAG CTCTGCCAGC ATCAAGGCGC GCGGAATAAC
201 GGGAAATTGC CGCTCCAACG CAgcgacaAC TTCGGgattT TCTTTCTTGA
251 CGGCGGTAGA GGCAACGACG ACATccgcAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

```
g094.pep
1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101 WPG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTA GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTCCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAAACGAC ACATCCGCAC CGTTAACGTG TTCGGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

```
m094.pep
1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRISSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

```
m094/g094

          10      20      30      40      50      60
m094.pep  MYSPLPKRALVPAALSLPPIITKVGSSPAAPRMEAVRLVVVVLPVPCVPAMAMPSRKRISSAN
          |||
g094       MYSPLPKRALVPAALSLPPIITKVGSSPAAPRMEAVRLVVVVLPVPCVPAMAMPSRKRISSAS
          10      20      30      40      50      60

          70      80      90      100
m094.pep  IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
          :|||
g094       IKARGITGICRSNAATTSGFSFLTAVEATTTSAPLTCSAVWPGX
          70      80      90      100
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```
a094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTCCCGGC AATGGCGATC
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAAACGAC ACATCCGCAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 326; ORF 094.a>:



a094.pep  
 1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM  
 51 PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV  
 101 WPG\*

m094/a094 100.0% identity over a 103 aa overlap

	10	20	30	40	50	60
m094.pep	MYSPLPKRALVPAALSLPPI	TKVGSSPAAPRMEAVRLVVV	VLPCVPAMAMPSRKRINSAN			
a094	MYSPLPKRALVPAALSLPPI	TKVGSSPAAPRMEAVRLVVV	VLPCVPAMAMPSRKRINSAN			
	10	20	30	40	50	60

	70	80	90	100
m094.pep	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX			
a094	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

g095.seq  
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTGTC GCGCCGACGT  
 51 TTTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA  
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC  
 151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA  
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG  
 251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA  
 301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTGCCC TTGCCCCAAG  
 351 CGGGCGTTGG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

g095.pep  
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV  
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK  
 101 EASDRRLRQR CIRLCPGRW CLRR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

m095.seq  
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTGTC GCGCCGACGT  
 51 TTTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA  
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC  
 151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA  
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG  
 251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG  
 301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTGCCC TTGCCCCAAG  
 351 CGGGCGTTAG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

m095.pep  
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV  
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK  
 101 DASDRRLRQR CIRLCPGRX CLRR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

	10	20	30	40	50	60
m095.pep	MSFHLNMDGEFHLRADVFDV	GGVDVGGIVQTVSSIRFAHF	GQNRADVFAVNTQKGF	AVEG		

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
1   ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGCTTC TCAACACTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
1   MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMFVDIGN DGHNRCQCRK
101 DASDRRLRQR CIRLCPSGRW CLRR*

```

m095/a095 96.0% identity in 124 aa overlap

```

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
a095      HTVDEIDKRLMQLLNTVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
1   ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGTGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGAtaat ggtgTCGTCT CGGttgtaCt

```

g096.pap

1 MAGHTGGQVD FQIEFAVGI FEEIDAAAF RTDCLCAANR QFAHQAFFGF  
51 GQIFRRTLIN GVVSVVLGFV VVKLGCDDV YAGQPFVQD GAGIFAAADK  
101 TFGNDFAPEG VSILRKRFSD GLFL\*

**m096.seq**

m096.pwp

m096/g096 96.0% identity in 124 aa overlap

a096.seq

a096.ppt

1 MAGHTGQGVDFQIEFAVGI FEEIDAHAAR RTDCLRAANR OFAHCAFFGF

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK  
101 PFGNDFAXES VSILRKRFSD GLFL\*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDCLRAANRQFAHQAFFGFGQIFRRTLIN				
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDCLRAANRQFAHQAFFGFGQIFRRTLIN				
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVKLGCNDVYAGQPFVQDGAGIFAAADKTFGND	FAXEGVSILRKRFSD				
a096	GVVAVVLGFVVIKLRGDDVYAGQAFVQHRAGIFAAADKPF	GNDFAXESVSILRKRFSD				
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

1	ATGGATATTT	CAAAACAAAC	ATTGCTGGAT	AGGGTTTTTA	ACCTGAAGGC
51	AAACGGTACG	ACGGTACGTA	CCGAGTTGAT	GGCGGGTTTG	ACGACCTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAATC	CCCTGATTTT	GGGCGAGACC
151	GGAATGGATA	TGGGGGCGGT	ATTCGTCGCT	ACCTGTATCG	CATCCGCCAT
201	CGGCTGTTTT	GTTCATGGGT	TTATCGGCAA	CTATCCGATT	GCGCTTGCCC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCCTT	GGCAGGTGGC	GTTGGGTGCG	GTGTTTCATT	CCGGTCTGAT
351	TTTCATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAATG	TCGATTGCCG	CCGGTATCGG	TTGTTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCGCG	TTGGGCGATA	TTTCATCAGC	CAGCGCACTG	TTGGCATTGT
551	TCGGTTTTGT	CATGGTGGTC	GTATTGGGGT	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTCTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAGTTT	CACGGCGTGG	TCGGCGAAGT	ACCGGGCATT	GCGCCGACCT
701	TTATGCAGAT	GGATTTTAAA	GGTCTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATTTGTTT	GACAGTACCG	GAACGCTGGT
801	CGGCGTATCC	CACCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TGGCGTGTCT	GATGTTCTCC	CCATTGGCGA	AAAGTGTGCC	GGTATTTGCC
1051	ACCGGCGCCG	CACTGCTTTA	TGTCGGCAGC	CAGATGCTCC	GCAGTGCAG
1101	GGACATTGAT	TGGGACGATA	TGACTGAAGC	CGCGCCCGCG	TTCTTGACCA
1151	TTGTCTTCAT	GCCGTTTACC	TATTCGATTG	CAGACGGCAT	CGCCTTCGGC
1201	TTTCATCAGC	ATGCCGTGGT	CAAACCTTTT	TGTCGCCGGA	CTGGGGACGT
1251	GCCGCCTATG	GTATGGGTTG	TTGCCGTATT	GTGGGCATTG	AAATTCTGGT
1301	ATTGGGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

1	MDISKQTLTD	RVFNKANGT	TVRTELMAGL	TTFLTMCYIV	IVNPLILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFIGNYPI	ALAPGMGLNA	YFTFAVVKGM
101	GVPMQVALGA	VFISGLIFIL	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL	LALFGFVMVV	VLGYFRVQGA
201	IIITILTITV	IASLMGLNEF	HGVVGEVPGI	APTQMMDFK	GLFTVSMVS
251	IFVFPLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSTTPYV	ESAAGVSAGG	RTGLTAVTVG	VLMLACLMPF	PLAKSVPVFA
351	TAPALLYVGT	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG

This corresponds to the amino acid sequence <SEQ ID 342; ORF 097>:

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng)

from *N. gonorrhoeae*:

[illegible]

301

m097.pep	FSFFKVR	EMLVNAL	PMGLKMS	IAAGIGL	FLALISL	KGAGII	VANPATL	VGLGDI	HQPSAL
g097	FSFFKVR	EMLVNAL	PMGLKMS	IAAGIGL	FLALISL	KGAGII	VANPATL	VGLGDI	HQPSAL
		130	140	150	160	170	180		
m097.pep	LALFGF	AMVVVL	GHFRVQ	GAIIIT	ILTITV	IASLMGL	NEFHGI	GEVPSI	APTQMDFE
g097	LALFGF	AMVVVL	GHFRVQ	GAIIIT	ILTITV	IASLMGL	NEFHGI	GEVPSI	APTQMDFE
		190	200	210	220	230	240		
m097.pep	GLFTVS	MVSVI	FVFFLV	DLFDST	GTTLVG	ISHRAG	LLVDGK	LRLKR	ALLADST
g097	GLFTVS	MVSVI	FVFFLV	DLFDST	GTTLVG	ISHRAG	LLVDGK	LRLKR	ALLADST
		250	260	270	280	290	300		
m097.pep	LGTSS	TPYVES	AAGVS	AGGRT	GLTAVT	VGVLML	ACL	MFSP	LAKSV
g097	LGTSS	TPYVES	AAGVS	AGGRT	GLTAVT	VGVLML	ACL	MFSP	LAKSV
		310	320	330	340	350	360		
m097.pep	QMLRS	ARDID	WDDMT	EAA	PAFLT	IVFMP	PFTYS	ADG	IAFGF
g097	QMLRS	ARDID	WDDMT	EAA	PAFLT	IVFMP	PFTYS	ADG	IAFGF
		370	380	390	400	410	420		
m097.pep	VWIVAV	LWALK	FWYL	LGX					
g097	VWVAV	LWALK	FWYL	LGX					
		430							

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

```

1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AACCGGTACG ACGGTGCGTA CCGAGTTGAT GCGGGGTTTG ACAACTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCTGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCTGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GCGGTGCCCT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTCATCCTG TTCAGCTTTT TTAAAGTCAG GGAATGCTG GTCAACGCAC
401 TGCCTATGGG TTTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCCGC TTGGGCGATA TTCATCAGCC GTCCCGCTTG TTGGCACTGT
551 TCGGTTTTGC CATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTTTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAATTT CACGGCATCA TCGGCGAAGT GCCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTAAA GGGTTGTTTA CCGTCAGCAT GGTGAGCGTG
751 ATTTTCGTCT TTTTCTAGT CGATCTGTTT GACAGTACCG GAACACTGGT
801 CGGTGTATCG CATCGTCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CTATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTCAACCAC GCCTTATGTG GAAAGTCCG GGGCGGTATC
951 GCGAGCGCGG CGGACAGGTC TGACGCGCGT TACCGTCCG GTATTGATGC
1001 TGGCTGCTCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTCCGCACG CAGATGCTCC GCAGTGCGAG
1101 GGACATCGAT TGGGACGATA TGACGGAAGC CGCACCCGCA TTCCTGACCA
1151 TTGTCTTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCCGCGCA CCAAGACGCT
1251 TCCGCCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT

```

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence &lt;SEQ ID 344; ORF 097.a&gt;:

a097.pep

```
1  MDTSKQTLLD GIFKLGKANGT TVRTELMAGL TTFLTMCIYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHERVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VIMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*
```

m097/a097 99.3% identity in 436 aa overlap

m097.pep	10	20	30	40	50	60
	MDTSKQTLLD	GIFKLGKANGT	TVRTELMAGL	TTFLTMCIYIV	IVNPLILGET	GMDMGAVFVA
a097	MDTSKQTLLD	GIFKLGKANGT	TVRTELMAGL	TTFLTMCIYIV	IVNPLILGET	GMDMGAVFVA
m097.pep	70	80	90	100	110	120
	TCIASAIGCF	VMGFVGNYP	I ALAPGMGLNA	YFTFAVVKGM	GVPWQVALGA	VFISGLIFIL
a097	TCIASAIGCF	VMGFVGNYP	I ALAPGMGLNA	YFTFAVVKGM	GVPWQVALGA	VFISGLIFIL
m097.pep	130	140	150	160	170	180
	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL
a097	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL
m097.pep	190	200	210	220	230	240
	LALFGFAMVV	VLGHERVQGA	IIITILTITV	IASLMGLNEF	HGIIGEVPSI	APTFMQMDFE
a097	LALFGFAMVV	VLGHERVQGA	IIITILTITV	IASLMGLNEF	HGIIGEVPSI	APTFMQMDFK
m097.pep	250	260	270	280	290	300
	GLFTVSMVSV	IFVFFLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRKRALLA	DSTAIVAGAA
a097	GLFTVSMVSV	IFVFFLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRKRALLA	DSTAIVAGAA
m097.pep	310	320	330	340	350	360
	LGTSSTTPYV	ESAAGVSAGG	RTGLTAVTVG	VIMLACLMFS	PLAKSVPAFA	TAPALLYVGT
a097	LGTSSTTPYV	ESAAGVSAGG	RTGLTAVTVG	VIMLACLMFS	PLAKSVPAFA	TAPALLYVGT
m097.pep	370	380	390	400	410	420
	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG	FISYAVVKLL	CRRTKDVPPM
a097	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG	FISYAVVKLL	CRRTKDVPPM
m097.pep	430					
	VWIVAVLWAL	KFWYLGX				
a097	VWIVAVLWAL	KFWYLGX				

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng)

from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

a098.seq

```
1  ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51 TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCGAG GCTGGCGATC
```



304

```

101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTTAA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GGCGACTTCT TCAAACCTCGC
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVR1 LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

```

              10      20      30      40      50      60
m098.pep      MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA
              |||||
a098           MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA
              10      20      30      40      50      60

              70      80      90      100     110     120
m098.pep      GTHYVHRMGMCRAQFQNFNHTDRQAAHGFEFGFISGQLEFVGQMAVNQQVGDFFKLAFLC
              |||||
a098           GTHYVHRMGMCRAQFQNFNHTDRQAAHGFEFGFISGQLEFVGQMAVNQQVGDFFKLAFLC
              70      80      90      100     110     120

m098.pep      QIRMSX
              |||||
a098           QIRMSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGG
101 CACTGACCGA ATTCTTGCGT AAAGAGCGCG TGGTCGGGGC GTTGTGCGAA
151 TTTTTCGGCG AGGCGCGGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGAAACCTA CGCCAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCCGTTTATC CGCGCTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTGG CCGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CTTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTTGTCG CGCCGCGACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTGAAAGAA GCAGGCTTGT
701 TGCCCCGAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcG CGCGCTcgac CCGAAAATCC AACAAGAAAT
801 CATCGACCGC GATttgtacg cCACCGCCGT ATGTTCAGGC AACCAGCACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTTCT CGCTTCGCCT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCCGTCC GCCCTATTGG GAAGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCGGC GATTTTGGCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCCA TTTTGCCCGG cagTGCcgca ggtgaATATT

```

```

1301 TGGCGAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GGCGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTCACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVE
51 FPEGARSLIS IGDRTISNM TPEFGATAAM FAIDAQTI DY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEEPSDQOM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSFPAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQEIIDR DLYATAVLGS NRNFDGRIHP YAKQAFASP
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEVVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRPPYEW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGO GSSRDWAAGK VRLAGVEAIA AEGFERIHRT
551 NLIGMGVLP LQKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEALVY EAGVLRFA QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGGCAGG CGGCGATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGCG GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCGGTTTATC CTCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCGAAC
451 GCCGATTGCG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCGCAGCGCT CGGTATCATC CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTGTACG CCACCGCCGT ATTATCAGGC AACCGCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCCA TTTTGGCCGT CAGTGCCGCA GCGGAGTATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGCGC CAAGGCTCGT
1451 TGCCCCGCGT CGAACCCGAA GGCGAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

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1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATAC TG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGGCG GCGTGTGCA ACGGTTTGCA CAGGATTTT
1901 TGAAGGGAA CGCGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
51  FFGEGARSLs IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEESPdGQM PDGSVIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWKSSFAPG SKVAEIYLKE AGLLPEMEKL GFGIVAFACt
251 TCNGMSGALD PKIQKEIIDR DLYATAVLsG NRNFDGRIHP YAKQAFLASp
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351 PQQFRDYYVP MFDTGTAQKA PSPLYDWRPM STYIRR?PYW EGALAGERTL
401 RGMRLAILP DNITDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501 ETYMNKQPL IIAAGADYQ GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551 NLIGMGVLP LQPKDPTNRHT LQLDGTETD VVGERTPRCD LTLVIHRKNG
601 ETVEVPVTC LDTAEVLVY EAGGVLRFA QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLs					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLs					
	10	20	30	40	50	60
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDY LKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDY LKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGSVIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGAIVIAAI					
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGSVIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGAIVIAAI					
	130	140	150	160	170	180
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
m099.pep	GFGIVAFACtTCNGMSGALDPKIQKEIIDRDLYATAVLsGNRNFdGRIHPYAKQAFLASp					
g099	GFGIVAFACtTCNGMSGALDPKIQKEIIDRDLYATAVLsGNRNFdGRIHPYAKQAFLASp					
	250	260	270	280	290	300
m099.pep	GFGIVAFACtTCNGMSGALDPKIQKEIIDRDLYATAVLsGNRNFdGRIHPYAKQAFLASp					
g099	GFGIVAFACtTCNGMSGALDPKIQKEIIDRDLYATAVLsGNRNFdGRIHPYAKQAFLASp					
	250	260	270	280	290	300
	310	320	330	340	350	360

307

m099.pep	PLVVAYALAGSIRFDIENEVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVIYP
g099	PLVVAYALAGSIRFDIENEVLGVADGREIRLKDIWPTDEEIDAIVA EYVKPQQFRDIYIP
	310 320 330 340 350 360
m099.pep	370 380 390 400 410 420
	MFDTGTAQKAPSPLYDWRPMSTYIRPPYWEALAGERTLRGMRPLAILPDNITTDHLSP
g099	MSDTGTAQKAPSPLYDWRPMSTYIRPPYWEALAGERTLRGMRPPAILPDNITTDHISP
	370 380 390 400 410 420
m099.pep	430 440 450 460 470 480
	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
	430 440 450 460 470 480
m099.pep	490 500 510 520 530 540
	QGSFARVEPEGETMRMWEAIETYMNKQPLIIAGADYQGSSRDWAAKGVRLAGVEAIV
g099	QGSLARVEPEGQTMRMWEAIETYMNKQPLIIAGADYQGSSRDWAAKGVRLAGVEAIA
	490 500 510 520 530 540
m099.pep	550 560 570 580 590 600
	AEGFERIHRTNLIGMGVLPLOPKPDTNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHRTNLIGMGVLPLOPKPGTNRHTLQLDGTETYDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099.pep	610 620 630 640
	ETVEVPVTCCLDTAEVLVYEAGGVLRFAQDFLEGNAAX
g099	ETVEVPVTCRPDTAEALVYEAGGVLRFAQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099.seq

```

1  ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51  GCTGAACGGC AAACGGAAGG CGGGCATTAC GCGCAGCGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGTCGCGGC GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCAGCGCGC TTTGCGACC
451 GCCGATTTGG CCGGCAAAGG CTTGGCTAAA CCTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCCTGTA
551 CCAATACTTC CAATCCGCGC AACGTTGTCG CGCCCGCGCT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GCAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCAGATCTGC
701 TGCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTTGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAGCGG CGCGCTGGAT CCGAAAATCC AGAAAAGAAAT
801 CATCGACCGC GATTTGTACG CCACCGCCGT ATTGTCAGGC AACCGCAACT
851 TTGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCTT CGCTTCGCCT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGCGTTG CAGACGGCAA AGAAATCCGC CTGAAAGACA
1001 TTTGGCCTAC CGATGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAAT TTCGCGACGT TTATATCCCG ATGTTGACGA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGTCCAATG TCTACCTATA
1151 TCCGCCGCCC ACCTTACTGG GAAGGCGCAC TGGCAGGGGA ACGCACATTA
1201 AGCGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA

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1251 TCTCTCGCCA TCCAATGCGA TTTTGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCTT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTCCGC
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```

1 MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRTISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNP HARFAT
151 ADLAGKGLAK PYEEPSDQGM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK FWVKSSFAPG SKVAEIIYLKE ADLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAF LASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVIYP MFDGTGTAQKA PSPLYDWRPM STYIRRPYVW FGALAGERTI
401 SGMRLAILP DNITTDHLSN SNAILASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNRRQPL IIIAGADYGO GSSRDWAAGK VRLAGVEAIV AEGFERIHR
551 NLIGMGVLP LQFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLRFA QDFLEGNA*

```

m099/a099 97.5% identity in 639 aa overlap

m099.pep	10	20	30	40	50	60
	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
a099	MLGRASMMRLPDIVGVELNGKRKAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
	AVYPRVLKFDLSSVTRNMAGPSNP HARFATADLAKGLAKPYEEPSDQMPDGSVIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNP HARFATADLAGKGLAKPYEEPSDQMPDGAIIAAI					
	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRKPWKSSFAPGSKVAEIIYLKEADLLPEMEKL					
	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNENFDGRIHPYAKQAF LASP					
a099	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNENFDGRIHPYAKQAF LASP					
	250	260	270	280	290	300
m099.pep	310	320	330	340	350	360
	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVIYP					

q102.seq

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.ppt

310

```

1  MSAKTPSLFG  GAMIIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLGGMVLTF  IWATGGLVAD  AKPSVLFDTQ  APVGTGYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQLSVLNETL  SKFAQTGDM  KILSLFPYMA  IATSFGLVTL
301 GLFDNIADIF  KWNDSMSGRG  TKTVALNFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGGWLWMLV  FLFGIANIAA
401 QVLSQMEVLP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGC  GGC GCGATGA  TTATCGCCGG
51  CACGGTCATC  GCGCGAGGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCCACGG  GCCTGATGAT  TTTGGAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGGCGGCGA  CCTGACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGGCAG  GTTTCACCTA  CCGTCGGACA  ACTCGTCTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTCGACCG  CTTACCCGGC
451 GTCCTTATCG  GCGGCATGGT  ATTGACCTTT  ATTTGGGCGG  CCGCGGGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCCTCTT  CGATACCCAA  GCGCCGCGCG
551 GCACAAACTA  CTGGATTAC  GCGGCCACCG  CCCTGCCCGT  CTGCGCTCGT
601 TCCTTCGGCT  TCCACGGCAA  CGTCTCAGC  CTGCTCAAAT  ACTTTAAGG
651 CGACGCGCCC  AAAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCCTCTGG  CAAACCGCCA  TCCAAGGCAA  CCTGCCGCGC
751 AACGAGTTCG  CCCCCTCAT  CGCCGCCGAA  GGGCAAGTCT  CCGTCCTCAT
801 CGAAACCCTG  TCCAAATTCG  CCCAAACCGG  CAATATGGAC  AAAATATTGT
851 CCCTGTTTTC  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCGCAAC  AAAACCGCGC  CGCTGACCTT  CCTGCCGCCC  CTGATTTCCT
1001 GCTGCTCTT  CCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 GCGGCAACCG  TCTGGACAGG  CATCATCCCC  GCCATGTGTC  TCTACCGTTC
1101 GCGCAAAAAA  TTCGGCGCAG  GCAAAACCTA  TAAAGTTTAC  GCGCGCTTGT
1151 GGTGTATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTAGGCC  AAATGGAAC  CGTCCCGTA  TTTAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLTYWFSM
51  LSSGLMILEV  NTHYPHASF  DTMVKDLLGR  GWNIIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLIGGMVLTF  IWAAGGLIAD  AKPSVLFDTQ  APAGTNYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWGT  LIALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  QQSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSFGLVTL
301 GLFDYIADIF  KWNDSISGRT  KTAALTFLLP  LISCLLFTG  FVTAIGYVGL
351 AATVWTGII  P  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAQ
401 VLSQMEVLPV  PKG*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFEGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLTYWFSMLSSGLMILEV					
g102	MSAKTPSLFEGGAMIIAGKVIAGMFPNPTANLGDGLIGSLIVLLTYWFPFSSGALMILEV					
	10	20	30	40	50	60
m102.pep	NTHYPHASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	70	80	90	100	110	120
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
g102	ISLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAATGGLVADAKPSVLFDTQ					
	130	140	150	160	170	180
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					
g102	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					
	190	200	210	220	230	240

a102.seq

1	ATGCCACCA	AAACCCCTTC	ACTGTTCCGGC	GGCGCATGA	TTATCGCCGG
51	CACGNTCATC	GGCGCAGGTA	TGCTCGCCAA	CCCACCCGCC	ACATCCGGCG
101	TATGGTTTAC	CGGCTCGCTG	GCCGTGTTGC	TGTACACCTG	GTTTTCATGT
151	CTCTCCAGCG	GCGTATGAT	TTTGGAACT	AACACCCACT	ACCCCCACGG
201	CGCGANCTTC	GACACCATGG	TAAAGACCT	GCTCGGACGG	AGCTGGAACA
251	TCATCAACGG	CATCCCGGTC	GCCTTCGTTT	TATACCTGCT	TACTTACGCT
301	TATATCTTCG	TCGGCGCGCA	CCTGACCGCC	AAAGGCTTAG	CGACGCGCGC
351	AGGCGGCAAT	GTTTCACTCA	CCGTCCGACA	ACTGCTCTTC	TCGGGCATTC
401	TCGCCTTTTG	CGTATGGGCA	TCCGCACGCT	TGGTCGACCG	ATTCAACAGC
451	GATCTCATCG	CGCGCATGTT	ATTAACCTTT	ATTTGGGCAA	CCGGCGGCCT
501	GTTTCGCGAT	GCACAACTGC	CCGCTCTCTT	CGACACCCAA	CGCCCTACCG
551	GCACCAACTA	CTGGATTAT	GTCGCCACCG	CCCTGCCCGT	CTGCCTTGCG
601	TCATTCGGTT	TCCACGGCAA	CGTCTCCAGC	CTGCTCAAT	ACTTTAAAGG
651	CGACGCGGCC	AAAGTGCTCA	AATCCCATCTG	GACGGGCACA	CTGATTTGCGC
701	TGGTAATTFA	CGTCTCTGG	CAAACCGCCA	TCCAANGCAA	CTGCGCGCGC
751	AACGAGTTTCG	CCCCCGTGAT	TGCCGCCGAA	GGGCAAGTCT	CCGTCNTGAT
801	TGAAACCCGT	TCCAAATTTCG	CCCAAACCGG	CAATATGGAC	AAAATATTGT
851	CCCTGTTTTC	CTATATGGCG	ATGCCCACTC	CGTTTTTAGG	CGTAACGCTC
901	GGACCTCTTCG	ACTACATCGC	CGACATCTTC	AAATGGAACG	ACAGCGTGTC
951	CGGCCGCACC	AAACCCGCGC	CGCTGACCTT	CCTGCCGCCT	NTAATTTCCT
1001	GCTGTGCTCT	CCCCACCGCG	TTTGTATCCG	CCATCGGNTA	CGTCGGGCTC
1051	CGCGCAACCG	TCTGGACAGG	CATCATCCCC	GCGATGCTGC	TNTACCGTTC
1101	GCGCAAAAAA	TTCGGCGCAG	GCAAAACCTA	TAAAGTTTAC	GGCGGCTTGT
1151	GGCTGATGGT	TGGGTCTTTC	CTTTTCGGCA	TCNTCAACAT	CGCCGCACAN
1201	GTATTGAGCC	AAATGGAATC	CGTCCCCGTA	TTTAAAGGAT	AA
1202					

**a102.pep**

1	MPTKTPSLFG	GAMIIAGTXI	GAGMLANPTA	TSGVWFTGSL	AVLLYTWFMS
51	LSSGLMILEV	NTHYPHGAXF	DTMVKDLLGR	SWNIINGIAV	AFVLYLLTYA
101	YIFVGGDLTA	KGLGSLAGLN	VSLTVGQVDF	FGILAFVCWA	SARLVDRFES
151	VLIGMGVLT	IWATGSLIAD	AKLPVPLEDT	APTGTNYWIY	VATLVPCLCA
201	SPFGHGNVSS	LLKYFKGDAP	KVAKSIWTGT	LIALVIYVLW	QTAIQXNLPR
251	NEFAPVIAAE	GQVSXKIETL	SKFAQTGNMD	KILSLFSYMA	IATSFLGVTL
301	GLFDYIADIF	KWNDSVSGRT	KTAALTFLPP	XISCLLFPTG	FVTAIGYVGL
351	AATVWVTGIIP	AMLLYRSRKK	FGAGKTYKVY	GGLWLMVWVF	LFGIXNIAAX
401	VLSEMELVPV	FKG*			

m102 / a102 95.9% identity in 413 aa overlap



m102.pep	10	20	30	40	50	60
	MPNKTPSLFGGAMI IAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWF SMLSSGLMILEV					
a102	MPTKTPSLFGGAMI IAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWF SMLSSGLMILEV					
m102.pep	70	80	90	100	110	120
	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGN					
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFVCWASARLVDRFTSVLIGGMVLTFFIWAATGGLIADAKLPVLFDTQ					
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVL IETLSKFAQTGNMDKILSLSYMAIATSFLGVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSX IETLSKFAQTGNMDKILSLSYMAIATSFLGVTL					
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDSISGRITKTAALTFLPPLISCLLFTGFTVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDSVSGRITKTAALTFLPPXISCLLFTGFTVTAIGYVGLAATVWTGIIP					
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGI VNI AAQVLSQME LVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGI XNIAAXVLSQME LVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

```

1   Atgtccgcag aaaCATACac acAAAtcggc tGGgtaggct taggGcaaatt
51  gGgtctgcct atgGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCcgC CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATt GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAACTCG TCTTGAATC GCTCTTAGG ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAAACAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CTTGCCTTGT
701 CACTCAAACA CGCTTCCAAA GacctTAACC TCGccgtcAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 364; ORF 105.ng>:

```
g105.pep
1  MSAETTYQIG WVGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVYGSTAELV RACPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLILFGG SEAVLNPLQK
151 IFSLVGKKTFF HFGDVGKGSF AKLVLSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GYVLKLAEH
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

```
m105.seq
1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGaTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAm ATCATCGTCA ACATGAGCAC CATCTCCCGG
301 ACCGAAAaGC TCGCCGTCAA AGCACTTGTC GAAGCGCAGm GaCAGTTTGC
351 CGAAGCACCC GTTTCGGAT CGGTCGGGCC CGCCACCAAC GGCACGCTGC
401 TGATCTGTGT CGGCGGCAGC GAACCGtTT AAACCCGCTG CAAAAATAT
451 TTTCCCTCGT CGGCAAAAA ACCTTCCATT TCGGCGATGT CGGCAAAGGT
501 TCGGGCGCGA AACTCGTCTT GAACTCGCTC TTGGGCATT TCGGCGAaCG
551 TAcAGCGAAs GmTgCTGATG GCGCGGCAGT TCGGCATCGA TACCGACACC
601 ATCGTCGAAG CCATCGGsGA CTCGGCAATG GACTCGCCCA TGTTCCAAAC
651 CAAAAAATCC CTGTGGGCAA ACCGCGAATT CCCGmCCGmC TTCGCCCTCA
701 AACACGCCTC CAAAGACCTC AACCTCGCCG TCAAAGAGCT TGAACAGGCA
751 GGCAACACCC TGCCCGCCGT CGAAACCGTT GCTGCCAGCT ACCGCAAAGC
801 AGTCGAAGCC GGCTACGGGA CACAGGACGT TTCCGGCGTT TACCTGAAAC
851 TGGCAGAACA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

```
m105.pep
1  MSANEYAQIG WIGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVYGNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGX IIVNMSTISP
101 TEKLAVKALV EAQRQFAEAP VSGSVGPATN GTLLILFGGS EPFXTRCKKY
151 FPSSAKKPSI SAMSAKVRAR NSSXTRSWAF SANVQRXXLM ARQFGIDTDT
201 IVEAIGDSAM DSPMFQTKS LWANREFPXX FALKHASKDL NLAVKELEQA
251 GNTLPAVETV AASYRKAVEA GYGTQDVSGV YLKLAEH
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

```
m105/g105

          10      20      30      40      50      60
g105.pep  MSAETTYQIGWVGLGQMGLPMVTRLLDGGIEGVYNRSPDKTAPISAKGAKVYGSTAELV
          |||:  |||:  |||:  |||:  |||:  |||:
m105      MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEGVYNRSPDKTAPISAKGAKVYGNTAELV
          10      20      30      40      50      60

          70      80      90     100     110     120
g105.pep  RACPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
          |  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
m105      RDYPVIFLMVSDYAAVCDILNGVRDGLAGXIIIVNMSTISPTENLAVKALVEAQR-QFAEA
          70      80      90     100     110

          130     140     150     160     170     180
g105.pep  PVSGSVGPATNGTLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSAGKLVLSLLG
          |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
m105      PVSGSVGPATNGTLILFGGSEPFXTCKKYFPSSAKKP-SISAMSAKVRARNSSXTRSW
          120     130     140     150     160     170
```

a105.seq

1	ATGTCGCCAA	ACGAATACAC	ACAAATCGGC	TGGATAGGCT	TAGGGCAAAT
51	GGGTCTGCCT	ATGGTAACGC	GGCTCTTGGA	CGGCGGCATC	SAAGTCGCGC
101	TATACATACC	CTCGCCCGAC	AAAACCTGCC	CCATCTCCGC	CAAAGGCGCA
151	AAAGTTTACG	GCAACACCGC	CGAACTCGTC	CGCGACTATC	CCGTCAATTT
201	CCTGATGGTT	TCCGACTATG	CGCGCGTGTG	CGACATCTCG	AACGGAGTCC
251	GCGACGGATT	GGCCGGCAAA	ATCATCGTCA	ACATGAGCAC	CATCTCCCGC
301	ACCGAAACCC	TCCCGCTCAA	AGCACTTGTC	GAAGCCGCAG	GCGGCACAGT
351	TGCCGAAGCA	CCCGTTTCCG	GATCGGTCTG	GCGCCGCACC	AACGGCAGCC
401	TGCTGATTCT	GTTTCGCGCG	AGCGAAGCCG	TTTTAAACCC	CTGCAAAAAA
451	ATATTTTCCC	TCGTGGGCAA	AAAAACCTTC	CATTTTCGGC	ATGTCTGGCA
501	AGGTTTCGGC	GCGAAACTCG	TCTTGAACTC	GCTCTTGGGC	ATTTTCGGCG
551	AAGCGTACAG	ACGAGCGATG	CTGATGGCCG	GGCAGTTCCG	CATCGATACC
601	GACACCATCG	TCGAAGCCAT	CGGCGGCTCG	GCAATTGGAT	CGCCCATGTT
651	CCAAACCAAA	AAATCCCTGT	GGGCAAAACG	CGAATTCCCA	CCGCCCTTCG
701	CCCTCAAACA	CGCCTCCAAA	GACCTCAACC	TCGCCGTCAA	AGAGCTTGAA
751	CAGGCAGGCA	ACACCTTGCC	CGCGTCGAA	ACGTTGCTG	CCAAGTACCG
801	CAAAGCAGTC	GAAGCCGGCT	ACGGCGAACA	GGACGTTTCC	GGCGTTTACC
851	TGAAATTGGC	AGAACACTGA			

a105.pep

1	MSANEYTOIG	WIGLGQMGLP	MVIRLLDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYQNTAELV	RDYPIVFLMV	SDYAADVCDIL	NGVRDLGLAK	IIVNMSTISP
101	TENLAVKALV	EAAQGVGFAEA	PVSQVSGVPTA	NGTLILILEGG	SEAMNLPLOK
151	IFSLVGKKTFF	HFGDVGKGS	AKLVLSNLLG	IFGEAYSEAM	LMARQFGIDT
201	DTIVEAIGGS	AMDSPMFQTK	KSLWANREFP	PAPAFKHAHK	DLNLAVKELE
251	OAGNTLPAVE	TVAASYRKAV	EAGYGEQDVS	GVLVKLAE*	

**m105/a105** 96.5% identity in 289 aa overlap

		10	20	30	40	50	60	
m105.pep		MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVDNRSPDKTAPISAKGAKVYGN					TAE LV	
a105		MSANEYTQIGWIGLGQMGLPMVTRLLDGGIEVGVDNRSPDKTAPISAKGAKVYGN					TAE LV	
		10	20	30	40	50	60	
		70	80	90	100	110	119	
m105.pep		RDYPVIFLMVS DYAA VCDILNGVRDGLAGKIIVNMSTISP					TENLAVKALVEAAG-QFAEA	
a105		RDYPVIFLMVS DYAA VCDILNGVRDGLAGKIIVNMSTISP					TENLAVKALVEAAGGQFAEA	
		70	80	90	100	110	120	
		120	130	140	150	160	170	179
m105.pep		PVSGSVGPATNGTLLI LFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLV					LNS LLG	
a105		PVSGSVGPATNGTLLI LFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLV					LNS LLG	
		130	140	150	160	170	180	
		180	190	200	210	220	230	

q105-1.seq

1	ATGTC	CCG	CAG	AAAC	TACAC	ACAAAT	CGGC	TGGT	TAGGCT	TAGGG	CAAAT
51	GGGT	CTGCCT	ATG	TACA	ACGC	GGCT	CTTGGCA	CGGC	CGGCATC	GAAG	TGGCG
101	TATACA	ACCG	CTCG	CCGC	GAC	AAACT	CGCC	CAATC	CTCGC	CAAA	GAGCAGCA
151	AAAGT	TTACG	GCAG	CACCGC	CGAACT	CGTC	CGCG	CCTGCC	CCGT	CATTTT	
201	CCGT	GATGGTT	TCCG	CAAT	TATG	CCCG	CGGTG	CGCAT	ACTCTG	ACCG	AAGGATCC
251	CGAC	CGGAT	GGCC	GGC	CAAA	ATCAT	CGTC	CA	TGAGAC	CATC	TCCCCG
301	ACCG	AAAAACC	TCGCC	GTCAA	AGCACT	TGTC	GAAG	CCGCAG	GCGG	CACGTT	
351	TGCC	GAAGCA	CCCT	TTTCCG	GAT	CGGTG	CGC	ACCC	CGCAACC	AACG	CACAC
401	TGCT	GATTCT	TGTC	GGCGC	AGCC	AAGCCG	TTTT	AAAAACC	GCTG	CAAAA	
451	ATATT	TTCCC	TTGTC	GGCAA	AAAA	ACCTTC	CATTT	CGCGC	ATGTC	GGCAA	
501	AGCT	CTGGC	CGGAA	ATCTG	CTT	GGAATC	GCTC	TTAGGC	ATTTT	CTGGCG	
551	AAGC	GTACAG	CGAAG	CGATG	CTGAT	GGCGC	GGC	AGTT	TCGG	CATG	CATACC
601	GACAC	CATCG	TCGA	AGCCAT	CGGC	GGCTCG	GCAAT	TGGACT	CGCT	TATGTT	
651	CTAA	CAAAAA	AAAT	CACTAT	GGGCA	TAACCG	TGAGT	GGCTC	CTG	CTTTTG	
701	CACT	CAACA	CGCT	TCCAAA	GACCT	TAAAC	TCGCG	CTCAA	AGAG	CTGAAA	
751	CAGG	CAGGCA	ACACC	CTGCC	CGCG	CTCGAA	ACC	GTTGCTG	CCAG	CTACCG	
801	CAAG	CAAGTT	GAA	CGCGCT	ACGCG	CAACA	GGAC	GTTTCC	GGCG	TTTACC	
851	TGAA	ATTGCT	AGAA	CACTGA							

g105-1.pep

1	5	1	MSAETYTQIG	WVGLGQMLP	MVTRLDDGGI	EVGVYNRSPD	KTAPISAKGA
51	10	6	KVYGSTAEVL	RACPVIFLMV	SDYAAVCDIL	NGVRDGLAGK	IIVMNSTTSP
101	15	7	TENLAVKALV	EAGGQGFAEA	SVDSVGVPAT	NGTLILFEGG	SEAVNLPLOK
151	20	8	IFSLVGKKTf	HFGDVGKGSG	AKLVLSLLC	IFGEAYSEAM	LMARQFGIDT
201	25	9	DTIVTEAIGS	AMDSMPFOKT	KSLSWANREFP	PAFLAKHASK	DLNLAVKELE
251	30	10	OAGNTLPAVE	TVAASYRKAV	EAGYGEODVS	GVFLKLAEH*	

m105-1.seq

1	ATGTCGCGAA	ACGAATACGC	ACAAATCGGC	TGGATAGGCT	TAGGGCAAA
51	GGGTCTGCTT	ATGTGTAACG	GGGCTTGGGA	CGCGCGCATC	GAAGTCTGGCG
101	TATACAACCG	CTCGGCCGAC	AAAATCGCC	CCATCTCCGC	CAAAAGGCGCA
151	AAAGTTTACG	GCAACACCGC	CGAACTCGTC	CGCGACTATC	CCGTCATTT
201	CCGTGATGGT	TCGCAGTATG	CGCCGGCTGT	GCAGATCTCG	AACGGAGTCC
251	GCGACGGATT	GGCCGGCAAA	ATCATCTGTA	ACATGAGACG	CATCTCCCGC
301	ACCGAAAACC	TCGCCGTCAA	AGCACTTGTG	GAAGCCGACG	GCGGACAGTT
351	TGCCGAAGCA	CCCGTTTCCG	GTCGCGTCTG	GTTCCGCCAC	AACCGCACGC
401	TGCTGATTCT	GTTCTGGCGG	AGCGAAGCG	TTTTAAACCC	GCTGCAAAAA
451	ATATTTTCCC	TCGTCGGCAA	AAAAACCTTC	CATTTCCGGC	ATGTCGGCAA
501	AGGTCGGCG	GCGAAATCTG	CTTGAAGACT	GCTCTGGGCG	ATTTTCCGCG
551	AAGCGTACAG	CGAATCGATG	TGTATGGCG	GCGAGTTCCG	CATCATACCC
601	GACACCATCG	TCGAAGCCAT	CGGSGACTCG	GCAATGGACT	CGCCCATGTT
651	CCAAACCAAA	AAATCTCTGT	GGGCAACCG	CGAATCCCGC	CCGCGCTTCG
701	CCCTCAACAA	CGCCTCCAA	GACCTCAACC	TCGCGCTCAA	AGAGCTTGAA
751	CAGGCAGGCA	ACACCTCGCC	CGCCGTCGAA	ACCCTTGTCT	CCAGTACCCG
801	CAAGACAGTC	GAACCCGGCT	ACGGCGAACA	GGAGCGTTTC	CGCGTTTACC
851	TGAACATGGC	AGAACATCTA			

m105-1.pgp

1 MSANEYAQIG WIGLGQMLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA  
51 KVGNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLQMGMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGCNTAELV					
g105-1	MSAETYYTQIGWVGLQMGMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m105-1.pep	RDYPVIFILMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA					
g105-1	RACPVIFILMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSGAKLVLSNLLG					
g105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSGAKLVLSNLLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m105-1.pep	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
g105-1	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	190	200	210	220	230	240
	250	260	270	280	290	
m105-1.pep	DLNLAVKELEQAGNTLPVAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX					
g105-1	DLNLAVKELEQAGNTLPVAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX					
	250	260	270	280	290	

```

a105-1.seq
1  ATGTCCGCAA  ACGAATACAC  ACAAATCGGC  TGGATAGGCT  TAGGGCAAAT
51  GGGCTTGCCT  ATGGTAACGC  GGCTCTTGGA  CGGCGGCATC  GAAGTTCGGC
101 TATACAACCG  CTCGCCGCAC  AAAACTGCCC  CCATCTCCGC  CAAAGGCGCA
151 AAAGTTTACG  GCAACAACCG  CGAACTCGTC  CGCGACTATC  CCGTCATTTT
201 CCTGATGGTT  TCCGCAATG  CGCCCGTGTG  CGACATCTGT  AACGGAGTCC
251 GCGACGGATT  GGCCGGCAAA  ATCATCGTCA  ACATGAGCAC  CATCTCCCCG
301 ACCGAAAACC  TCCCGGTCAA  AGCACTGTCT  GAAGCCCGAC  GCGGACAGTT
351 TGCCGAAGCA  CCGGTTTCGG  GATCGGTCCG  GCCCGCCACC  AACGGCACGC
401 TGCTGATTCT  GTTCGGCGGC  AGCGAAGCGC  TTTTAAACCC  GCTCGAAAAA
451 ATATTTTCCC  TCGTCGGCAA  AAAAACCTTC  CATTTCCGGC  ATGTCGGCAA
501 AGGTTTCGGG  CGGAACTCG  TCTTGAACTC  GCTCTTGGCC  ATTTTCCGGC
551 AAGCGTACAG  CGAAGCGATG  TCGTGGCGCG  GGCAGTTTCG  CATCGATACC
601 GACACCATCG  TCGAAGCCAT  CGCGGGCTCG  GCAATGGAAT  CGCCCATGTT
651 CCAAACCAA  AAATCCCTGT  GGGCAAAACG  CGAATTCCCA  CCCGCTTGGT
701 CCTCAACAA  CGCCTCAAAA  GACCTCAACC  TCGCCGTCAA  AGAGCTTGAA
751 CAGGCAGGCA  ACACCTTGCC  CGCCGTCGAA  ACCGTTGCTG  CCAGCTACCG
801 CAAAGCAGTC  GAAGCCGGTC  ACGGCGAACA  GGACGTTTCC  GGCCTTTACC
851 TGAATTGGC  AGAATCTGA

```

a105-1.pep

1	MSANEY	TQIG	WIGLG	QMGLP	MVTRL	LDGGI	EVGVN	NRSPD	KTAPIS	AKGA
51	KVYGNT	AEVL	RDYPV	IFLMV	<u>SDYAP</u>	<u>CDIL</u>	NGVRD	GLAGK	IIVMST	SGP
101	TENLAV	KALV	EAAGG	QFAEA	PDVSG	VGPAT	NGTL	LILFGG	SEAVLN	PLQK
151	IFSLVG	GKKT	HFGDG	KGKSG	AKLVL	NSLLG	IFGEAY	SEAM	LMARQF	GD
201	DTIVFA	IGGS	AMDS	PMFQK	KSLWAN	REFP	PAFALK	HASK	DLNLAV	KELE
251	QAGNTL	PAVE	TVAAS	YRKAT	EAGYGE	QDVS	GVIYK	LAEH*		

MSANEYQTIGWIGLGQMGLPMVTRLDDGGIEVGYNRSPDKTAPISAKGAKVYGNTAELV

317

m105-1	MSANEYAQIGWIGLQMGMLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV
	10 20 30 40 50 60
a105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
	70 80 90 100 110 120
m105-1	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
	70 80 90 100 110 120
a105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
	130 140 150 160 170 180
m105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
	130 140 150 160 170 180
a105-1.pep	IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
	190 200 210 220 230 240
m105-1	IFGEAYSEXMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
	190 200 210 220 230 240
a105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAHX
	250 260 270 280 290
m105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAHX
	250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

g107.seq

```

1  ATGGTATTAA CCTTTATTG GGCACCGGC GGCCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTCGACA CCCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCcttggtta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg cgcagaggca actCTCCGTC CTgaatgaaa cccTGtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc caccctcttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cgcacccaaa
501 accgtcgcgc tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

g107.pep

```

1  MVLTFIWAATG GLVADAKPSV LFDTOAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAABRQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

m107.seq

```

1  ATGGTATTGA CCTTTATTG GGCAGCCGCG GGCCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTCGATA CCCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGs CACCGCCCTG CCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTACGTCC
251 TCTGGCAAAC CGCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

m107.pep..

```

1  MVLTFIWAAG GLIADAKPSV LFDTOAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWGTGLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY  
 151 IAHLMERQH LRAAPKPPR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng)

from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLT	FIWAAGGLIADAKPSVL	FDTQAPAGTNYWIYAX	TALPVCLASFGFHG	NVSSLLKYF	
g107	MVLT	FIWATGGLVADAKPSVL	FDTQAPVGTGYWIYA	TALPVCLASFGFHG	NVSSLLKYF	
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPK	VAKSIWGTGLIALVIY	VLWQTALIQGNLPRNE	FAPVIAAEGQVSVLI	ETLSKFAQ	
g107	KGDAPK	VAKSIWAGTLVALVIY	VLWQTALIQSNLPRNE	FAPVIAAERQLSVL	NETLSKFAQ	
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDK	ILSLFSYMAIATSF	LGVTLGLFDYIA-H	LQMERQHLRAAPKPPR		
g107	TGDMDK	ILSLFPYMAIATSF	LGVTLGLFDNIAGH	LQMERQYVRAAPKPSR		
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTTG EGCAACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGG3CA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGCGGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCGGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTTCCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAAA ACCTATAAAG TTTACGGCGG CTTGTGGCTG ATGTTTGGG
701 TCTTCCTTTT CGGCATC3TC AACATCGCCG CACAGGTATT GAGCCAAAT
751 GAACTCGTCC CCGTATT1AA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWATG GLIADAKLPV LFDTQAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTALIALV IYVLWQTALIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGGWL MVWVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLT	FIWAAGGLIADAKPSVL	FDTQAPAGTNYWIYAX	TALPVCLASFGFHG	NVSSLLKYF	
a107	MVLT	FIWATGGLIADAKLPV	LFDTQAPTGTNYWIYV	ATALPVCLASFGFHG	NVSSLLKYF	
	10	20	30	40	50	60

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```

              70      80      90      100      110      120
m107.pep      KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              |||||
a107           KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              70      80      90      100      110      120

              130      140      150      160      170
m107.pep      TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIAHLQMERQHLRAAPKPPRX
              |||||
a107           TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL
              130      140      150      160      170      180

a107           LFPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGGLWMVWVFLFGIV
              190      200      210      220      230      240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

```

g108.seq
1   ATGttgccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AACggCGCAT AAAACGCCGc ccTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGCG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCCGC GGCACACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGGAATTG
301 GACAGGCGCA GCGAATGGCG TTTGACCGCG CTGGCGATGA GTGCCGAAAA
351 ACAGGCGGAA TGGGAAAACA AGATTTCGG CTGCGCTACC GAAGAAGCAC
401 CTAACCAGCT GACCGGCAAC GATGTGATGC AGATGCTGaa ccagtccacG
451 CGCaatcagg cacTtgccgc CCTgaccgTC AAAacgggTT CcgctgcgTT
501 CAAacgcctg tACCGCTaa

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

```

g108.pep
1   MLPGFNRIFK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRAL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EEAPNQLTGN DVMQMLNQST
151 RNQALAAALT KTVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

```

m108.seq
1   ATGTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGTG GCAATCTTAC TCGGCGGCTG
201 CGCCGCCGGA GCGGTAACA CATTGCGCAG CTTAGACGGT GGCACAGGCA
251 TGGGCGGCAG CATCGTCAAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTTC CGCTTGCGTC GCCCAAGAAG
401 CACCCGAACG GATGACCGGC AACGATGTGA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCACTTGC CGCCTGACC GCCAAAACGG TTCCCGCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

```

m108.pep
1   MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLILPV AILLGGCAAG GNTFGSLDGG GTGMGGSIVK MAVSQCRAB
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAALT AKTVSACFKH LYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng)

from *N. gonorrhoeae*:

m108/g108



a108.seq

```

1   ATGTTGCCGG  GCTTCAACCG  GATATTCAA  CGGTTTGTT  CAACACTCGG
51  AACGGCGCAT  AAAACGCCGC  CCTTCGCGT  ATCCCGAAC  GGGCGGCTAA
101 TCAGATTCTA  TCGCCATAAA  AGGCGGGGT  TCAACCGAA  AGGAATTGAG
151 ATGAATAAAA  CCTTGTCTAT  TTTGCCGGT  GCAATCTAC  TCGGCGCGTG
201 CGCCGCCGGG  GGGCGGTACA  CATTCCGCG  CTTAGACGG  GCGACAGGTA
251 TGGCGCCGCG  CATCTGTCAA  ATGCGGGTA  AAGCCAATG  CCGTGCGGAA
301 TTGAACAAC  GCAGCGAATG  GCGTTTGAC  GCGCTGGCG  TGAGTGCCGA
351 AAAACAGCG  GAATGGGAAA  ACAAGATTG  CGCTTGCCT  GCCCAAGAAG
401 CACCCAACCA  GCTGACCGGG  AACGATGTG  TGAGATGCT  GGATCCGTCC
451 ACCGCGCAAT  AGGCATCTGC  GCGCCTGAC  GCCAAACGG  TTTCCGCGTG
501 CTTCAACAC  CTGACTCGCT  AA

```

a108.pep

1 MLPGFNRIKF RFVPTLGTAH KTPPFALSRT GLRIRFYRHK RRGFNRRKGIE  
51 MNKTL~~SL~~ILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE  
101 LNKRS~~EW~~RLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS  
151 TRNQALAA~~LT~~ AKTVSACFKH LYR\*

**m108/a108** 96.5% identity in 173 aa overlap

	10	20	30	40	50	60
m108.pep	MLPGFNRI	FKRFVPTL	GTAHKTPP	FALSRTGR	LIRFYRHK	RGRGFNRK
a108	MLPGFNRI	FKRFVPTL	GTAHKTPP	FALSRTGR	LIRFYRHK	RGRGFNRK
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCA	AAGGGNTF	GSLDGGTG	MGGSI	VKMAVGSQ	CRAELDKR
a108	AILLGGCA	AAGGGNTF	GSLDGGTG	MGGSI	VKMAVESQ	CRAELNKR
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKICAC	VQAQEAPE	RMTGNDVM	QMLAPSTR	NQALAA	LAKTVSAC
a108	EWENKICAC	VQAQEAPE	NQLTGNDV	QMLDPSTR	NQALAA	LAKTVSAC
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

321

g109.seq  
 1 ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGCGC  
 51 AGCCGGTATT GATCGTAGGC GTATGCTTAC CGCTTTTGA AGCGGGCATG  
 101 GAAATGACGC GCAAAGGCAA AACCACCCAA TCCGCCGCCA TCGTGGTGT  
 151 CTCTCCGTC TGGTCAATCC GGTTTTCGGC TGGGCGTTGA CGATGCTGTT  
 201 GGATAATTTG GGCTTAATCG GCTGCAAAGA ACGCAGCGCG CAATTAGGTT  
 251 TTGTCGGACG AGTATTGATA CCCGCACTAG GTTCTTAAT CTTGTGTGTG  
 301 GCGATGGGTG CGGTCGGGAT GCTGCCCGGT ATCCCTCCGT TTTGGAGCA  
 351 GTTCAAATCT TTGGGCTAG

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

g109.pep  
 1 MYRRVVGSL DGLGDLAAGI DRRRLTAFG SHGNDAQRO NHPIRRHRGV  
 51 LFRVNPVFG WALTMLLDNL GLIGCKERSA QLGFGVRLI PAVGFLILCV  
 101 AMGAVGMLPG IPPFLEQFKS LG

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 389>:

m109.seq  
 1 ATGTATTATC GCCGGGTTAT GGGGCTATCC GATGGACTTG GCGATTGCGC  
 51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG  
 101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC  
 151 CATCGTGGTG TTCTCTCCG CCTTGTCAT CCGGTTTTCG GCTGGGCGTT  
 201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAA GAGCGCAGTG  
 251 CGCAATTAGG TTTCGCCGGA CGCGTGTGA TACCCGCACT AGGTTTCTTG  
 301 ATCTTGTTG TGGCGATGGG TGCGGTCGGG ATGCTGCCCG GTATCCCGCC  
 351 GTTTTGGAA CACTTCAAAT CTTTGGGCTA G

This corresponds to the amino acid sequence <SEQ ID 4; ORF 109>:

m109.pep  
 1 MYRRVMGLS DGLGDLAAGI ERSLGRRRIL TAFSGHGNDA AQRQNHPIRR  
 51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSALGFAG RVLI PAVGFL  
 101 ILCVAMGAVG MLPGIPPFLE HFKSLG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 109 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 109.ng)

from *N. gonorrhoeae*:

m109/g109

	10	20	30	40	50	60
m109.pep	MYRRVMGLSDGLGDLAAGIERSLGRRIITAFSGHGNDAQRQNHPIRRHRGVLFRLVN					
	:       :    :					
g109	MYRRVVGSLDGLGDLAAGIDR---RRLTAFGSGHGNDAQRQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	
	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLI PAVGFLILCVAMGAVGMLPGIPPFLE					
	:       :					
g109	PVFGWALTMLLDNLGLIGCKERSAQLGFVGRVLI PAVGFLILCVAMGAVGMLPGIPPFLE					
	60	70	80	90	100	110
m109.pep	HFKSLGX					
	:					
g109	QFKSLGX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq  
 1 ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGCGC  
 51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG  
 101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC  
 151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

This corresponds to the amino acid sequence <SEQ ID 392; ORF 109>:

1 MYYYRVVGLS DGLGLAAGI ERLGRRRII TAFSGSHGND AQRQNHPIRR  
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFTG RVLIIPVVGFL  
101 ILCVAMGAVG MLPGIPPFLE HFKSLG\*

		10	20	30	40	50	60
m109.pep		MYYYRRVMGLSDGLGDLAAGIERSLGRRRILTAFGSGHGNDQAQRQNHPIRRHRGVLFRLVN					
		:					
a109		MYYYRVVGLSDGLGDLAAGIERSLGRRRILTAFGSGHGNDQAQRQNHPIRRHRGVLFRLVN					
		10	20	30	40	50	60
		70	80	90	100	110	120
m109.pep		PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIIPAVGFLILCVAMGAVGMLPGIPPFLE					
a109		PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLIIPVVGFLILCVAMGAVGMLPGIPPFLE					
		70	80	90	100	110	120
m109.pep		HFKSLGX					
a109		HFKSLGX					

```
g111.seq
1  ATGCCGCTCTG  AAACACGCCT  GCCGAACCTT  ATCCGCGCCT  TGATATTTCG
51  CTTGGGTTTC  ATCTTCTCTGA  ACGCTGTGTC  GGAcaaacC  CGCGAaacctg
101 TTAACCTCGA  AGGACGAAACG  ATGGGTACGA  CCLATACGT  CAAATACCTT
151 TCAAATAATC  GGGACAAACT  CCCCTCCCT  GCCAAAATAC  AAAAGCGCAT
201 TGATGATGCG  CTTAAAGAAG  TCAACCGGCA  GATgtccaCC  TACCAGACCG
251 ATTCCGAAAT  CAGCGCGTt  atacagacan  atgctggaga  gctcttcgcg
301 tntcatgcag  ntctataac  tgattccgcc  gaagactgtc  tgccataac
351 qcctatctca  tcqgcqctct  qa
```

```
g111.pep
      1  MPSETRLPNL  IRALIFALGF  IFLNACSEQT  AQTVTLQGET  MGTTYTVKYL
     51  SNNRDKLPSP  AKIQKRIDDA  LKEVNRQMS  YQTDSEISRF  IQTAGELFAH
    101  ASITDSAEDC  LPTNPISAL  *
```

```
m111.seq
1  ATGCCGTC TG AAACACGCCT GCCGAAC TTT ATCCGCGTCT TGA TATTTCG
51  CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAAACCG
101 TACCCCTGCA AGCGGAAACG ATGGGCACGA CCTATAYcGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AWAACCGCAT
201 CGATGACGCG CTTAAAGAAK TCAACCGGyA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCACACA CAGCCGGCAA GCCCCTCCCG
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCGCTCC GCTCGAACCG
351 CCTGACACAC GCGCGCGTGG ACCTAACCCT CGGCCCTT TGCTAACCTTT
401 GGGGATTTCG CCCCACAAA TCCGTATACC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAG CGGCATCTTA TACGGGCATA CACAAAATCA TTTTGAACAA
501 AGGCAAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTCG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGGAA
```

```
m111.pep
1  MPSETRLPNF  IRVLIFALGF  IFLNACSEQT  AQTVTLQGET  MGTTYXVKYL
51  SNNRDKLPSP  AEIXKRIDDA  LKEXNRXMST  YQPDSEISRF  NQHTAKGPLR
101 ISSDFAHVTA  EAVRLNRLTH  GALDVTVGPL  VNLWGFQDPK  SVTREPSEQE
151 IQQAASYTGI  DKILKQGGK  YASLSKTHPK  AYLDLSSIAK  GFGVDKVAE
201 LEKYGIQNYL  VEIGGELHGK  GKNARGEPWR  IGIEQPNIVQ  GGNQTQIVPL
251 NNRSLATSGD  YRIFHVDKNG  KRLSHIINPN  NKRPISHNLA  SISVVADSAM
301 TADGLSTGLF  VLGETEALKL  AEREKLAVPL  IVRDKGGYRT  AMSSEFEKLL
351  *

```

m111.pep/g111.pep

**a111.seq**

1	ATGCCGCTCTG	AAACACGCCT	GCCGAAC TTT	ATCCGCACCT	TGATATTTGC
51	CCTGAGTTT	ATCTTCTCTGA	ACGCTGTGT	GGAAACAAACG	GCGCAAAACCG
101	TTACAGTTC	AGGTGAACG	ATGGGCACGA	CCTATACCGT	CAAAATACCTT
151	TCAAATTAAT	GGGACAACT	CCCTTCACCT	GCGGAAATAC	AAAAGCGCAT
201	CGATGACGCG	CTTAAAGAAG	TCAACCGGCA	GATGTCCACC	TATCAGCCCG
251	ACTCCGAAAT	CAGCCGGTTC	AACCAACACA	CAGCCGGGAA	GCCCTCTCGC
301	ATTTCAAGCG	ACTTCGCACA	CGTTACTGCC	GAGCGCTGCC	ACCTGAACCG
351	CTCGACACAC	GCCCTGCTGG	ACGTAACCGT	CGGCCCTTG	TGTAACCTTT
401	GGGGATTTCG	CCCCGACAAA	TCCGTTACCC	GTGAACCGTC	GCCGGAACAA
451	ATCAAAACAAG	CAGCATCTTA	TACGGGCATA	GACAAAAATCA	TTTTGAAACA
501	AGGCAAGAT	TAGCTTTCCT	TGAGCAAAAC	CCACCCCAAG	GCCATTATTGG
551	ATTTATCTTC	GATTGCCAAA	GGCTTCGGCG	TTGATAAAGT	TGCGGGCGAA
601	CTGGA AAAAT	ACGGCATTCA	AAATTATCTG	GTGGAATCG	GCGGCGAGTT
651	GCACGGCCAA	GGCAAAATAC	CGCGCGGCGA	ACCTTGGGCG	ATCGGCATCG
701	AACAGCCCAA	CATCTTCCAA	GGCGGCAATA	CGCATAGGAT	CGTCCCGCTG
751	AACAACCGTT	CGTTGCCAC	TTCCGGCGAT	TACCGTATT	TCCACGTCGA

324

```

801 TAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCTGC TGTTCCTG ATTGTCAGGG
1001 ATAAAGCGG .CTACCGACC GCCATGTCTT CCGAATTGA AAAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

```

1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFDPK SVTREPSPEQ
151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQT AQTVTLQGETMGTITYVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIFLNACSEQT AQTVTLQGETMGTITYVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEXNRXMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKILKQKGDYASLSKTHPK					
a111	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKILKQKGDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRIGIEQPNIVQ					
a111	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVADSAM					
a111	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVADSAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

```

1  ATGCCGCTCG AACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51  CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAaCCG
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCTT GCCAAATAC AAAAGCGCAT
201 TGATGATGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TACCAGACCG

```

325

```

251 ATTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ATTTGCGACA CGTTACCGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACTCAC GGCACACTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGGTTTCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACA
501 AGGCAAAAGT TACGCTTCCT TGAGCAAAAC CCACCCCAA GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGC AAA GGC AAAAATG CGCACGGCGA ACCGTGGCGC ATCGGTATAG
701 AGCAACCCAA TATcatccaa ggcggcaata cgcAGattat cgtcccgcgtg
751 aaCaaccgtt cgcttgccac ttccggcgat taccgtaTTT tccacgtcga
801 TAAAAACGGC Aaacgccttt cccacATCAT CAATCCCAAC AACAAACGAC
851 CACTCAGCCA CAACctcgcc tcCATCagCg TGGTCTCAGA CAGTGCATG
901 ACGGCGGACG GTTTATCCAC AGGATTATTT GTTTTAGGCG AAACCGAAGC
951 CTTAAGGCTG GCAGAACAG AAAAATCTCG TGTTTTCTTA ATTGTCCGGG
1001 ATAAGGCGG CTACCCGACC GCCATGTCTT CCGAATTGTC CAAGCTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 400; ORF 111-1.ng>:

```

g111-1.pep
1  MPSETRLPLN  IRLIFALGF  IFLNACSEQT  AQTVTLQGET  MGTTYTVKYL
51  SNNRDKLPSP  AKIQKRIDDA  LKEVNRQMS  YQTDSEISRF  NQHTAGKPLR
101 ISSDFAHVTA  EAVRLNRLTH  GALDVTVGPL  VNLWGFDPK  SVTREPSFEQ
151 IKQAASYTGI  DKILQQKGD  YASLSKTHPK  AYLDLSSIAK  GFGVDKVAGE
201 LEKYGIQNYL  VEIGGELHGK  GKNAHGEPWR  IGIEQPNIIQ  GGNTQIIIVPL
251 NNRSLATSGD  YRIFHVDKNG  KRLSHIINPN  NKRPISHNLA  SISVVSDSAM
301 TADGLSTGLF  VLGETEALRL  AEQEKLAFL  IVRDKDGYRT  AMSSEFAKLL
351 R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 401>:

```

m111-1.seq
1  ATGCCGCTCG  AAACACGCTT  GCCGAACTTT  ATCCGCGTCT  TGATATTTGC
51  CCTGGGTTTC  ATCTTCCTGA  ACGCCTGTTC  GGAACAAACC  GCGCAAACCG
101 TTACCCCTGCA  AGGCGAAACG  ATGGGCACGA  CCTATACCGT  CAAATACCTT
151 TCAATAATC  GGGACAAACT  CCCCTCACCT  GCCGAAATAC  AAAACGCAT
201 CGATGACGCG  CTTAAAGAAG  TCAACCGGCA  GATGTCCACC  TATCAGCCCG
251 ACTCCGAAAT  CAGCCGGTTC  AACCAACACA  CAGCCGGCAA  GCCCCTCCGC
301 ATTTCAAGCG  ACTTCGCACA  CGTTACTGCC  GAAGCCGTCC  GCCTGAACCG
351 CCTGACACAC  GGCAGCGCTG  ACGTAACCGT  CGGCCCTTTG  GTCAACCTTT
401 GGGGATTTCG  CCCCACAAA  TCCGTTACCC  GTGAACCGTC  GCCGGAACAA
451 ATCAAACAGG  CGGCATCTTA  TACGGGCATA  GACAAAATCA  TTTTGAACA
501 AGGCAAAAGT  TACGCTTCCT  TGAGCAAAAC  CCACCCCAAG  GCCTATTGG
551 ATTTATCTTC  GATTGCCAAA  GGCTTCGGCG  TTGATAAAGT  TCGGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGC AAA GGC AAAAATG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GGCAGCAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCTCG TGTTTTCTG ATTGTACGGG
1001 ATAAGGCGG CTACCCGACC GCCATGTCTT CCGAATTGTA AAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 402; ORF 111-1>:

```

m111-1.pep
1  MPSETRLPNF  IRLIFALGF  IFLNACSEQT  AQTVTLQGET  MGTTYTVKYL
51  SNNRDKLPSP  AEIQKRIDDA  LKEVNRQMS  YQPDSEISRF  NQHTAGKPLR
101 ISSDFAHVTA  EAVRLNRLTH  GALDVTVGPL  VNLWGFDPK  SVTREPSFEQ
151 IKQAASYTGI  DKILQQKGD  YASLSKTHPK  AYLDLSSIAK  GFGVDKVAGE
201 LEKYGIQNYL  VEIGGELHGK  GKNAHGEPWR  IGIEQPNIVQ  GGNTQIIIVPL
251 NNRSLATSGD  YRIFHVDKNG  KRLSHIINPN  NKRPISHNLA  SISVVSADAM
301 TADGLSTGLF  VLGETEALKL  AEREKLAFL  IVRDKGGYRT  AMSSEFEKLL
351 R*

```

m111-1/g111-1 96.6% identity in 351 aa overlap

```

10      20      30      40      50      60
m111-1.pep  MPSETRLPNFIRVLIFALGFIFLNACSEQAQTVTLQGETMGTTYTVKYLNNRDKLPSP
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g111-1      MPSETRLPLNIRLALIFALGFIFLNACSEQAQTVTLQGETMGTTYTVKYLNNRDKLPSP

```

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	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
g111-1	70	80	90	100	110	120
m111-1.pep	130	140	150	160	170	180
g111-1	130	140	150	160	170	180
m111-1.pep	190	200	210	220	230	240
g111-1	190	200	210	220	230	240
m111-1.pep	250	260	270	280	290	300
g111-1	250	260	270	280	290	300
m111-1.pep	310	320	330	340	350	
g111-1	310	320	330	340	350	

## g111-1/p44550

sp|P44550|YOJL\_HAEIN\_HYPOTHETICAL\_LIPOPROTEIN\_HI0172\_PRECURSOR >gi|1074292|pir||C64144  
hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)  
lipoprotein, putative [Haemophilus influenzae Rd] Length = 346  
Score = 349 bits (885), Expect = 2e-95  
Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQVTVLQGETMGTTYXVKYLSNNRDKLPSPAEIXKRIIDALKEKNRMSTYQ 62  
L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+  
Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVKYLDGGSITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRFNQHT-AGKPLRISSDFAHVTAEAVALNRLTHGALDVTGVLVNLWGFPGPKS 141  
DSE+SRFNQ+T P+ IS+DFA V AEA+RLN++T GALDVTGVP+VNLWGFPGP+K  
Sbjct: 75 KDSELSRFNQHTQVNTPIEISADFAKVLAEAILRLNKVTEGALDVTGVPVNLWGFPGPEKR 134

Query: 142 VTREPSPEQIKQAASVTGIDKIILKQKDYASLSKTHPKAYLDLSSIAKGFVGVKAGEL 201  
++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKGFVGV+VA +L  
Sbjct: 135 PEKQFTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKGFVGVQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIVPLNNRSLATSGDY 261  
E+ QNY+VEIGGE+ KGN G+PW+I IE+P + ++ LNN +A+SGDY  
Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKPWQIAIEKPTTGERAVEAVIGLNNHMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321  
RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A  
Sbjct: 255 RIY-FEENGKREAFHEIDPKTYPIQHHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAVFLIVRDGGYRTAMSSEFEKL 349  
E+ LAV+LI+R G+ T SS F+KL  
Sbjct: 314 EKNNLAVYLIIRTDNFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

## a111-1.seq

```
1  ATGCCGCTCTG  AAACACGCTT  GCCGAACCTT  ATCCGCACCT  TGATATTTGC
51  CCTGAGTTT  ATCTTCTGA  ACGCCTGTTC  GGAACAAACC  GCGCAAACCG
101  TTACCCTGCA  AGGTGAAACG  ATGGGCACGA  CCTATACCGT  CAAATACCTT
151  TCAAATAATC  GGGACAAACT  CCCCTCACCT  GCCGAAATAC  AAAAGCGCAT
201  CGATGACGCG  CTTAAAGAAG  TCAACCGGCA  GATGTCCACC  TATCAGCCCG
251  ACTCCGAAAT  CAGCCGGTTC  AACCAACACA  CAGCCGGCAA  GCCCTCCGCG
301  ATTTCAAGCG  ACTTCGCACA  CGTTACTGCC  GAAGCCGTCC  ACCTGAACCG
```

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```

351 CCTGACACAC GGC GCGCTGG ACCTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGC AAAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACACCGTT CGTTGCCAC TTCCGGCGAT TACCGTATT TCCACGTCGA
801 TAAAAGCGGC AAACGCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG CTTGTCCAC AGGATTATTC GTATTGGCGC AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCGC TGTTCCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGCTT CCGAATTGA AAAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

```

a111-1.pep
1  MPSETRLNPF IRTLIFALSF IFLNACSEOT AOTVTLOGET MGTITYVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQST YOPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
251 NNRLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

a111-1.pep	10	20	30	40	50	60
	MPSETRLNPFIRTLIFALSFI	FLNACSEQTAQVT	LOGETMGTITYVKYLS	SNNRDKLPSP		
m111-1	MPSETRLNPFIRVLIFALGF	IFLNACSEQTAQVT	LOGETMGTITYVKYLS	SNNRDKLPSP		
a111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQSTY	QPDSEISRFNQHTAGKPL	RISDFAHVTA	EAVHLNRLTH		
m111-1	AEIQKRIDDALKEVNRQSTY	QPDSEISRFNQHTAGKPL	RISDFAHVTA	EAVRLNRLTH		
a111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFPGDK	SVTREPSPEQIKQAASYT	GIDKILKQKGDYASLSK	THPK		
m111-1	GALDVTVGPLVNLWGFPGDK	SVTREPSPEQIKQAASYT	GIDKILKQKGDYASLSK	THPK		
a111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKFGVDKVAGE	LEKYGIQNYLVEIGGELHG	GKGNARGEPRWIGIEQPN	IVQ		
m111-1	AYLDLSSIAKFGVDKVAGE	LEKYGIQNYLVEIGGELHG	GKGNARGEPRWIGIEQPN	IVQ		
a111-1.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSG	DYRIFHVDKSGKRLSHI	INPNKRPISHNLASISV	VADSAM		
m111-1	GGNTQIIVPLNNRSLATSG	DYRIFHVDKSGKRLSHI	INPNKRPISHNLASISV	VADSAM		
a111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALK	LAEREKLAVFLIVRDKG	GYRTAMSSEFEKLLRX			
m111-1	TADGLSTGLFVLGETEALK	LAEREKLAVFLIVRDKG	GYRTAMSSEFEKLLRX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

```

g114.seq
1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGGACGAG TATGGGGCGG TCAATGTCGG

```



g114.pep  
1 MASITSPLHG AQQECSTKFL CPPGGTSMGR SMSVTVGLFC VSINLTISVE  
51 YGQSGYFTRA AECKTGCQGI SPSCLNERTV CEVTIKWSSS ETSTDMACA  
101 SRLVNMSSC EGSGEPPGWL CAIIRLSAYS SNASLTISRM \*

```
m114.seq
  1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCACAGAG AATGCAGCAA
51  GACTTTTTTA TGTCCACC GG GCGGGACGAG TATAGGGCGG TCAATGTGCG
101 TAACGGTAGG TTTGTTTGT GTTTCATTA ACTTAACAAT ATCTGTTGAA
151 TACGGTTGAA GCGGCTATTT TATCAGAGCC GCGGCATGA AAACAGAGTG
201 TCAGGGCATC AACCCGAGCT GTCTGAACGA ACAGACGCTT TGCGAKGTAA
251 CGATAAAATG GTCGAGCAGC GACACATCGA CCAGCGACAT TGCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCTTCG GAATGTTcG GCGAGCCGcC
351 CGGTATGGTT TGCGCAATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA
```

m114.pep

1	MASITSPLHG	AHRECSKTF	CPPGGTSIGR	<u>SMSVTVGLFC</u>	<u>VSINLTISVE</u>
51	YGXSGYFIRA	AACKTECQGI	NPSCLEQTL	CVTIKWSSS	DTSTSDIACA
101	SRLVNMSSC	EXSGEPPGWL	CAIIRLSAYS	SNASLTISM	*

```

a114.seq
1  ATGCCGGAGG CAAGCATCGC CTCATCACT TCGCCGCTGC ACGGGGCGCA
51  ACAGGAATGC AGCAAGACTT TTTATGTCC GCCGGGCGGG ACGAGTATGG
101 GCGCGTCAAT GTCGGTAACG GTAGGTTTGT TTTGTGTTTC CATTAACTTA
151 ACGATATCTG TCGAATACGG TGAAGCGCG TATTTTATCA GAGCCGCCGC
201 ATGTAAAACA GGGTGTCAAG GCATCAGCCC GAGCTGCCTG AACGAACGGA
251 CGGTTTGC GCATTACGATA AATGGTTCGA GCAGCGACAC ATCGACCAGC
301 GACATTGCCT GTGCCAGCCG CCTTGTGAAC ATGATGTCTT CCTGCGAAGG
351 TTCGGGCGAG CCGCCGGATG GGTGTGCGC GATAATCAGG CTGTCCGCAT
401 ATTCTGCCAA TGCCAGTTTG ACAATTTTCA CGATGTAA

```

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This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1 MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRSMSTV VGLFCVSINL
51 TISVEYG*SG YFIRAAACKT GCQGISPSCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCAIIR LSAYSSNASL TISRM*

```

m114/a114 92.9% identity in 140 aa overlap

```

          10      20      30      40      50
m114.pep  MASITSPLHGAHRECSKTFLCPPGGTSIGRSMSTVGLFCVSINLTISVEYGXSG
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114       MPEASIASITSPLHGAQQECSTFLCPPGGTSMGRSMSTVGLFCVSINLTISVEYGXSG
          10      20      30      40      50      60

          60      70      80      90     100     110
m114.pep  YFIRAAACKTECQGINPSCINLEQTLXVTKWSSSDTSTSDIACASRLVNMSSCEXSGE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114       YFIRAAACKTGCQGISPSCLNERTVCAVTIKWSSSDTSTSDIACASRLVNMSSCEGSGE
          70      80      90     100     110     120

          120     130     140
m114.pep  PPGWLCAIIRLSAYSSNASLTISRMX
          |||||:|||||:|||||
a114       PPGWLCAIIRLSAYSSNASLTISRMX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1 atgggtcgacg aactcgacCT GCTGCCCGAT GCCGTCGCCG CCACCTGCT
51 TGCCGACATC GGACGCTACG TCCCGGATTG GAACCTATTG GTTTCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTGtga CGAAGTGCAG
151 AAACCTTACCC ACTTCGCCCG GGTGGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TGCGGAAAAT GCTGCTGGCg atggttaccg
251 Acatccgcgt cgtatTAATC AAACCTGGCGA TGCGTaccgc caccCTGeta
301 ttTTtaagCA ACGCCCCGA CAGCCCTGAA AAACgcgccg TCgcaaaAga
351 aacccTCGAC ATCTTCGCCC CGCTCGCCAA CCGCTTGGGC GTGTGGCAGC
401 TCAAATGGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGCGAAA TCGCCCTGCT TTGGGACGAA AAACGCACCG AACGCCTCGA
501 ATACATCGAA AACTTCCTCG ATATCCTGCG TACGGAACCTC AAAAAATACA
551 ATATCCACTT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTAC
601 AAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgctTGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTCG ATACCGTCCC CGaGTGTAC ACCACGCTGG
701 gcaTCGTCCA CAGCCTCTGG CAGCCCATTC CCGGCGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaA CGgttATAAA AGtTTGCACA CCGTCATCGT
801 cggccccGGAa gacaaagggt tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTCa CgaatTeggt gtcgccgCCC ACTGGCGtta caaagaaggc
901 ggcaaaaggc attccGCCTa cgaacaaaAAA ATcgccTggt TCGcceaACT
951 CTGGACTGG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCGAGCTT TTCAACGACA CGATTATGT TTTGACCCCG
1051 CACGGCAAAG TCCTCTCTCT GCCAACGGGC GCAACCCCCA TCGACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcggCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCCGCTG TCCACCCCGC TCGAAACCGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGtC aAATCCGCA AGGCCATCGG caaAATCCGC GCCTAcatCC
1301 GCCAGcaaaAa cgCgaCACC GTGCGCGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CCAAACTCAC GCCCAAACCC AACCTGCAAG AGCTTgcca
1401 aaATCTCGGC tacaAAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaaatttc caaccgcgcc atCcaaaaag cctgcggcac GCTgaacgaa
1501 ccgccccCGG TGCCCGTCAG CGCAACCACC ATCGTCAAAAC AGTCCAAAAA

```

```

1551 CAAAAAAGGT GGCAAAACCG GCGTGCTCAT CGACGGCGAA GACGCGTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAAACCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTCG GTCCACCGCA AAACCTGCCC
1701 CTCTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAAGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTCACG CTCGAAGTCA AACAAGtCAA CGacCTCCCG
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAA GCGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

```

g117.pep
1 MVDELDLLPD AVAATILLADI GRYVPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVVL I KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFLDILRTEL KKYNIHFEVA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGEPDDY
251 IANPKGNGYK SLHTVIIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 GKGDSEYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLTP
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLT PKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLINE
501 PPPVPVSATT IVKQSKIKKG GKTGVLIDGE DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTA VQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDKV GVLSTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

```

m117.seq (partial)
1 ..GTGAACTCA AGAAATACAA TGTCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCCTCTT TGACATCCGC GCCGTGCCGA TTCTGGTTGA TACCGTCCCC
151 GAGTGTTTACA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTCACAC CGTCATCGTC GGCCCGGAAG ACAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCGGTG TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAATC TTGGACTGGC GCGAAAACAT GGCGGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAA ACCGAGCTTT TCAACGACAC
501 GATTATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCCGCT
651 CGAAAACGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCGCGTC CAACTCGACA AACAGCTTGC CAAACTCACG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT ACAAAAAGCC AGAAGACCTC
901 TACACGCGCG TCGGACAAGG CGAAATTTC AACCGCGCCA TCCAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCAACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCCCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTCAG
1151 TGCACCGCAA AwyyTkCyCG TCTTCCAAC ACCTCGCGA ACACGCGCCC
1201 GAwAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCGGTCGAT ATCGAAATCC GCGCCCAAGA CCGTCCGGG CTTTTCGCG
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAC TCAACGTAC CCGGTGCAA
1351 ACCCAGTCCC GCGACTTGGA AGCCAGCATG AGGTTCACGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCCGC GCGTCCTCGC CAGCCTCGG GACGTCAAAG
1451 GCGTATTGAG CGTTACCCCG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)

Homology with a predicted ORF from *N. gonorrhoeae*

m117/q117

		10	20	30
m117.pep		VKLKKNVHFEVAGR	PKHIYSIYKKMVKKKL	
		:	:	
g117	EKYREIALLLDEKRTERLEYIENFLDILRTELKKYNIHFEVAGR	PKHIYSIYKKMVKKKL		
	150	160	170	180 190 200
		40	50	60 70 80 90
m117.pep	SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPI	PGFEDDYIANPKNGYKSLHTVIVG		
g117	SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPI	PGFEDDYIANPKNGYKSLHTVIVG		
	210	220	230	240 250 260
		100	110	120 130 140 150
m117.pep	PEDKGVEVQIRT	FDMHQFNEFGVAAHWRYKEGGKGD	SAYEQKIANLRQLLDWRENMAESG	
g117	PEDKGVEVQIRT	FDMHQFNEFGVAAHWRYKEGGKGD	SAYEQKIANLRQLLDWRENMAESG	
	270	280	290	300 310 320
		160	170	180 190 200 210
m117.pep	KEDLAAAFKTELFNDTIYVLTPHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEGQIV	
g117	KEDLAAAFKTELFNDTIYVLTPHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEGQIV	
	330	340	350	360 370 380
		220	230	240 250 260 270
m117.pep	PLSTPLENGQ	RVEIITAKEGHPSVNWLYEGWVKS	NKAIGKIRAYIRQONADTVREEGRVQ	
g117	PLSTPLENGQ	RVEIITAKEGHPSVNWLYEGWVKS	GKAIGKIRAYIRQONADTVREEGRVQ	
	390	400	410	420 430 440
		280	290	300 310 320 330
m117.pep	LDKQLAKLTPKPNLQELAENLGYKKPED	LYTAVGQGEISNRAIQKACGTLNEPPVPVSE		
g117	LDKQLAKLTPKPNLQELAENLGYKKPED	LYTAVGQGEISNRAIQKACGTLNEPPVPVSA		
	450	460	470	480 490 500
		340	350	360 370 380 390
m117.pep	TTIVKQSKI	KKGGKNGVLIDGEDGLMTTLAKCCKPAPPDDI	IGFVTRERGISVHRKXXXS	
g117	TTIVKQSKI	KKGGKTGVLIDGEDGLMTTLAKCCKPAPPDDI	AGFVTRERGISVHRKTCPS	
	510	520	530	540 550 560
		400	410	420 430 440 450
m117.pep	FQHLAEHAPXKVL	DASWAALQEGQVFAVDIEIRAQDRSGLLRD	VS DALARHKLNVTAVOT	

a117.seq

1	ATGGTTCATG	AACCTGCACCT	GCTCCCCGAT	GCCGTCGCCG	CCACCCTGCT
51	TGCCGACATC	GGAGGCTATG	TCCCCGACTG	GAACCTATTG	GTTTCCGAAC
101	GCTGCAACAG	TACCGTTCAG	GAGCTGGTCA	AAGGTGTGGA	CGAAGTGCAG
151	AAACTCACCC	ACTTCGCCCG	GGTGGACAGC	CTCGCCACGC	CGGAAGAAAG
201	CGCCACGACG	GCAGAAACTA	TGCGGAAAAA	GCTGCTGGCC	ATGGTTACCG
251	ACATCCGCGT	CGTGTTAATC	AAACTGGCGA	TGCGTACGCG	CACCCCTGAA
301	TTTTTAAGCA	ACGCCCCCGA	CAGCCCCGAA	AAACGCGCCG	TGCCCCAAGA
351	AACCTCGAC	ATCTTCGCCC	CGCTCGCCAA	CCGTTTGGGC	GCTGTGGCAG
401	TCAAATGGCA	GCTCGAAGAT	TTGGGCTTCC	GCCATCAAGA	ACCCGAAAAA
451	TACCGCGAAA	TCGCCCTGCT	TTTGGAGCGA	AACGCACCGC	AACGCCTCGA
501	ATACATCGAA	AACTTCTCTA	ATATCCTGCG	TACGGAATCG	AAAAAATACA
551	ATATCCACTT	TGAAGTCGCC	GGCCGTCCGA	AACACATCTA	CTCCATTATC
601	AAAAAAATGG	TGAAGAAAAA	ACTCAGCTTC	GACGGGTTGT	TCGACATCCG
651	CGCGGTGCGG	ATTCTGTTTG	ATACCGTCCC	CGAGTGTATT	ACCACTACTG
701	GCATTGTCCA	CAGCCTCTGG	CAGCCCATTC	CCGGCGAGTT	CGACGACTAC
751	ATCGCCAACC	CGAAAGGCAA	CGGTTATAAA	AGTTTGCACA	CGGTATCGT
801	CGGCCCGGAA	GACAAAGGCG	TGGAAGTGCA	AATCCGCACC	TTCGATATGC
851	ACCAATTCAA	CGAATTCCGT	GTCGCGCGCG	ACTGGCGTTA	CAAAGAGGGC
901	GGCAAAGGCG	ATTCCGCCTA	CGAACA AAAA	ATCGCTTGGT	TACGCCAACT
951	TTTGACTGG	CGGAAACA	TGGCGAAAG	CGGCAAGGAA	AGCGCTCGCG
1001	CGCGCTTCAA	AACCGAGCTT	TTCAACGACA	CGATTTATGT	TTTGACCCCG
1051	CACGGCAAAG	TCCTCTCCCT	GCCCACAGGC	GCGAGCCCCA	TCGACTTCGC
1101	CTACGCCCTG	CACAGCAGCA	TCGGCGACCG	TTGCCGCGGT	GCGAAAGTCG
1151	AAGGGCAGAT	TGTGCCCGTG	TCCACCCCGC	TCGAAAACGG	ACAGCGTGTC
1201	GAATCATFTA	CGCGCAAAGA	AGGGCATCTT	TCGGTCAACT	GCGTTTACGA
1251	AGGCTGGGTC	AAATCCAACA	AGGCAATCGG	CAAAATCCGC	GCCTACATCC
1301	GCCAGCAAAA	CGCCGACAGC	GTGCGCGAAG	AAGCGCCGAT	CCAACTCGAC
1351	AAACAGCTTG	CCAAACTCAC	GCCCAAAACC	AACCTGCAAG	AGCTTGCCGA
1401	AAATCTCGGC	TCAAAAAAGC	CGAAGACCTT	CTACACCGCC	TCGGGACAAG
1451	GCGAAATTTT	CAACCGCGCC	ATCCAAAAAG	CCTGCGGCAC	GCTGAACGAA
1501	CCGCGCGCCG	TACCCGTACG	CGAAACCCAC	ATCGTCAAAC	AGTGTAAAAT
1551	CAAAAACCCG	GGCAAAAAAG	GCGTGCTCAT	CGACGGCGAA	GACGGTCTGA
1601	TGACCACGCT	TGCCAAATGC	TGCAAAACCT	CGCCGCCCGA	CGACATTGTC
1651	GGCTTCGTTA	CCCGCGATCG	CGGCATTTCG	GTACACCGCA	AAACCTGCCC
1701	CTCTTTCCGA	CACCTCGCCG	AACACGCGCC	CGAAAAAGTA	CTGGACGCAA
1751	GTTGGGCGCG	GTTCGAGGAA	GGACAAGTGT	TCGCCGTCGA	TATCGAAATC
1801	CGGCGCCAAG	ACCGCTCGGG	GCTTTTGGCG	GACGTATCCG	ACCGCTCGCG
1851	CCGCCACAAA	CTCAACGTTA	CGCCCGTGCA	AACCCAGTCC	CGCGACTTGG
1901	AAGCGAGCAT	GAGGTTACAG	CTCGAAGTCA	AACAAGTTAC	CGACCTCCCA
1951	CGCGTCCCTG	CCAGCCTCGG	CGACGTCAAA	GGCGTATTGA	CGGTTACCCG
2001	GCTTTAA				

a117.pap

1	MVHELDLLPD	AVAATLLADI	GRYPDWNLL	VSERCNSTVA	ELVKGVDVQ
51	KLTHFARVDS	LATPEERAQ	AETMRKMLLA	MVPTDIRVVLI	KLAMRTHTEQ
101	FLSNAPDPSPE	KRAVAKETLE	I FAPLANRLG	VWLQKWLQEE	LGRFRHQLEP
151	YREIALLLDE	KRTERLEYIE	NFLNLTRLT	KKNYNHFEVA	GRPKHIYSIY
201	KKMVKKKLSF	DGLFDIRAVR	ILVDTVPECY	TTLGIVHSLW	QPIPGFDDY
251	IANPKGNGYK	SLHTVIVLDE	DKGEVQIRT	FDMHQFNEFG	VAAHWRYYKEG
301	KGKDSAYEQK	I AWRLQQLDW	RENMAESGKE	DLAAAFKTEL	FNDTYIYVLT
351	HGKVLSLPTG	ATPIDFAYAL	HSSIGDRCRG	AKAEGOIVPI	SPLENGORV

401 EIIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQQNADT VREEGRVQLD  
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTINE  
501 PPPVPVSETT IVKQSKIKKG GKNGVLIDGE DGLMTTLAKC CKPAPPDDIV  
551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFVAVDIEI  
601 RAQDRSGLLR DVSDALARHK LNVAVQTQS RDLEASMRFT LEVKQVTDLP  
651 RVLASLGDKV GVLVSVTRL\*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKNVHFEVAGR	PKHIYSIYKKMVKKKL	
a117	EKYREIALLLDEKRT	LEYIENFLN	ILRTELKKN	IHFEVAGR	PKHIYSIYKKMVKKKL	
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
	SFDGLFDIRAVRIL	VDTVPECYT	TTLGIVHSL	WQPIPGEF	DDYIANPKG	NGYKSLHTVIVG
a117	SFDGLFDIRAVRIL	VDTVPECYT	TTLGIVHSL	WQPIPGEF	DDYIANPKG	NGYKSLHTVIVG
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
	PEDKGVEVQIRTF	DMHQFNEF	GVAAHWRY	KEGKGDS	AYEQKIAW	LRLQLLDWRENMAESG
a117	PEDKGVEVQIRTF	DMHQFNEF	GVAAHWRY	KEGKGDS	AYEQKIAW	LRLQLLDWRENMAESG
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
	KEDLAAAFKTELF	NDTIYVLT	PHGKVL	SLPTGAT	PIDFAYAL	HSSIGDRCRGAKVEGQIV
a117	KEDLAAAFKTELF	NDTIYVLT	PHGKVL	SLPTGAT	PIDFAYAL	HSSIGDRCRGAKVEGQIV
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
	PLSTPLENGQ	RVEIITAKE	GHP	SVNWLYEG	WVKS	NKAIGKIRAYIRQQNADTVREEGRVQ
a117	PLSTPLENGQ	RVEIITAKE	GHP	SVNWLYEG	WVKS	NKAIGKIRAYIRQQNADTVREEGRVQ
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
	LDKQLAKLTPKPN	LQELAENL	GYKKPED	LYTAVG	QGEISNRA	IQKACGTLINEPPVPVSE
a117	LDKQLAKLTPKPN	LQELAENL	GYKKPED	LYTAVG	QGEISNRA	IQKACGTLINEPPVPVSE
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
	TTIVKQSKI	KKGGKNG	VLIDGED	GGLMTTL	AKCCKP	APDDIIGFVTRDRGISVHRKXXXS
a117	TTIVKQSKI	KKGGKNG	VLIDGED	GGLMTTL	AKCCKP	APDDIIGFVTRDRGISVHRKTCPS
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
	FOHLAEHAPXK	VLDASWA	ALQEGQV	FAVDIEI	RAQDRS	GLLRDVSDALARHKLNVAVQT
a117	FRHLAEHAPEK	VLDASWA	ALQEGQV	FAVDIEI	RAQDRS	GLLRDVSDALARHKLNVAVQT
	570	580	590	600	610	620
m117.pep		460	470	480	490	
	QSRDLEASMRFT	LEVQVND	LPRVLAS	LGDKV	GVLVSVTRLX	
a117	QSRDLEASMRFT	LEVQVND	LPRVLAS	LGDKV	GVLVSVTRLX	
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCTTGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGCGCG
201 GCGCGAAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CGGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GGAATAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCCGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTTC GGCTTCCGCC ATCAAGAACCC
651 CGAAAAATAC CGCGAAATCG CCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAAA TTCCTCGATA TCCTGCGTAC GGAACCTAAA
751 AAATACAATA TCCACTTTGA AGTCGCCGCG CGTCGGAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAAGT CAGCTTCGAC GGCCTGTTTCG
851 ACATCCGCGC CGTGCAGGAT CTGGTCGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCATTCCTCG GCGagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGT TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGcacc AATTcAaCga ATTCGGTGTc GCCGCCCACT GGCGTTACAA
1101 AGAAGGCGGC AAAGGCGGAT CCGCTACGA ACAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAAATATG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCCATCG
1301 ACTTTCGCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCAGGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGGCG AATTTCCAA CCGCGCCATC CAAAAAGCCT CGCGCACGCT
1701 GAACGAACCG CGCCCGGTGC CCGTCAGCGC AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGCGC TGCTCATCGA CGGCGAAGAC
1801 GGCTTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTGCGCGC TTCGTTACCC GCGAGCGCGG CATTTCCGTC CACCGCAAAA
1901 CCTGCCCTTC TTTCCGACAC CTTGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGG CAAGTGTTCG CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGCG GTCCTCGCCG GCCTCGGCGA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TAA

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This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

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1  MTAISPIQDT OSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDDEVOK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSIYK KMVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKYS LHTVIVGPPE KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWRQLLDWR ENMAESGKED
401 LLAAPFKTELF NDTIYVLTTPH GKVLSLPTGA TPIDFAYALH SSIIDRCRGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPS VNWLYEGWVK SGKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GGEISNRAI QKACGTLNEP PPVVSATTI VKQSKIKKGG RTGVLDIGED
601 GLMTTLAKCC KPAPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPERVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```

```

51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTTGCTGG CGCAGGAACA TTACCCCGCC
151 GATGCCGCCA CGCCGTATGS CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCGCAAATG GTTCATGAAC TCGACCTGCT CCCGATGCCG GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCAGCGCGG
401 AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAATAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACS CCCCGACAG CCCGAAAAA CGCGCCGTCG
551 CCAAGAAATC CCTCGACATC TTCGCCCCGC TCGCCAAACG TTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAAAGCC
651 CGAAAAATAC CGCGAAATCG CGCTGCTTTT GGACGAAAAA CGCACCGAAC
701 CCATCGAATA CATCGAAATC TTCTCAACA TCCTGCGCGG TGAATCAAG
751 AAATACAATG TCCATTTCGA AGTCGCCGCG CGCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAATC CAGCTTCGAC GGCCTCTTTG
851 ACATCCGCGC CGTCCGAATT CTGGTTGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGTA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAATCCCA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCCG CCCGGAAGAC AAAGGCGTGG AAGTACAAAT CCGCACCTTC
1051 GATATGCACC AATTCACGCA ATTCGGTGIC GCGCCCACTG GCGGTTACAA
1101 AGAGGGCGCG AAGGGCGATT CCGCCTACGA ACAGAAAAAT GCCTGGITGC
1151 GCCAACTCTT GGACTGGCGC GAAAACATCG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CTTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAGAGTCC TCTCCTGCGC CACGGGCGCG ACCCCCATCG
1301 ACTTCGCGTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTCGG
1351 AAAGTCGAAG GGCAGATTGT GCGCTGTGCC ACCCGCTCG AAAACGACAA
1401 CGCGTCGCAA ATCATTACCG CCAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAACCCCAAC CTGCAAGAGC
1601 TTGCGGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGTTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAGCCT CCGGACCGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAACAGT
1751 CCAAAATCAA AAAAGGCGCG AAAAAGCGCG TGCTCATCGA CGGCGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTATCGGC TTCTGTACCC GCGAGCGCGG CATTTAGTGC CACCGCAAAA
1901 CDTGCCCGTC TTTCACACAC CTGCGCGAAC ACGCGCCGGA AAAAGTGCTG
1951 GACGCAAGCT GGGCGGCATT GCAGGAAGGA CAAGTATTCG CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGCG GTCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

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This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

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1  MTAISPIQDT QSATLQELRE WFD SYCAALP DNDKNLIGTA WLLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPCA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLID FAPLANRLGV
201 WOLKWQLEDL GFRHQKPEKY REIALLLDEK RTERLEYIEN FLNILLRGELK
251 KYNVHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWO PIPGEFDDYI ANPKNGNYKS LHTVIVGPED KGVEVQIRTF
351 DMHOFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESSKED
401 LAAPFKTELF NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQRV E IITAKEGHPN VNWLYEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIIG FVTRERGISV HRKTCPSFQH LAEHAPKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLASLGDKVG VLSVTRL*

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m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120



m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
g117-1	PDHFLGAAQMVDELDDLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
	70 80 90 100 110 120
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRLQFLSNAPDSPEK
g117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRLQFLSNAPDSPEK
	130 140 150 160 170 180
m117-1.pep	RAVAKETLDIFAPLANRLGVWLKQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN
g117-1	RAVAKETLDIFAPLANRLGVWLKQLEDLGFRHQEPEKYREIALLLDEKRTERLEYIEN
	190 200 210 220 230 240
m117-1.pep	FLNLRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
g117-1	FLDLIRTELKKYNHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
	250 260 270 280 290 300
m117-1.pep	TLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVGPEKGVQIRTFDMHQFNEFGV
g117-1	TLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVGPEKGVQIRTFDMHQFNEFGV
	310 320 330 340 350 360
m117-1.pep	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLT
g117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLT
	370 380 390 400 410 420
m117-1.pep	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
g117-1	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	430 440 450 460 470 480
m117-1.pep	VNWLYEGWVKSNKAIGKIRAYIROQNADTVREEGRVQLDKQAKLTFKPNLQELAEENLGY
g117-1	VNWLYEGWVKSGKAIGKIRAYIROQNADTVREEGRVQLDKQAKLTFKPNLQELAEENLGY
	490 500 510 520 530 540
m117-1.pep	KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSETTIVKQSKIKKGGKNSVLIDGED
g117-1	KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSATTIVKQSKIKKGGKTVLIDGED
	550 560 570 580 590 600
m117-1.pep	GLMTTLAKCKKPAPDDIAGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG
g117-1	GLMTTLAKCKKPAPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG
	610 620 630 640 650 660
m117-1.pep	QVFAVDIEIRAQDRSGLLRDVSALARKHLNVTAVQTQSRDLEASMRFTLEVQVNDLPR
g117-1	QVFAVDIEIRAQDRSGLLRDVSALARKHLNVTAVQTQSRDLEASMRFTLEVQVNDLPR
	670 680 690 700 710 720
m117-1.pep	VLASLGDVKGVLVSVTRLX
g117-1	VLASLGDVKGVLVSVTRLX
	730
m117-1/RelA	

sp|P55133|RELA\_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744  
Score = 536 bits (1366), Expect = e-151  
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRYVPDWNLLVSERCNSTVAELVKGVDVQKLTHFARVDSL 130  
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S  
Sbjct: 68 LSMDDDTLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVQMCAS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEKRAVAKETLDI 190  
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I  
Sbjct: 122 AEETAQAAQVDNIRRMLLSMVDDFRCVVIKLAERICNLREVQDQDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGFHQQKPEKYREIALLLDEKRTRELEYIENFLNLRGELK 250  
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K  
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDTYKQIAKQLSERRIDREDYITHFVDDLS DAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKKMKVKKLSFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQ 310  
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++  
Sbjct: 241 ASNIRAQVQGRPKHIYSIWKMKQKKSLEFDELFDVRAVRIAAELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEG- 369  
+P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHHW+YKEG  
Sbjct: 301 HLPKEFDDYVANPKNGYQSIHTVVLGPEGKTIEIQIRTKMHHESELGVAHHWKYKEG 360

Query: 370 --GKGDSAYEQKIAWLRLQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPHGKVLSP 427  
G SAY++KI WLR+LL W+E M++SG ++ ++++F+D +Y TP G V+ LP  
Sbjct: 361 ASGGAQSADEKINWLRLKLLAQEEMSDSG--EMLDELRSQVFDORVYAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQRVEIITAKEGHPSVNWLYE- 486  
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL  
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAKIGIRAYIRQONADTVREEGRVOLDKOLAKL--TPKPNLQELAENLGKYP 543  
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P  
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDNIIAGKEILEALVKIHATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQACGTLNEPPPPVPVSETTIVKQSKI-----KKGGKNGV 594  
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V  
Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLEKLSEASNQATSHKKPQORDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTREGRISVHRKTCPSFQHLAEHAPEKVLDASW 654  
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W  
Sbjct: 599 VVEGVNDLMTHLARCCQPIPGDDIQGFVTQGRGISVHRMDCEQLEELRHAPERI IDTVW 658

Query: 655 AALQEGQGVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQTQ--SRDLEASMRFTLEV 712  
G + + + + A +R+GLL++++ L K+ V +++++ + + M F LE+  
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLKELTNTLMNEKVKVAGMKSRVDYKKQMSIMDFEEL 717

Query: 713 KQVNDLPRVLASLGDVKGVLVSVTRL 737  
+ L RVL + VK V RL  
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

a117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACCAACGATA
101  AAAAAGTTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GCGCGAAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCGGCCA
251  CCTGTCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCGGAG CTGGTCAAAG GTGTGGACGA
351  AGTGCAAGAA CTCACCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401  AAGAAACGCGC CCAGCAGGCA GAAACTATGC GGAAATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501  CCGTCAATTT TTAAGCAACG CCCCCGACAG CCCCCGAAAA CGCGCCGCTG
551  CCAAAGAAAC CCTCGACATC TTCGCCCGCG TCGCCAACCG TTGGGCGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTG GGGTTCGCGC ATCAAGAACC
651  CGAAAAATAC CGCGAAATCG CCTGCTTTT GGACGAAAAA CGCACCGAAC
701  GCCTCGAATA CATCGAAAC TTCTTAATA TCCTGCGTAC GGAACTCAAA
751  AAATACAATA TCCACTTTGA AGTCGCCGGC CGTCCGAAAC ACATCTACTC
801  CATTTACAAA AAAATGGTGA AGAAAAAAGT CAGCTTCGAC GGGTTGTTCC

```

```

851 ACATCCGGCG CGTGCGGATT CTGGTTGATA CCGTCCCGGA GTGTTACACC
901 ACACCTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGGTGC GCCGCGCACT GCGGTTACAA
1101 AGAGGGCGCG AAAGGCGATT CCGCCTACGA AAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGACTGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCGCGCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAAGTCT TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCTCA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGTGTGCAA ATCATTACCG CCAACAAGG GCATCCTTCC CTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCAACAAG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCG AGCAAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAACCCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGCTC
1651 GGACAAAGGG AAATTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCCA AACCACCATC GTCAAACAGT
1751 CCATAATCAA AAAAGGCGCG AAAAAGCGCG TGCTCATCGA CGCGGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 CATTGTGCGG TTCGTTACCC GCGATCGCGG CATTTCCGTA CACCGCAAAA
1901 CCTGCCCCCT TTTCCGACAC CTCGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTCC CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAAAC CCAGTCCCGC
2101 GACTTGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTTACCGA
2151 CCTCCACCGC GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

a117-1.pep

```

1 MTAISPIQDT QSATLQELRE WFD SYCTALP NNDKKLVLA RSLAEAHYPA
51 DAATPYGEPL PDHFLGAAQM VHELDLLPCA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPERAQQA ETMRKMLLAM
151 VDIRVVLTK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQPEPEY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPED KGVEVOIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAPFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHFS VNWLYEGWVK SNKAIGKIRA
501 YIRQQNADTV REEGRVQLDX QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIQGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPSKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDKVG VLSVTRL*

```

a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD	SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL				
a117-1	MTAISPIQDTQSATLQELREWFD	SYCTALPNNDKKLVLAARSLAEAHYPADAATPYGEPL				
	10	20	30	40	50	60
m117-1.pep	PDHFLGAAQMVHELDLLPD	AVAATLLADIGRYVPDWNLLV	SERCNSTVAELVKG	DEVQK		
a117-1	PDHFLGAAQMVHELDLLPD	AVAATLLADIGRYVPDWNLLV	SERCNSTVAELVKG	DEVQK		
	70	80	90	100	110	120
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAM	VDIRVVLIKLAMRTRTLQFLSNAPDSPEK				
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAM	VDIRVVLIKLAMRTRTLQFLSNAPDSPEK				
	130	140	150	160	170	180
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
	190	200	210	220	230	240

	250	260	270	280	290	300
m117-1.pep	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
a117-1	FLNILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m117-1.pep	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
a117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m117-1.pep	AAHWRYKEGKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH					
a117-1	AAHWRYKEGKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH					
	370	380	390	400	410	420
	430	440	450	460	470	480
m117-1.pep	GKVLSTPTGATPIDFAYALHSSIGDRCRGARVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	GKVLSTPTGATPIDFAYALHSSIGDRCRGARVEGQIVPLSTPLENGQORVEIITAKEGHPS					
	430	440	450	460	470	480
	490	500	510	520	530	540
m117-1.pep	VNWLYEGWVKSNAIGKIRAYIRQONADTVREEGRVOLDKOLAKLTPKPNLQELAENLGY					
a117-1	VNWLYEGWVKSNAIGKIRAYIRQONADTVREEGRVOLDKOLAKLTPKPNLQELAENLGY					
	490	500	510	520	530	540
	550	560	570	580	590	600
m117-1.pep	KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
a117-1	KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
	550	560	570	580	590	600
	610	620	630	640	650	660
m117-1.pep	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFOHIAEHAPEKVLDAASWALQEG					
a117-1	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWALQEG					
	610	620	630	640	650	660
	670	680	690	700	710	720
m117-1.pep	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR					
a117-1	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR					
	670	680	690	700	710	720
	730					
m117-1.pep	VLASLGDKGVLSVTRLX					
a117-1	VLASLGDKGVLSVTRLX					
	730					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1   ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAT TCATTTATTG GCAAATGGTA TGATCAGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAG
251 CTTCCCCTTG GTTGCCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAPGACA TAGTCAACGT
351 GCGATTTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1   MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRRK
51  YFYPMDIPRD IVIGIGTIID FLMVPPNWELF EIKASPWLPD SVGIHERYER
101 FTTMLRYIFT EKDIYVNVRFD YYNKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTCATTG GAATCGGTAC
201 CATTTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
1  MCEFKDIIRN VPYFEGYDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRKK
51  YPYPM DIPRY VVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

          10      20      30      40      50      60
m118.pep  MCEFKDIIRNVPYFEGYDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118      MCEFKDFRRNIPCFEEDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60

          70      80      90      100     110     120
m118.pep  VVIGIGTIIDFLMVPNWKLFEIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118      IVIGIGTIIDFLMVPNWELFEIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          70      80      90      100     110     120

m118.pep  YYNKKX
          |||||
g118      YYNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAATTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
1  MCEFKDFRRN IPCFEEDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRKK
51  YPYPM DIPRD IVIGIGTIID FLMVPNWELF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep  MCEFKDIIRNVPYFEGYDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a118      MCEFKDFRRNIPCFEEDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60
```

341

	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLFEIKAS	PWLPDSVGIHERYERFTTMLRYIFTEK	DIVNVRF			
a118	IVIGIGTIIDFLMVPNWELFEIKAS	PWLPDSVGIHERYERFTTMLRYIFTEK	DIVNVRF			

m118.pep	YYNKKX
a118	YYNKKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

```

g120.seq
1  ATGATGAAGA CTTTAAATAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTGCGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGCC TGAATAAGGC GGTACGGGA AAATACAGCA Taggcggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGGTGGC GCGCGGCGAC GATACGGTAA
551 CGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACgaCG GCAAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

```

g120.pep
1  MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

```

m120.seq
1  ATGATGAAGA CTTTAAATAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTGCGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGGC GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

```

m120.pep
1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILS	SAALPCAYAAGLPQSA	VLXYSYGI	PATMTFERSG	NAYKIVSTIK	
g120	MMKTFKNIFSAAILS	SAALPCAYAARLPQSA	VLHYSYGI	PATMTFERSG	NAYKIVSTIK	
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVV	GNLHPTYYRDIRRG	KLYAEAKFADG	SVTYGKAGESKTE	QSPKAM	
g120	VPLYNIRFESGGTVV	GNLHPAYYKDIRRG	KLYAEAKFADG	SVTYGKAGESKTE	QSPKAM	
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAK	LPGLKITNGKKLYSV	GGLNKAGTGKYSIG	GGVETE	VVKYRVR	RGD
g120	DLFTLAWQLAANDAK	LPGLKITNGKKLYSV	GGLNKAGTGKYSIG	GGVETE	VVKYRVR	RGD
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNI	PAQIGYTDGKTYTL	KLKSVQINGQA	AKP		
g120	DTVTYFFAPSLNNI	PAQIGYTDGKTYTL	KLKSVQINGQA	AKPX		
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

```

1  ATGATGAAGA CTTTAA AAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTC ACGTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAGAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAACCGGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

```

1  MMKTFKNIFS AAILS AALPC AYAAGLPQSA VLHYSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPEGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILS	SAALPCAYAAGLPQSA	VLXYSYGI	PATMTFERSG	NAYKIVSTIK	
a120	MMKTFKNIFSAAILS	SAALPCAYAAGLPQSA	VLHYSYGI	PATMTFERSG	NAYKIVSTIK	

343

	10	20	30	40	50	60
m120.pep	70	80	90	100	110	120
	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFAJGJSV'TYKGAGESKTEQSPKAM					
a120	70	80	90	100	110	120
	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFAJGJSV'TYKGAGESKTEQSPKAM					
m120.pep	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE'VVKYRVRRGD					
a120	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE'VVKYRVRRGD					
m120.pep	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					
a120	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAACAC AGCTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51  GGCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTCGCGCG CAAATTGCTG
151 GATTTCGAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACAGCGCAAAC CGCCGCGCGA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACAGCGCCGGA ACACGGTtac AGCATAACAG TTGCCGATT
351 GCGGCTGCTG GCGGAACTGa cgcggatttT TACCGTCggc gacttcCGCA
401 GCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGCGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cactGGcagc TGCCTTACGA CAAAacggt gcAAAGgcg cacaAGGCAA
651 catatTGcG cAACTGCTCG gcaggtGCT CGCCcaccCG TATTCTCAC
701 AACCcacc aaAAAGCAG GGgcGCGaac TgtttgcccT AAattggctc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgta- tgcggacgt
801 ttcccgattc accgcgcaaA ccgTttggga cgcggtctca CACGACGCG
851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGCGAGA ATGTTTCGCG ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATTTg
1001 cgtggttgG GCGGTGTTGG ATTAACCGCA TTCCCGTAG TCCGCACAA
1051 GCGACCGCG CATCAAACC GTGTATTCTG GCGCGGGAT ATTATTATG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSNDGADA VLVRMDGGKW LGAEGHAFT? YPDRLRRKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPGP NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVWDVAV HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAACAC AGCTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCGCGCA GGTACGCGC CCAATTGCTG

```



```

151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTG
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCCGTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxGAGC TTCCTTACGA CAAAACGGT GCAAAGTCG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGSCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGT'TGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILF QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDVAVS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTPYPDLRRKLDDLQDTGTDEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAAGGQCAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILFQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTPGNMLMDAWTOAHWQLPYDKNGAKAACGNILPOLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVAVSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIENPV					
	250	260	270	280	290	300

345

```

          310      320      330      340      350      360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPOQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
          |||||:|||||
g121      LMADLAECFGTRVSLHSTAE LNLDPOQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
          310      320      330      340      350      360

m121.pep  XAGYYYY
          |||||
g121      GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTAGTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCGCGCA GGTACGCGC CAAATTGCTG
151 GATTTCGAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCCGCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAATCA GCGTACTCCC CCGCGACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCACCC TAAAAGCACG GGGCGGAAC TGTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATT ACCGCGCAA CCGTTTCGA CGCGTCTCA CACGACGCG
851 CAGATGCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCG CATCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRLKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPOQWVEA AAFWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

```

          10      20      30      40      50      60
m121.pep  METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRLQLDQDTGADEL
          |||||:|||||
a121      METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRLQLDQDTGADEL
          10      20      30      40      50      60

          70      80      90      100     110     120
m121.pep  HRSRILSOELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL
          |||:|||||
a121      HRSRMLSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESYSVQLADLPLL
          70      80      90      100     110     120

```

346

	130	140	150	160	170	180
m121.pep	XX					
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
a121	XX					
	190	200	210	220	230	240
m121.pep	250	260	270	280	290	300
a121	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADAROMYICDGGIRNPV					
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
a121	LMADLAECFGTRVSLHSTADLNLDPOWVEAAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
a121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGCGATGCC GTACTGATAC GGATGGACGG CGGCAAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCGGGCA GGTACGCGG CCAATTGCTG
151 GATTTCGAGG ACACAGGCGC AGACGAAC TG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCTTAT ATGCGCAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCGCGC ACAGCGCCGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTT TACCGTCGGC GACTTCGCA
401 GCCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCACTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGCGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGCGCGGGC AATATGCTGA TGGACGCGTG GACGCAGGCA
601 CACTGCGCAG TCCTTACGCA CAAAACGGT GCAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 ACCCCACCCC TAAAAGCAGC GGGCGCGAAC TGTTCGCCCT AAATTGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTGCGA CGCGCTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG CGCGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAC CTGAACCTCG ATCGCAATG GGTGGAAGCC GCCGNATTTG
1001 CGTGGTTTGG GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGCGCG CATCAAACC GTGTATTCTG ANCGCGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  NETQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFPT YPGRLLRQLL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAFEHGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDVSH HAAADAROMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

m121-1.pep	METQLYIGIMSGTSMDGADAVLIRMGGKWLGAEGHAFTYPGRLLRQLLDLQDTGADEL
g121	METQLYIGIMSGTSMDGADAVLVRMDGGKWLGAEGHAFTYPDRLLRQLLDLQDTGTDEL
	10 20 30 40 50 60
m121-1.pep	70 80 90 100 110 120
g121	70 80 90 100 110 120
m121-1.pep	130 140 150 160 170 180
g121	130 140 150 160 170 180
m121-1.pcp	190 200 210 220 230 240
g121	190 200 210 220 230 240
m121-1.pep	250 260 270 280 290 300
g121	250 260 270 280 290 300
m121-1.pep	310 320 330 340 350 360
g121	310 320 330 340 350 360
m121-1.pep	XAGYYYYX
g121	GAGYYYYX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1 ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51 GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGGCGGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTTACGGCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAATCG CACCGCAGCA GGATGTTGTC
201 CGAAGAACTC AGCCGCGTGT ACAGCGCAAC CGCCGCGGAA CTGCTGTGCA
251 GTCAAAACCT GCGCGCGTGT GACATTACCG CCTCTCGGCT CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TGTCGCCCGC GGACAAAGGG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGGTCCGCGA GCACAGGCGAA ACACGCGCGG TACTGAACAT
501 CGCGGGGATT GCCAACATGA GCGTACTFCC CCCGACGCGA CCCGCCTTCC
551 ECTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGACGGCA
601 CACTGGCAGC TTCTTTACGA CAAAAACGGT GCAAAGCGCG CACAGGCGAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTCGCAC
701 AACCCACACC TAAAGACAGC GGGCGGCAAT TGTTTGCCCT AAATTGGGCTC
751 GAAACCTACC TTAGCAGCGG CGAAAACCGA TACGACGTAT TCGCGACGCT
801 TTCCCATTTC ACCGCGCAAA CCGTTTTCGA CGCCGCTCTC CACGCAGCGG
851 CAGATGCCCG TCAAAATGAC ATTTGCGCGC GCGGCATCTG CAATCCTGTT
901 TTAATTGGCG ATTTGGCAGA ATGTTTTCGG ACACGCTGCT CCCGTCACAG
951 CACCGCGCAA CTGAACCTCG ATTCGCAATG GGTAGAAGCC CGCTGGCTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

a121-1.pap

```
1  METQLYIGIM  SGTSMGADA  VLIRMDGGKW  LGAEGHAFTP  YPGRLRRLKL
51  DLQDTGADEL  HRSRLMSQEL  SRLYAQTAAE  LLCQNLPAS  DITALGCHGQ
101 TVRHAPESHY  SVQLADLPLL  AERTQIFTVV  DFRSRDLAAG  GQGAPLVPFA
151 HEALFRDDRE  TRAVLNTGGI  ANISVLPPDA  PAFGDTGPG  NMLMDAWNMA
```

201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL  
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV  
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK  
 351 ATGASKPCIL GAGYYY\*

m121-1/a121-1 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRLR	ROLLDLQDTGADEL		
a121-1	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRLR	ROLLDLQDTGADEL		
	10	20	30	40	50	60
m121-1.pep	70	80	90	100	110	120
a121-1	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRS	DLAAGGQGAPLVPA	FHEALFRDNRETRAV	LNIGGIANISVLP	PPDA	
a121-1	AERTRIFTVGDFRS	DLAAGGQGAPLVPA	FHEALFRDNRETRAV	LNIGGIANISVLP	PPDA	
	130	140	150	160	170	180
m121-1.pep	190	200	210	220	230	240
a121-1	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	250	260	270	280	290	300
a121-1	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	310	320	330	340	350	360
a121	310	320	330	340	350	360
m121-1.pep	XAGYYYY					
a121	GAGYYYY					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGGA AAAAGGCGAA GtcatCGTAC
101 TGCTGGGCCC gTccggtgc ggCAAATCCA CCTTcstgcg ctgcgtcaaC
151 GGTTTGGAGC CGCACCAagg cgGCAGCATC GTGATGGACG GTgtcgGCCA
201 ATTcggcAAA GACGTTTCCT GGCAAACCGC CCGCAAAAa gtcggtatgg
251 tctttcaaag taacgAactg Tttgcccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAAcCgc gaccgtgccc aagcaGAGGC
351 gCAAGCCGGC AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GGCGGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGACG AAATCACC GC
501 CGCACTTGAC CCCGAAATGG TGCGCGAAGT CITGGAAGTG GTTTTGGAAC
551 TCGCCCGCGA AGGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCCGAAA CCTTTTTTTC CGCACCAAAA AGCGAACGCG
701 CCCGCCAATT TCTGGCAGGT ATGGACTACT GA
```

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

## g122.pep

```

1  MALLSIRKLIH KQYGSVTAIQ SLDLDLEKGE VIVLLGPSGC GKSTLLRCVN
51  GLEPHQGGSI VMDGVGEFGK DVSWQTARQK VGMVFQSNEL FAHMTVIENI
101 FLGPVKEQNR DRAEAEAQAG KLLERVGLLD RKNAYPRELS GGQKQRIATV
151 RALCLNPEVI LLDEITAALD PEMVREVLEV VLELAREGMS MLIVTHEMGF
201 ARKVADRIVF MDKGGIVESS DPETFFSAPK SERARQFLAG MDY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 447>:

## m122.seq

```

1  GTTGTCAATGA TTAAATCCG CAATATCCAT AAGACCTTTG GCGAAAACAC
51  TATTTTGCGC GGCATCGATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGcC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAG TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TCGCGCGCAA ATCAKGCATG GTGTTTCAAC AATACAaCT CTTTCCGCAC
301 AAAACCGCCT TGGAAAACGT AATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTGAG
451 CAGCAGCGCG TCGGCATTGC CCGCGCATTC GCGATTTCAGC CTGAACTGAT
501 GCTGTTTGAC GAACCGACTT CCGCGCTCGA TCCTGAATTG GTGCAAGATG
551 TTTTGGATmC CATGAAGGAA TTGGCGCAAG AAGGCTGGAC CATGGTTGTC
601 GTTACGCATG AAATCAAGTT CGCCTTAGAA GTGGCAACCA CCGwCGTCGT
651 GATGACrGC GGCCTTATTG TCGAACAAGG CAGCCCGCAA GATTTGTTG
701 ACCACCCCAA ACACCAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
751 ACCAAGATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 448; ORF 122>:

## m122.pep

```

1  VVMIKIRNIH KTFGENTILR GIDL DVCKGQ VVILGPSGS GKTTFLRCLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSXM VFQYQNLFPH
101 KTALENVMEG PVAVQGKPAA QAREEALKLL EKVGLGDKVD LYPYQLSGGQ
151 QQRVGIALAL AIQPELMLFD EPTSALDPEL VQDVLDXMK E LAQEGWTMVV
201 VTHEIKFALE VATTXVMDX GVIVEQGS PQ DLFDPKHER TRRFLSQIQS
251 TKI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng)

from *N. gonorrhoeae*:

## m122/g122

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKT	FGENTILRGID	LDVCKGQVVV	ILGPSGSGKT	TFRLRCINALE	MPEDGQI
g122	MALLSIRKLIH	KQYGSVTAIQ	SLDLDLEKGE	VIVLLGPSGC	GKSTLLRCVN	GLEPHQGGSI
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKID	FSKKPSKHDIL	ALRRKSXMVF	QYQNLFPHK	TALENVMEGP	VAVQGKPAA
g122	VMDGVGEFGK	DVSWQTA-----	RQKVMVFQSN	ELFAHMTVI	ENIFLGPVKE	QNRDRA
	70	80	90	100	110	
	130	140	150	160	170	180
m122.pep	QAREEALKLLE	KVGLGDKVDL	YPYQLSGGQ	QQRVGIALAL	AIQPELMLFD	EPTSALDPEL
g122	EAEAQAGKLL	ERVGLLDKRN	AYPRELSGG	QKQRIATV	RALCLNPEVI	LLDEITAALDP
	120	130	140	150	160	170
	190	200	210	220	230	240
m122.pep	VQDVLDXMKEL	AQEGWTMVV	VTHEIKFALE	VATTXVMDX	GVIVEQGS	PQDLFDPKHER
g122	VREVLEVVL	EAREGMSML	IVTHEMGF	ARKVADRIV	FMDKGGIV	ESSDPETFFS

350

	180	190	200	210	220	230
	250					
m122.pep	TRRFLSQISTKIX					
	: : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```

a122.seq
1   GTTGTCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTTTGC GC GGCATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGC GCCGCAA ATCAGGCATG GTGTTTCAAC AATACAACCT CTTCCGCAC
301 AAAACCGCCT TGGAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTGAT
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTGAGC CCGAGCTGAT
501 GTTGTGTTGAC GAACCCACTT CCGCGCTTGA CCCCAGTTG GTGCAAGACG
551 TGTTGAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGTTATCG TAGAGCAGG CAGCCGAAA GAGTTGTTG
701 ACCACCCCAA ACACGAACG ACGCGGAGAT TTTAAGCCA AATCCAATCT
751 ACCAAGATT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```

a122.pep
1   VVMIKIRNIH KTFGNTILR GINLDVCKGQ VVVILGPSGS GKTTFLRCLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSGM VFQYQNLFPH
101 KTALENVM EG PVAVQGKPA QAREEALKLL EKVLGDKVD LYPYQLSGGQ
151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVNLAMKE LAREGWTM VV
201 VTHEIKFALE VATTVVMDG GVIVEQGS PK ELFDHPKHER TRRFLSQIQS
251 TKI*
  
```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFGNTILRGIDLVDCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQI					
a122	VVMIKIRNIHKTFGNTILRGIDLVDCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSGMVVFQYQNLFPHKTALENVM EGPVAVQGKPA					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSGMVVFQYQNLFPHKTALENVM EGPVAVQGKPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
a122	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m122.pep	VQDVLDMKELAQEGWTVVVVTHEIKFALEVATTXVVMXG VIVEQGSQDLFDHPKHER					
a122	VQDVLNAMKELAREGWTM VVVVTHEIKFALEVATTXVVMXG VIVEQGSQDLFDHPKHER					
	190	200	210	220	230	240
	250					
m122.pep	TRRFLSQISTKIX					

351

|||||  
a122 TRRFLSQIQSTKIX  
250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq  
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT  
51 GCGCGGCATC GATTTGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG  
101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCGCTGCCT AAACGCGTTG  
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG  
201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC  
251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC  
301 GTGTTGGAAA ACGTGATGGA AGGGCCGGTT GCCGTACAGG GCAAGCCTGC  
351 CGCCCAAGCG CGCGAAGAGG CTTTGAAGCT GCTGGAAGAA GTCCGCTTGG  
401 GCGATAAAGT GGATTGTGAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG  
451 CGTGTCCGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT  
501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTGTT  
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC  
601 CACGAAATCA AGTTACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA  
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC  
701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCCAAG  
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep  
1 MIKIRNIHKT FGENTILRGI DLDVKGQVV VILGPSGSGK TTFLRCLNAL  
51 EMPEDGQIEF DNRPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT  
101 VLENMVEGPV AVQKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ  
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT  
201 HEIKFTLEVA TNVVMDGGV IVEQSGPKEL FDHLKHERTR RFLSQIQSAK  
251 I\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq  
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACATTTT  
51 GCGCGGCATC GATTTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG  
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG  
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA  
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC  
251 GCAAATCAGG CATGGTGTTC CAACAATACA ACCTCTTCCC GCACAAAACC  
301 GCCTTGGAAA ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC  
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAGAA GTCCGCTTGG  
401 GCGACAAAGT GGATTGTGAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG  
451 CGCGTCGGCA TTGCCCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT  
501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG  
551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTGCTTACG  
601 CATGAAATCA AGTTCCGCTT AGAAGTGGA ACCACCGTCG TCGTGATGGA  
651 CGGCGGCGTT ATTGTCGAAC AAGGCAGCCC GCAAGATTG TTCGACCACC  
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG  
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep  
1 MIKIRNIHKT FGENTILRGI DLDVCKGQVV VILGPSGSGK TTFLRCLNAL  
51 EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT  
101 ALENMVEGPV AVQKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ  
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT  
201 HEIKFALEVA TTVVMDGGV IVEQSGPDQL FDHPKHERTR RFLSQIQSTK  
251 I\*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKTFGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
g122-1	MIKIRNIHKTFGENTILRGIDLDVKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					



352

	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAQA					
g122-1	DNERPLRIDFSKKTSKHDILALRRKSGMVFQQYNLFPHKTVLENVMEGPPVAVQGKPAQA					
	70	80	90	100	110	120
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTTSALDPELVQ					
g122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTTSALDPELVQ					
	130	140	150	160	170	180
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGSPPDLFDHPKHHERTR					
g122-1	DVLDMKELAREGWTMVVVTHEIKFTLEVATNVVMDGGVIVEQGSPPKELFDHLKHHERTR					
	190	200	210	220	230	240
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAATAA  TCCGCAATAT  CCATAAGACC  TTCGGCAAAA  ATACCATTTT
51  GCGCGGCATC  AATTTGGATG  TGTGCAAAGG  GCAGGTGGTC  GTCATCCTCG
101  GGCCCTCCGG  CTCAGGCAAA  ACGACGTTTC  TGCGATGCCT  AAACGCGTTG
151  GAAATGCCCG  AAGACGGACA  AATCGAGTTC  GACAACGAGC  GACCGCTGAA
201  AATCGATTTT  TCTAAAAAAC  CAAGCAAACA  CGATATTTTG  GCACTGCGCC
251  GCAATCAGG  CATGGTGTTC  CAACAATACA  ACCTCTTTTC  GCACAAAACC
301  GCCTTGGAAG  ACGTGATGGA  AGGACCGGTT  GCCGTACAGG  GCAAGCCTGC
351  CGCCCAAGCG  CGCGAAGAGG  CTCTGAAACT  GCTGGAAAAA  GTCGGCTTGG
401  GCGACAAAGT  GGATTGTAT  CCCTACCAGC  TTTCCGGCGG  TCAGCAGCAG
451  CGCGTCGCGA  TTGCCCGAGC  ATTGGCGATT  CAGCCCGAGC  TGATGTTGTT
501  TGACGAACCC  ACTTCCGCGC  TTGACCCCGA  GTTGGTGCAA  GAUGTGTGA
551  ACGCCATGAA  GGAATTGGCG  CGGGAAGGTT  GGACGATGGT  CGTCGTTACC
601  CACGAAATCA  AGTTCGCGCT  GGAAGTTGCC  ACGACCGTTG  TCCTGATGGA
651  CGGCGGCGTT  ATCGTAGAGC  AGGCGAGCCC  GAAAGAGTTG  TTCGACCACC
701  CCAAACACGA  ACGGACGCGG  AGATTTTAA  GCCAAATCCA  ATCTACCAAG
751  ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT  FGKNTILRGI  NLDVCKGQVV  VILGPSGSGK  TFLRCLNAL
51  EMPEDGQIEF  DNERPLKIDF  SKKPSKHDIL  ALRRKSGMVF  QQYNLFPHKT
101  ALENVMEGPV  AVQGKPAQA  REEALKLLEK  VLGDKVDLY  PYQLSGGQQQ
151  RVGIARALAI  QPELMLFDEP  TSALDPELVQ  DVLNAMKELA  REGWTMVVVT
201  HEIKFALEVA  TTVVVMDDGG  IVEQGSPEL  FDHPKHHERTR  RFLSQIQSTK
251  I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGENTILRGIDLVDCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAQA					
	70	80	90	100	110	120
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTTSALDPELVQ					
m122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTTSALDPELVQ					

	130	140	150	160	170	180
	190	200	210	220	230	240
a122-1.pep	DVLNAMKELAREGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGS	PKELFDHPKHERTR				
m122-1	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGS	PQDLFDHPKHERTR				
	190	200	210	220	230	240
	250					
a122-1.pep	RFLSQIQSTKIX					
m122-1	RFLSQIQSTKIX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 457>:

```

g125.seq
1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGGT
51  TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TCGCCCCCTT GGGCTGGCAG CGCGGTCTGG CGGCCCTGCT TTTGGGTGAT
151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GTGTGCGCCT GTCGTTCCGC AAATGCGGTT
251 CAGTGCTGTT TTCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGTCGGCGC AacggTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACggc gaATCCTTTG TCTGGTGGGC ATTGGCAAAC GGCGCACTGA
401 TCGTGCTGTG GCTGGTTTTT GCGGCACGCA GAACGGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GCTTGCCGTG TTGTGGTTGA GCGTCGAAGT
501 GTTCGCTTCG TCCGGCACAA ACGCCGCGCC CGCCGTTTCA GACGGCATGA
551 CCTTCGGAAC GGCAGTCGAA CTGTCCGCCG TCATGCCGCT TTCCTGGCTG
601 CCGCTGGCCG CCGACTACAC GCGCCAAGCA CGCCGCCCGT TGGCGGCAAC
651 CCTGACGGCA ACGCTCGCCT ATACGCTGAC GGGCTGCTGC ATGTATGCCT
701 TGGGTTTGGC GCGGCTCTG TTTACCGGAG AAACCGACGT GCGGAAAATC
751 CTGTTGGGCG CGGGCTTGGG CATAACGGGC ATTCTGGCAG TCGTCCTCTC
801 CACCGTTACC ACAACGTTTC TCGATACCTA TTCCGCCGGC GCGAGTGCGA
851 ACAACATTTT CCGCGCTTTT GCGGAAATAC CCGTCGCTGT CGGCGTTACC
901 CTGatccgca cegtgccttc cgtcatgctg cccgttaccg aatataaaaa
951 cttcctgctg cttatccgct cggatatttg gccgatggcg ggtggttttg
1001 attgccgaCT TTTttgtctt AAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 458; ORF 125.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 459>:

```

m125.seq
1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCTCCGCCA TCGGGCTGAT
51  TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TTGGCCTTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTACT TTTGGGTGAT
151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCCGC AAACGCGGTT
251 CAGTGCTGTT TTCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTT GCGGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAAT
501 CTTTTCACG GCAGGCAGCA CCGCCGACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCGCTTTC CTGGCTGCCG
601 CTTGCCCGCG ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCCCT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GCGCTTGTTC ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAG GTTTGgGTGC GGCAGGCATT TTGGCGGTGC TCCTCTCCAC
801 CGTTACCACA ACGTTTCTCG ATGCCTATTC CGCCGGCGCG AGTGCGAACA

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851 ACATTTCCGC GCGTTTTGCG GAAACACCCG TCGCTGTCrG CGTTACCCTG  
 901 ATCGGCACGG TACTTGCCGT CATGCTGCCC GTTACCGAAT ATGAAAACCTT  
 951 CCTGCTGCTT ATCGGCTCGG TATTGCGCC GATGGCGGgC GGTTTTGATT  
 1001 GCGGACTTTT TCGTCTTGAA ACGGCGTGA

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

m125.pep  
 1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH  
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA  
 101 VMYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT  
 151 VSMLLMLLAV LWLSAEVFST ACSTAAQVSD GMSFGTAVEL SAVMPLSWLP  
 201 LAADYTRHAR RPFATLTAT LAYTLTGCM YALGLAAALF TGETDVAKIL  
 251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL  
 301 IGTVLAVMLP VTEYENFLLL IGSVFAPMAG GFDCLFRLE TA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

m125/g125

m125.pep	10	20	30	40	50	60
	MSGNASSPSSSSAIGLIWFGAAVSI AEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA					
g125	MSGNASSPSSSSAIGLVWFGAAVSI AEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA					
	10	20	30	40	50	60
m125.pep	70	80	90	100	110	120
	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVAGATVSSALGKVLWDG					
	70	80	90	100	110	120
m125.pep	130	140	150	160	170	179
	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	180
m125.pep	180	190	200	210	220	230
	DGMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAL					
g125	DGMTFGTAVELSAVMPLSWLPLAADYTRQARRPFAATLTATLAYTLTGCMYALGLAAL					
	190	200	210	220	230	240
m125.pep	240	250	260	270	280	290
	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	250	260	270	280	290	300
m125.pep	300	310	320	330	340	
	LIGTVLAVMLPVTEYENFLLLIGSVFAPMAGGFDCLFRLETA					
g125	LIRTVLAVMLPVTEYKNFLLIRSVFGPMAGGFDCLFCLKTAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

a125.seq  
 1 ATGTCGGGCA ATGCCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT  
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC  
 101 TTGCGCCTTT GGGCTGGCAG CCGGCTCTGG CGGCTCTGCT TTTGGGTCAT

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151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTTCGGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTT GCGGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGCTGA GTGCCGAAGT
501 CTTTTCACG GCAGGCAGCA CCGCCGACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTA TGCCGCTTTC TTGGCTGCCG
601 CTGGCCGCCG ACTACACGCG CCACGCGCGC CGCCCCTTTC CGGCAACCC
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTGGCAGC GCGCTTGTTC ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAG GTTGGGTGCG GCGAGGCATT TTGGCGGTCG TCCTGTGCGA
801 CGTTACCACC ACTTTTCTCG ATGCCTACTC CGCCGGCGTA AGTGCCAACA
851 ATATTTCCGC CAACTTTTCG GAAATACCCA TCGCCCTTGC CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCCG GTTACCGAAT ATGAAAACCT
951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCG.GC GGTTTTGATT
1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1  MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWC RGLAALLLGH
51  AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFVA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RPFATLTAT LAYTLTGCMW YALGLAALF TGETDVAKIL
251 LGAGLGAAGI LAVVLSTVTT TFLDAYSAGV SANNISAKLS EIPIAVAVAV
301 VGTLLAVLLP VTEYENFLLL IGSVFAPMAX GFDCRLFRLE TA*

```

m125/a125 95.6% identity in 342 aa overlap

```

m125.pep      10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQRGLAALLLGHAVGGALFFAA
|||||:|||||
a125          10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQRGLAALLLGHAVGGALFFAA

m125.pep      70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
|||||:|||||
a125          70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFVANMLQLAGWTAVMIYAGATVSSALGKVLWDG

m125.pep     130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLMLLAVLWLSAEVFSTAGSTAAQVSD
|||||:|||||
a125         130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLMLLAVLWLSAEVFSTAGSTAAQVSD

m125.pep     190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAALF
|||||:|||||
a125         190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAALF

m125.pep     250     260     270     280     290     300
TGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
|||||:|||||
a125         250     260     270     280     290     300
TGETDVAKILLGAGLGAAGILAVVLSTVTTTFLDAYSAGVSANNISAKLSEIPIAVAVAV

m125.pep     310     320     330     340
IGTVLAVMLPVTEYENFLLIGSVFAPMAGGFDCRLFRLETAX
:|||||:|||||
a125         310     320     330     340
VGTLLAVLLPVTEYENFLLIGSVFAPMAXGFDCRLFRLETAX

```

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310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```

g126.seq
  1  AtgccgtcTG AAaccCcaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
 51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101  CTTTCCCTTC GCGGCTGCTg cteggcacgG eggcctacCC GACCCCTGAA
151  ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201  GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTGGT
251  CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301  CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351  TGAAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401  AGCCGGACGT GTTCCAACTC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451  GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501  CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551  GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601  CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651  CCAAGCGGCA CAAGTGATGG AATGGGTTT TGACGGCGTA TTGTTAAACA
701  CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751  CTCGCCGTCG AATCCGGACG GCTGGCATTG GAAGCCGGGC CGGTCGAAGC
801  GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTGGC
851  ATTCGGCGGA ATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```

g126.pep
  1  MPSETPKARR RLSGDIASDN HTKESIMLTLY YGETFPSRL L LGTAAYPTPE
 51  ILKQSVRTAR PAMITVSLRR TGCGGEAHGQ GFWSLLQETG VVPLPNTAGC
101  QSVQEAHTTA QMAREVPETD WIKLELIGDD DTLQPDVFQL VEAAILIKD
151  GPKVLPYCTE DLIACRLLLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201  RLPDTPLIID AGLGLPSQAA QVMEWGFDGV LLNTAVSRSG DPVNMARAF
251  LAVESGRLAF EAGPVEARTK AQASTPTVGQ PFWHSAEY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```

m126.seq (partial)
  1  ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
 51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCG GAAATCCTCA
101  AACATCCAT CCAAACCGCC CAGCCTGCGA TGAATTACCGT CTCGCTGCGC
151  CGCGCGGGAA GCGGCGGCGA GCGCACGGT CAGGGGTTT GGTGCTGCT
201  TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251  TGCAGGAAGC GGTAACGACG GCGCAAATGG CGCGGAAGT GTTTGAAACC
301  GATTGGATAA AATTGGAAC TATCGGAGAT GACGACACCT TGCAGCCGGA
351  TGTGTTCCAG CTTGTCGAAG CGGCGGAAAT CTTGATTAAA GACGGCTTCA
401  AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451  GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCGGA TCGGCACGGG
501  TTTGGGCGCG GTTCACGCCT ACGCGTTGAA CGTCCTGCGC GAACGCCTGC
551  CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601  GCACAAGTGA TGGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651  TTCCCGCAGC GCGGATCCGG TCAATATGGC ACGCGCCTTC GCACTCGCCG
701  TCGAATCCCG ACGGCTGGCA TTTGAAGCGG GACCGGTGCA AGCAGCGGAC
751  AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTT GGCATTGCGC
801  GGAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```

m126.pep (partial)
  1  ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
 51  RAGSGGEAHG QGFWSLLQET GVPVLPNTAG CQSVQEAHTT AQMAREVPET

```

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```

101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRLL
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLRL ERLPDTPLII DAGLGLPSQA
201 AQVMEWGFDG VLLNTAVSRS GDPVNMARAF ALAVESGRLA FEAGPVEARD
251 KAQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep      .  HYTKPEIMLTLYGETFPSRLLLGTAAAYPTPEILKQSIQTAQ
                  ::||| ||||| ||||| ||||| ||||| ||||| |||||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSRLLLGTAAAYPTPEILKQSVRTAR
                  10      20      30      40      50      60

                                50      60      70      80      90      100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  70      80      90      100      110      120

                                110      120      130      140      150      160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  130      140      150      160      170      180

                                170      180      190      200      210      220
m126.pep      APIGTGLGAVHAYALNVLRLERLPTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRLERLPTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  190      200      210      220      230      240

                                230      240      250      260      270
m126.pep      DPVNMARAFALAVESGRLA FEAGPVEARDKAQASTPTVGQPFWHSAEYX
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMARAFALAVESGRLA FEAGPVEARTKAQASTPTVGQPFWHSAEYX
                  250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

al26.seq

```

1   TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCCT TCGCGGCTGC TGCTCGGCAC AGCCGCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACC GCCCGGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CCGCGGCGAG GCGCACGGTC AGGGGTTTTC
201 GTCGCTGCTT CAAGAAACCG GCGTTCCCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAACTC ATCGGCGACG ACGACACCTT
351 GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC GCGGAAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCGGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCUA CGCGTTGAAC GTCCTGCCGC
551 AACGCTGCC CGACACGCCG CTGATTATCG ACGCGGCTT GGGTTTGCC
601 TCACAGGCGG CACAAGTGAT GGAATGGGCG TTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCCTTCG
701 CACTCGCCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCAGCGACA AAGCGAAGC CAGCAGCCG ACAGTCGGAC AACCGTTTTG
801 GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
1  LLIHYTKPEI MLTYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101 FETDWIKLEL IGDGDTLQPD VFQLVAAEI LIKDGFKVLP YCTEDLIACR
151 RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201 SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251 ARDKAQASTP TVGQPFWWSA EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

          10      20      30      40      50
m126.pep  HYTKPEIMLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE
          |||
a126      LLIHYTKPEIMLTLYSETFP SRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE
          10      20      30      40      50      60

          60      70      80      90      100     110
m126.pep  AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD
          |||
a126      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD
          70      80      90      100     110     120

          120     130     140     150     160     170
m126.pep  VFQLVAAEILIKDGFKVLPYCTEDLIACRLLDAGCQALMPWAAPIGTGLGAVHAYALN
          |||
a126      VFQLVAAEILIKDGFKVLPYCTEDLIACRLLDAGCQALMPWAAPIGTGLGAVHAYALN
          130     140     150     160     170     180

          180     190     200     210     220     230
m126.pep  VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG
          |||
a126      VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG
          190     200     210     220     230     240

          240     250     260     270
m126.pep  RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX
          |||
a126      RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX
          250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
1  ATGCTCACCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  GSCCGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GSCCGCGGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151 GTGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CTTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 C3CAATGGC GCGCGAAGTG TTTGAAACCG ATTTGGATAAA ATTGGAAGTC
301 ATCGGCGAGC ACGACACCTT GCAGCCGGAC GTGTTCCAAC TCGTCGAAGC
351 GSCGGAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCTTGCCGC CGCTTGCTCG ATGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCTA
501 TCGCTCAAAA ATCTTGCGCG AACGCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601 TTTGACGGCG TATTGTAAA CACCGCGGTT TCCCGCAGCG GCGACCCCGT
651 CAACATGGCG CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG GCCGCTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTGT GCATTGGCGG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
1  MLTYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRTGCGGE
```

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```

51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MFWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWWSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

## m126-1.seq

```

1  ATGCTCACCC TATACGGCGA AACTTTCCCC TCGCGGCTGC TGCTCGGCAC
51  GGCTGCTTAC CCGACCCCGG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CCGAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATGGGAATC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCCAGC TTGTCGAAGC
351 GCGGGAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCGGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CCGGTTGAAC GTCCTGCGCG AAGCCTGCGC CGACACGCGG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCAGCCCG
751 ACAGTCGGAC AACCGTTTTG GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

## m126-1.pep

```

1  MLTYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MFWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTYGETFP	SRLLLGTAAY	PTPEILKQSI	QTAQPAMITV	SLRRAGSGGE	AHGQGFWSLL
g126-1	MLTYGETFP	SRLLLGTAAY	PTPEILKQSV	RTARPAITV	SLRRAGSGGE	AHGQGFWSLL
	70	80	90	100	110	120
m126-1.pep	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQVLEAAEI
g126-1	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQVLEAAEI
	130	140	150	160	170	180
m126-1.pep	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGT	LGAVHAYALN	VLRERLPDTP
g126-1	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGT	LGAVHAYALK	ILRERLPDTP
	190	200	210	220	230	240
m126-1.pep	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSGDPVNMA	RAFALAVESG	RLAFEAGPVE
g126-1	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSGDPVNMA	RAFALAVESG	RLAFEAGPVE
	250	260				
m126-1.pep	ARDKAQASTP	TVGQPFWSAEYX				
g126-1	ARTKAQASTP	TVGQPFWSAEYX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

## a126-1.seq

```

1  ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  AGCCGCTTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GCGCCCGGAT GATTACCGTC TCGCTGCGCC GCGCGGATG CGGCGGCGAG

```



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```

151 GCGCACGGTC AGGGGTTTTG GTCGCTGCIT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCCT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAATC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTCCAAC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTCCGGC GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

a126-1.pep

```

1  MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAQVMWEG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFAEGPVE ARDKAQASTP
251 TVGQPFWHSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

a126-1.pep	10	20	30	40	50	60
	MLTLYSETFP SRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGEAHGQGFWSLL					
m126-1	MLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAPAMITVSLRRAGSGGEAHGQGFWSLL					
	10	20	30	40	50	60
a126-1.pep	70	80	90	100	110	120
	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQLVEAAEI					
m126-1	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQLVEAAEI					
	70	80	90	100	110	120
a126-1.pep	130	140	150	160	170	180
	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALNVLRERLPDTP					
m126-1	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALNVLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	190	200	210	220	230	240
	LIIDAGLGLPSQAQVMWEGFDGVLLNTAVSRSGDPVNMA RAFALAVESGRLAFAEGPVE					
m126-1	LIIDAGLGLPSQAQVMWEGFDGVLLNTAVSRSGDPVNMA RAFALAVESGRLAFAEGPVE					
	190	200	210	220	230	240
a126-1.pep	250	260				
	ARDKAQASTPTVGQPFWHS AEYX					
m126-1	ARDKAQASTPTVGQPFWHS AEYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

1  ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCGATACG
51  CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GGCGCAAATT CAAACGCTGG
251 CTTTGTGCGAT GTTTGCGGTG GCGGCGGCGG TCGTCTGGC GACAAAAGAA
301 CTGATTATGT GTCTGTCGGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCGCGC ACAATATTTT GGGCGACTAT GTCATCCATA

```

```

551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGGCC GCGCGTTACC CCGGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGC GCGTACA ATACCGCTG TTAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

```

g127.pep
1  MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLNI HFRRHPDFGI
51  ESKRRFLVAS RNITLLLVL FSLAFIWSAQI QTLALSMFAV AAADVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

```

m127.seq
1  ATGGAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51  TGGCGAGGCG GTCGAATCCG TGGCGGCGGT TGGCGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCCGCATC
151 GAAAGCAAGC GCGGCTTTTT GGTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCGAAATC CAAACGCTGG
251 CTTTGTGCGAT GTTTGCGGTG GCGGCGGCGG TCGTCTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCCGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGACAGC TTGCGGGAAC CACCGTTTCT TCCCCCAACA GCCTGTGTGT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA
551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGGsAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGACC GCGCGTTACC CCGGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGC GCGTACA ATACCGCTG TTAATCACC
851 CCGCCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

```

m127.pep
1  MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLNI HFRRHPDFGI
51  ESKRRFLVAS RNITLLLVL FSLAFIWSAQI QTLALSMFAV AAADVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

m127/g127

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAESVAAVAALLLARA_LLLNIHFRRHPDFGIESKRRFLVAS					
	:         :					
g127	MEIWNMLNTWPDVPIRAEAESVAAVAALLLARA_LLLNIHFRRHPDFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG					
g127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDCAVCRKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDCAVCRKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

```

a127.seq
1  ATGGAAATAT  GGAATATGTT  GGACACTTGG  CTCGGTGCCG  TCCCGATACG
51  TGCAGAGGCG  GTCGAATCCG  TGGCGGTGGT  CGCGGCTTTG  CTGCTGGCGC
101 GCGCCCTTCT  GTTGAATATC  CACTTCAAAC  GGCATCCGGA  TTTCGGCATC
151 GAAAGCAAGC  GCGCGTTTTT  GGTGCCAGC  CGCAATATAA  CGCTGCTTTT
201 GGTGCTGTTT  TCGCTGGCAT  TTATCTGGTC  GGCGCAAATC  CAAACGCTGG
251 CTTTGTGCGT  GTTGGCGGTG  GCGGCGGCGG  TCGTCGTGGC  GACGAAGGAA
301 CTGATTATGT  GTCTGTGCGG  CAGCATTTTA  AGGTCTGCCA  CCCAGCAATA
351 CTCGGTCGGC  GACTATATCG  AAATCAACGG  CCTGCGCGGG  CGCGTGGTCG
401 ACATCAACCT  GTTGAACACG  CTGATGATGC  AGGTCGGTCC  GAACCCCTTG
451 GTCGGACAGC  TTGCGGGAAC  CACCGTTTCT  TTCCCAACA  GCCTGTTGTT
501 GAGCCACCCC  GTGCGCCGCG  ACAATATTTT  GGGCGACTAC  GTCATCCATA
551 CGGTCGAAAT  CCCGGTTCCC  ATCCATTGG  ATTCGGATGA  AGCCGTATGC
601 CGTCTGAAAG  CCGTACTCGA  GCCCTTGTGC  GCGCCCTACA  TCCCCGCCAT
651 CCAACGGCAT  TTGGAAGACG  TGCAGGCGGA  AAAACTGTTT  ATCACGCCCG
701 CCGCCAAACC  GCGCGTTACC  CGCGTCCGT  ACGATGACAA  GGCATACCGC
751 ATCATCGTCC  GCTTCGCCTC  CCCCCTTCA  AAGCGGCTGC  AAATCCAACA
801 GCGCGTTATG  GACGAATTTT  TCGCGGTACA  ATACCGCTCG  TTAAATTACC
851 CCGCCGGCTC  CGAAACACTT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

```

a127.pep
1  MEIWNMLDTW  LGAVPIRAEA  VESVAVVAAL  LLARALLNI  HFKRHPDFGI
51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAADVATKE
101 LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151 VGQLAGTTVS  FPNSLLLSHF  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201 RLKAVLEPLC  APYIPAIQRH  LENVQAEKLF  ITPAAKPRVT  RVPYDDKAYR
251 IIVRFASPV  KRLEIQQAVM  DEFLRVQYRL  LNYPAGSETL  *

```

m127/a127 98.6% identity in 290 aa overlap

```

m127.pep
10 20 30 40 50 60
MEIWNMLDTWLGAVPIRAEAESVAVVAALLARALLNIHFKRHPDFGIESKRFLVAS
|||||
a127
10 20 30 40 50 60
MEIWNMLDTWLGAVPIRAEAESVAVVAALLARALLNIHFKRHPDFGIESKRFLVAS

70 80 90 100 110 120
RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG
|||||
a127
70 80 90 100 110 120
RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG

```

363

	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNI LGDY					
a127	DYIEINGLRGRVVDINLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNI LGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASFVSKRLEIQQAVMDEFRLVQYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASFVSKRLEIQQAVMDEFRLVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

```

1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACAtca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGCGCGATT TCGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TCGCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCGCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGccaaa cTGCTCGGCT TTAAAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTTA CGCGGAAAA GACCTCGCGG AAGTCAAAGC
951 CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GTACGCGCG CGAAAAATG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTGCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGCGG TTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTaca AAGGCCGCCG CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCTTAC CTGCTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCAGCC TCTTCCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCGGCAT CAACggcgtA GAATGGGACG CGGTGCAACT GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 TCCGAAGAA AccgGCGAGC CCTGCGGAA AGAACTCTT GACAAAATGC
1601 TcgCGCCAA AAATCTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 TCcggcGGCT ATTCCGCGAG CTATTACAGC TACGCATGGG CCGAAGTCCt
1851 cAGCACCGAT GCCTACGCGC CTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTCTTGCGAA GAAAtccttg ccgtcggcgg ctCCCGCAGC
1951 gcgGCGGAAT CCTCAAAGC CTTCGCGGA GCGGAACCGA GCATAGACGC

```

2001 ACTGCTGCGC CAAagcggtT TCGACAACGC gGCttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1  MIDNALLHLG  EEPFRNQIQT  EDIKPAVQTA  IAEARGQIAA  VKAQHTTGWA
51  NTVERTLGIT  ERVGRIWGVV  SHLNSVVDTP  ELRAVYNELM  PEITVFFTEI
101 GQDIELYNRF  KTIKNSPEFA  TLSPAQKTKL  DHDLRDFVLS  GAELPPERQA
151 ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201 AAQSEGKTGY  KIGLQIPHYL  AVIQYAGNRE  LREQIYRAYV  TRASELSNDG
251 KFDNTANIDR  TLENALKTAK  LLGFKNYAEL  SLATKMADTP  EQVLNFLHDL
301 ARRAKPYAEK  DLAEVKAFAR  EHLGLADPQP  WDLSYAGEKL  REAKYAFSET
351 EVKKYFPVGK  VLAGLFAQIK  KLYGIGFAEK  TVPVWHKDVR  YFELQONGKT
401 IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFA  DGTQLQLPTAY  LVCNFAPPVG
451 GKEARLSHDE  ILTLFHETGH  GLHLLLTQVD  ELGVSGINGV  EWDAVELPSQ
501 FMENFVWEYN  VLAQMSAHEE  TGEPLPKELF  DKMLAAKNFQ  RGMFLVRQME
551 FALFDMMIYS  ESDECRLKNW  QQVLDSVRKE  VAVIQPPEYN  RFANSFGHIF
601 AGGYSAGYYS  YAWAEVLSTD  AYAAFEESDD  VAATGKRFWQ  EILAVGGSRS
651 AAESFKAFRG  REPSIDALLR  QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1  ATGACTGACA  ACGCACTGCT  CCATTTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCGCCCT  GCAAACCGCC  ATCGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCT  AACCCTGAC  CGGCATCACC  GAACGCGTCG  GCAGGATTIG
201 GGGCGTGGTG  TCGCACCTCA  ACTGCGTCGC  CGACACGCC  GAACTGCGCG
251 CCGTCTATAA  CGAACTGATG  CCCGAAATCA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAATTCCCC
351 CGAATTCGAC  ACCCTCTCCC  CCGCACAAA  AACCAAACTC  AACCAAC
1  TACGCCAGCG  AAAAAGTGG  CGAAGCCAAA  TACGCGTTCA  GCGAAACCGA
51  wGTCAAAAAA  TAYTCCCYG  TCGGCAAwGT  ATTAACCGA  CTGTTCGCC
101 AAmTCAAAAA  ACTmTACGGC  ATCGGATTTA  CCGAAAAAAC  yGTCCCGTCT
151 TGGCAAAAG  ACGTGCCTA  TTKTGAATTG  CAACAAACG  GCGAAmCCAT
201 AGGCGGCGTT  TATATGGATT  TGTACGCACG  CGAAGGCAAA  CGCGGCGGCG
251 CGTGGATGAA  CGACTACAAA  GGCCGCGCGC  GTTTTTCAGA  CGGCACGCTG
301 CAAYTGCCCA  CCGCTACCT  CGTCTGCAAC  TTCGCCCCAC  CCGTCGCGCG
351 CAGGGAAGCC  CGCyTGAGCC  ACGACGAAAT  CCTCATCCTC  TTCCACGAAA
401 CCGGACACGG  GCTGCACCAC  CTGCTTACCC  AAGTGGACGA  ACTGGGCGTA
451 TCCGCGATCA  ACGCGGTAKA  ATGGGACGCG  GTCGAACTGC  CCAGCCAGTT
501 TATGGAAAAT  TTCGTTTGGG  AATACAATGT  CTTGGCACAA  mTGTCAGCCC
551 ACGAAGAAAC  CGGcgTTCCC  yTGCGAAAG  AACTCTTsGA  CAAAwTGCTC
601 GCGGCCAAAA  ACTTCCAAsG  CGGCATGTTC  yTsGTCCGCG  AAwTGGAGTT
651 CGCCCTCTTT  GATATGATGA  TTTACAGCGA  AGACGACGAA  GGCCGTCTGA
701 AAAACTGGCA  ACAGGTTTTA  GACAGCGTGC  GCAAAAAAGT  CGCCGTCATC
751 CAGCCGCCCG  AATACAACCG  CTTGCGCTTG  AGCTTCGGCC  ACATCTTCGC
801 AGGCGGCTAT  TCCGCGCTn  ATTACAGCTA  CGCGTGGGCG  GAAGTATTGA
851 GCGCGGACGC  ATACGCGGCC  TTTGAAGAAA  GCGACGATGT  CGCCGCCACA
901 GGCAAACGCT  TTTGGCAGGA  AATCCTCGCC  GTCGGGGnAT  CGCGCAGCGG
951 nGCAGAATCC  TTCAAAGCCT  TCCGCGGCGG  CGAACCGAGC  ATAGACGCAC
1001 TCTTGCGCCA  CAGCGGTTTC  GACAACGCGG  TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1  MTDNALLHLG  EEPFRDQIKT  EDIKPALQTA  IAEAREQIAA  IKAQHTTGWA
51  NTVPLTLGIT  ERVGRIWGVV  SHLNCVADTP  ELRAVYNELM  PEITVFFTEI
101 GQDIELYNRF  KTIKNSPEFD  TLSPAQKTKL  NH

//
1  YASEKLREAK  YAFSETXVKK  YFPVGXVLNG  LFAQXKKLYG  IGFTEKTVPV
51  WHKDVRYXEL  QQNGEXIGGV  YMDLYAREGK  RGGAWMNDYK  GRRRFSDGTL
101 QLPTAYLVCN  FAPPVGGREA  RLSHDEILIL  FHETGHLHH  LLTQVDELGV
151 SGINGVXWDA  VELPSOFMEN  FVWEYNVLAO  XSAHEETGVP  LPKELXDKXL
201 AAKNFQXGMF  XVRQXEFALF  DMMIYSEDDE  GRLKNWQQVL  DSVRKKVAVI
251 QPPEYNRFAL  SFGHIFAGGY  SAAXYSYAWA  EVLSADAYAA  FEESDDVAAT

```

301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHSGF DNAV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPAQTAIAEAREQIAAIAKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDFVLGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
g128.pep				340	350	360
				YAGEKLREAKYAFSETEVKKYFPVGKVLG		
m128				YASEKLREAKYAFSETXVKKYFPVGKVLNG		
				10	20	30
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHBETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIYSESDECRLLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDDGRLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRGREPS					
	280	290	300	310	320	330

366

```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTGGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAACTC AACCACGATC
401 TCGCGGATTT CGTCCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTCACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCTATC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCGC CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAATCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCGC
1101 CCAATCAAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGTTTTCFA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAGC CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCACGCA
1401 AACCGGACAC GGCCTGCACC ACCTGCITAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAT ATTTGTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCGGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCCTA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGGC CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCGCCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTHTGWA
51  NTVPEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTYG KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VINGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

```

551 FALFDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF  
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS  
651 AAESFKAFRG REPSIDALLR HSGFDNAA\*

## m128/a128 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130	TLSPAQKTKLNH-----				
a128	130	140	150	160	170	180
	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSONVLDTDAFGIY					
m128.pep	-----					
a128	190	200	210	220	230	240
	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYV					
m128.pep	-----					
a128	250	260	270	280	290	300
	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
m128.pep	-----					
	140 150					
	-----YASEKLREAKYAFSETXVKKYFPVGX					
	:					
a128	310	320	330	340	350	360
	ARRAKPYAEKDIAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTVPVVHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600



q128-1.seq (partial)

This corresponds to the amino acid sequence <SEO ID 488; ORF 128-1.ng>:

g128-1.pep (partial)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 489>:

m128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTTGGGC	GAAGAACCCC	GTTTGTATCA
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATCGCCGAAG
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCATAC	CGGCTGGGCA
151	ACACTGTGTC	AACCCCTGAC	CGGCATACCC	GAACCGCGTC	CGAGGATTTC

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201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACCCGATC
401 TGCGCGATTT CGTCTCAGC GCGCGGAAC TGCGCGCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTGACGATG
551 CCGCACCGCT TGCGCGCATT CCGAAGACG CGTCGCCAT GTTTGCCGCG
601 GCGCGCAAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCGATTCC
651 AACTACCTC GCGTCTATCC AATACGCGCA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCAAA CTGCTCGGCT TCAAAACTA CCGCGAATTG TCGTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCGCG CCAAACCTA CGCGAAAAA GACCTCGCGC AGTCAAAGC
951 CTTCGCGCG GAAAGCCTGA ACCTCGCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCGAG CGAAAAACTG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGCGAAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAAAAAA CCGCGAAACC
1201 ATAGGCGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACCGCGCGG
1251 CCGGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTCG GACGCGACGC
1301 TGCAACTGCC CACCGCTTAC CTGCTGCA ACTTCGCCCC ACCCGTCGCG
1351 GGCAGGGAAG CCGCGCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGCGAT CAACGCGGTA GAATGGGACG CGGTGCAACT GCCCAGCCAG
1501 TTTATGAAA ATTTCGTTT GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGCGCTTC CCCTGCCGAA AGAATCTTC GACAAAATGC
1601 TCBCCGCCAA AAATCTCAA CGCGCATGT TCCTCGTCCG GCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCGCTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCGTCA
1751 TCCAGCGCGC CGAATACAAC CGCTTCGCT TGAGCTTCGG CCACATCTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGC CTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAAAAC CTTTGGCAG GAAATCTCG CCGTCGCGCG ATCGCGCAGC
1951 GCGCGAGAAT CCTTCAAAGC CTTCGCGCGC GCGCAACCGA GCATAGACGC
2001 ACTCTTCCG CACAGCGGTT TCGACAACGC GGTCTGA

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This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pcp.

```

1  MTDNALHLHLG EEPREFDIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY PDAAAPLAGI PEDALAMFAA
201 AAQSESTGY KIGLQIPHYL AVIQYADNRB LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLNALQTAQ LLGFKNYAEL SLATKMDATP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLPQ WDLGYASEKL REAKYAFSET
351 EVKKYPPVKG VLNLGFAQIK KLYGIGFTEK TVPVVHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMPLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESEFKAFRG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pcp MIDNALHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQTHTGWANTVERLTGIT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      MTDNALHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
g128-1.pcp ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

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370

	130	140	150	160	170	180
g128-1.pep	T L S P A Q K T K L D H D L R D F V L S G A E L P P E R Q A E L A K L Q T E G A Q L S A K F S Q N V L D A T D A F G I Y					
m128-1	T L S P A Q K T K L N H D L R D F V L S G A E L P P E Q Q A E L A K L Q T E G A Q L S A K F S Q N V L D A T D A F G I Y					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	F D D A A P L A G I P E D A L A M F A A A A Q S E K T G Y K I G L Q I P H Y L A V I Q Y A G N R E L R E Q I Y R A Y V					
m128-1	F D D A A P L A G I P E D A L A M F A A A A Q S E K T G Y K I G L Q I P H Y L A V I Q Y A D N R E L R E Q I Y R A Y V					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	T R A S E L S N D G K F D N T A N I D R T L E N A L K T A K L L G F K N Y A E L S L A T K M A D T P E Q V L N F L H D L					
m128-1	T R A S E L S D D G K F D N T A N I D R T L A N A L Q T A K L L G F K N Y A E L S L A T K M A D T P E Q V L N F L H D L					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	A R R A K P Y A E K D L A E V K A F A R E H L G L A D P Q P W D L S Y A G E K L R E A K Y A F S E T E V K Y F P V G K					
m128-1	A R R A K P Y A E K D L A E V K A F A R E S L N L A D L Q P W D L G Y A S E K L R E A K Y A F S E T E V K Y F P V G K					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	V L A G L F A Q I K K L Y G I G F A E K T V P V W H K D V R Y F E L Q Q N G K T I G G V Y M D L Y A R E G K R G G A W M					
m128-1	V L N G L F A Q I K K L Y G I G F T E K T V P V W H K D V R Y F E L Q Q N G E T I G G V Y M D L Y A R E G K R G G A W M					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	N D Y K G R R R F A D G T L Q L P T A Y L V C N F A P P V G G K E A R L S H D E I L T L F H E T G H G L H H L L T Q V D					
m128-1	N D Y K G R R R F S D G T L Q L P T A Y L V C N F A P P V G G R E A R L S H D E I L I L F H E T G H G L H H L L T Q V D					
	430	440	450	460	470	480
	490					
g128-1.pep	E L G V S G I N G V K					
m128-1	E L G V S G I N G V E W D A V E L P S Q F M E N F V W E Y N V L A Q M S A H E E T G V P L P K E L F D K M L A A K N F Q					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTC
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCGGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACACGATC
401 TGCGCGATTT CGTCCTCAGC GCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCCGCGAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCTATC AATACGCCA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 GCTACGCCG CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCG AAGTCAAAGC
951 CTTCGCCCGC GAAAGCCTCG GCCTCGCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCG CGAAAACTG CGCGAAGCCA AATACGATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAATCAAA AACTCTACG GCATCGGATT TACCGAAAA ACCGTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGCGC TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGCGCG

```

```
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGGCAGCG
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCGTGACAC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGAAAA ATTTCTTTTG GGAATACAAT GTCTTGGCGC AAAATGTCCGC
1551 CCACGAAGAA ACGGCGGTTT CCCTGCCGAA AGAACTCTTC CACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCTG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGC CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACAG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGA CCGGAACCGA GCATAGACGC
2001 ACTCTTGGCG CACAGCGGCT TCGACAACGC GCCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

```
a128-1.pep
1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGPKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFBLQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLEKN QVLDSEVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESEKAFRG REPSIDALLR HSGFDNAA*
```

m128-1/a128-1 97.8% identity in 677 aa cverlap

```
10 20 30 40 50 60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA IKAQHTGWANTVEPLTGIT
|||||
m128-1 MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA IKAQHTGWANTVEPLTGIT
10 20 30 40 50 60

70 80 90 100 110 120
a128-1.pep ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||
m128-1 ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
70 80 90 100 110 120

130 140 150 160 170 180
a128-1.pep TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
|||||
m128-1 TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
130 140 150 160 170 180

190 200 210 220 230 240
a128-1.pep FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
|||||
m128-1 FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
190 200 210 220 230 240

250 260 270 280 290 300
a128-1.pep TRASELSDDGKFDNTANIDRTLENALQTAKLLGPKNYAELSLATKMADTPEQVLNFLHDL
|||||
m128-1 TRASELSDDGKFDNTANIDRTLANALQTAKLLGPKNYAELSLATKMADTPEQVLNFLHDL
250 260 270 280 290 300

310 320 330 340 350 360
a128-1.pep ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVVGK
|||||
```

372

```
m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVSK
              310      320      330      340      350      360

a128-1.pep   370      380      390      400      410      420
              VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVMDLYARECKRGGAWM
              |||
m128-1      VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVMDLYARECKRGGAWM
              370      380      390      400      410      420

a128-1.pep   430      440      450      460      470      480
              NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHHLLTQVD
              |||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHHLLTQVD
              430      440      450      460      470      480

a128-1.pep   490      500      510      520      530      540
              ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              |||
m128-1      ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

a128-1.pep   550      560      570      580      590      600
              RGMFLVRQMEFALFDMMIYSEDEGRLLKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
              |||
m128-1      RGMFLVRQMEFALFDMMIYSEDEGRLLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIF
              550      560      570      580      590      600

a128-1.pep   610      620      630      640      650      660
              AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              |||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

a128-1.pep   670      679
              REPSIDALLRHSGFDNAAX
              |||
m128-1      REPSIDALLRHSGFDNAVX
              670
```

## a128-1/ P44573

sp|P44573|OPDA\_HAEIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlC) homolog  
- Haemophilus influenzae (strain Rd KW20)  
>gi|1573174 (U32706) oligopeptidase A (prlC) [Haemophilus influenzae Rd] Length = 681  
Score = 591 bits (1507), Expect = e-168  
Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

Query: 4 NALLHLGEEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXXHTGWANTVEPLTGITERV 63  
N LL++ P F QIK E I+PA++ H W N + PLT +R+  
Sbjct: 5 NPLLNIIQGLPFPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64 GRIWGVVSHLNSVTDTPELRAAYNELMPEITVFTEIGQDIELYNRFTKNSPEFDTLS 123  
R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S  
Sbjct: 65 NRAWSPVSHLNSVKNSTELREAYQTCLPLLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124 HAQKTKLHNDLRDPVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183  
AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++  
Sbjct: 125 IAQKKAIENSLRDFELSGIGLSEEKQRYGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYVTRA 243  
A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA  
Sbjct: 185 EAELAGLPEALQAAQSAESKGLGYRPTLEIPSYLPVMTYCENRALREEMRYAYATRA 244

Query: 244 SELSDD-GKFDNTANIDRTLENALQTAKLLGPKNYAELSLATKMATDTPQVLNFLHDLAR 302  
SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA  
Sbjct: 245 SEQGPNAGKWDNSKVMEEILTLRVBLAKLLGFNTYTELSLATKMAENPQQVLDLFLDLAE 304

Query: 303 RAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFFVGKVL 362  
RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFF +V+  
Sbjct: 305 RAKPQGEKELQELKGyceKEFGVTLELPWDIGFYSEKQKQHLVAINDEELRPYFFENRVI 364

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QONGETIGGVYMDLYAREGKRGGAWM 420  
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGGAWM  
 Sbjct: 365 SGLFELIKRIFNIRAVERRKGVDTWHKDVRFDDLIDENDOLRGSFYLDLYAREIHKRGGAWM 424

Query: 421 NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXXXXQVD 480  
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D  
 Sbjct: 425 DDCIGRKRKLDGSIETPVAYLTCNFNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540  
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ  
 Sbjct: 485 VSDVAGINGVPWDAVELPSQFMENWCWEEELAFISGHYETGEPLPKEKLTQLLAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDGRLQNWQQVLDVSRKEVAVVRPPEYNRPFANSFGHIP 600  
 MF++RQ+EF +PD ++ D + L SV+ +VAV++ ++ R +SF HIF  
 Sbjct: 545 AAMFILRQLSEFIPDFRLHHTFDAEKTNQILDTLKSVKSQVAVIKGVDWARAPHSPSHIF 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAESFKAFR 659  
 WAEVLSADAY+ FBE TKG F EIL GGS E FK FR  
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGGSEEPMELEFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676  
 GREP +DALLRH G N  
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq

```

1  ATGCTTTCAC CTCCTCGGCG TAAACGGCG GCACATCAAT CAAGCCGTCT
51  TTCATTTCGC TGCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAATCAAT
101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG
151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT
201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GCGGTCGAA TCCTGTTTCA
251 TCCGGACAAA CGCGTTGGCA GTCGGAAT CCGCCGCC GTGTCAAATA
301 ATGCGTACT TTGGCCGGT CTTGTCTTT GTAAGCGGCG GTCTTTTTTT
351 GCGCGCCATC CGCATCTGTT TGGGCGCAT GCAAACGGCG GCTGCCGTAC
401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCG ATGCCGCCG
451 ACATATCGAG CCGGTTTTG CCTATCCGAT TTGGCGCAT TTAGCCGGT
501 AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep

```

1  MLSPRRKTA AHQSSRLSFA CGKNAACRD QNQYRAASSP NRGLPRFPIT
51  PTAAAVHPYP RFRHLPFQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
151 TYRAGFCLSD LAAFRPVT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)

```

1  ..TATCTGCGCT TTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
51  ACAGGTAGCG GTCAATCCT GTTTCATCCA AATAACACG TTGGTAGTCG
101 GAAAATTTCG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGCTCTTG
151 TTCTTTGTAA GTGGTGTCT TTTTTCGCG GTTATCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTG GCGATTTCAT
251 GCAGATAGC ATCCGGGTGT TGCCCAACAT ATTGAGCCG TTTTTCCTA
301 TCCGATTGTA CGGCATTAG ACCGGTAACT TGA

```

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)

```

1  ..YLRHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
51  FVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL
101 SDLTAFRPVT *

```

Computer analysis of this amino acid sequence gave the following results:

# Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

						10	20	30
m129.pep						YLRFHYPFOAAGIGTEQVAVKSCFIQINT		
g129	RDQNQYRAASSPNRGLPRFPITPTAAAVHPYPRFRHLPFOAAGIGAEQAAVESCFIRNTA							
	30	40	50	60	70	80		
		40	50	60	70	80	90	
m129.pep	LVVGKFGRLCQIMRYFGRVLFVSGGLFLRVIPICLSAXQMVAAVQSKCLAIISCRXASGC							
	:							
g129	LAVGKSGRPCQIMRYFGRVLSFVSGGLFLRAIRICLGAWQTAAAVQSKCLAIISCRQASGC							
	90	100	110	120	130	140		
		100	110					
m129.pep	CPTYXAGFCLSDLTAFRPVTX							
g129	RPTYRAGFCLSDLAAFRPVTX							
	150	160						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

a129.seq (partial)

```

1  TATCTGCGCT TTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
51  ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
101 GAAAATTCGG CCAGCTGTGT CAAATAATGC GTTACTTTGG CCGGGCTTGG
151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCGC GTTATCCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTTCAT
251 GCAGATAGGC ATCCTGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCCTTA
301 TCCGATTTGA CGGCATTTAG ACCGTAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

a129.pep (partial)

```

1  YLRFHYPFO AAGIGTEQVA VKSCFIQINT LVVGKFGQLC QIMRYFGRVL
51  FVSGGLEFLR VIPICLSA*Q MVAAVQSKCL AISCR*ASWC CPTY*AGFCL
101 SDLTAFRPVT *

```

m129/a129 98.2% identity in 110 aa overlap

						10	20	30	40	50	60
m129.pep	YLRFHYPFOAAGIGTEQVAVKSCFIQINTLVVGKFGRLCQIMRYFGRVLFVSGGLFLR										
a129	YLRFHYPFOAAGIGTEQVAVKSCFIQINTLVVGKFGQLCQIMRYFGRVLFVSGGLFLR										
	10	20	30	40	50	60					
		70	80	90	100	110					
m129.pep	VIPICLSAXQMVAAVQSKCLAIISCRXASGCCPTYXAGFCLSDLTAFRPVTX										
a129	VIPICLSAXQMVAAVQSKCLAIISCRXASWCCPTYXAGFCLSDLTAFRPVTX										
	70	80	90	100	110						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

g130.seq

```

1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG TGGATCGTTC GCGATGTCG ATGCCACTAC GGAAGCGGCA
151 ACGCAGACCC GCATCCAGCC TGTCGGACAA TTGACGATGG GTGACGGCAT
201 CCCCCTCGGC GAACGCCAAG GCGAACAGAT TTTCGGCAA ATCTGTATCC

```

375

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAACTC AAACGGGCGA TTACCTACAT GCGCAATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG COGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCCG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAAGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGTTTGTAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
1  MKQLRDNKAQ  GSALFTLVSG  IVIVIAVLYF  LIKLAGSGSF  GDVDATTEAA
51  TQTRIQPVGQ  LTMGDGIPVG  ERQGEQIFGK  ICIQCHAADS  NVPNAPKLEH
101 NGDWAPRIAQ  GFDTLFQHAL  NGFNAMPAGK  GAADLTDQEL  KRAITYMANK
151 SGGSFNPNDE  AAPADNAASG  TASAPADSAA  PAEAKAEDKG  AAPAVGVDDG
201 KKVFEATCQV  CHGGSIPGIP  GIGKKDDWAP  RIKKKGKETH  KHALEGPNAM
251 PAKGGNAGLS  DDEVKAAVDY  MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
1  ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
51  CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACCGC
101 GTATCGGCAA GGCTTCGATA CCTTGTTCCA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAACTT
201 AAACGGGCGA TTACTTACAT GCGCAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGAGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACCCC TGCGGTCCGC GTTGACGGTA AAAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACAA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAArG CGgCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
1  ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDT LFOHALNGFN
51  AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAAPAEA KAEDKGAAPA VGVGKRVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPKXG NAGLSDEVK AAVDYMANKS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

m130/g130

```

m130.pep
10 20 30
GEQIFGKICQCHAADSNVPNAPKLEHNGD
|||||
g130  DATTEAATQTRIQPVGQ LTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
50 60 70 80 90 100

40 50 60 70 80 89
XAPRI-QGFDTLFQHALNGFNAMPAGKGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
|||||
g130  WAPRIAQGFDTLFOHALNGFNAMPAGKGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
110 120 130 140 150 160

```



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```

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||
g130       ADNAASGTASAPADSAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAADVYMANQSGAKFX
          |||||
g130       KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAADVYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC  TCCGCGACAA  CAAAGCCCAA  GGCTCTGCAC  TGTTTACCTT
51  TGTGAGCGGT  ATCGTTATTG  TTATTGCAGT  CCTTTATTTT  CTGATTAAGC
101 TGGCGGGCAG  CGGCTCGTTC  GGCGATGTCG  ATGCCACTAC  GGAAGCAGCA
151 ACGCAGACCC  GTATCCAGCC  TGTCGGACAA  TTGACGATGG  GCGACGGCAT
201 CCCCCTCGGC  GAACGCCAAG  GCGAACAGAT  TTTCGGCAAA  ATCTGTATCC
251 AATGCCACGC  GGCGGACAGC  AATGTGCCGA  ACGCTCCGAA  ACTGGAACAC
301 AACGGCGATT  GGGCGCCGCG  TATCGCGCAA  GGCTTCGATA  CCTTGTTCCA
351 ACACGCGCTG  AACGGCTTTA  ACGCCATGCC  TGCCAAAGGC  GGTGCGGTAG
401 ACCTGACCGA  TCAGGAATCT  AAACGGGCGA  TTACTTACAT  GCGGAACAAA
451 AGCGGCGGTT  CTTTCCCGAA  TCCTGATGAG  GCTGCGCCTG  CCGACAATGC
501 CGCTTCAGGA  ACAGCTTCTG  CTCCTGCCGA  TAGTGCAGCT  CCGGCAGAAG
551 CGAAGGCAGA  AGACAAGGGT  GCGGCAGCCC  CTGCGGTCGG  CGTTGACGGT
601 AAAAAAGTCT  TCGAAGCAAC  CTGTCAGGTG  TGCCACGGCG  GTTCGATTCC
651 CGGTATTCCC  GGCATAGGCA  AAAAAGACGA  TTGGGACCG  CGTATCAAAA
701 AAGGCCAAAG  AACCTTGCAC  AAACACGCCC  TTGAAGGCTT  TAACGCGATG
751 CCGCCAAAG  GCGGCAATGC  AGGTTTGAGC  GATGACGAAG  TCAAAGCGGC
801 TGTGACTAT  ATGGCAAACC  AATCCGGTGC  AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ  GSALFTLVSG  IVIVIAVLYF  LIKLAGSGSF  GDVDATTEAA
51  TQTRIQPVGQ  LTMGDGIPVG  ERQGEQIFGK  ICIQC:HAADS  NVPNAPKLEH
101 NGDWAPRIAQ  GFDTLFQHAL  NGFNAMPKAG  GAVDLTDQEL  KRAITYMANK
151 SGGSFNPDE  AAPADNAASG  TASAPADSAA  PAEAKAEDKG  AAPAVGVVDG
201 KKVFEATCQV  CHGGSIPGIP  GIGKKDDWAP  RIKKGKETLH  KHALEGFNAM
251 PAKGGNAGLS  DDEVKAAVDY  MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

```

          10      20      30
m130.pep  GEQIFGKICIQCHAADSNVPNAPKLEHNGD
          |||||
a130       DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90      100

          40      50      60      70      80      89
m130.pep  XAPRI-QGFDTLFQHALNGFNAMPKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP
          |||||
a130       WAPRIAQGFDTLFQHALNGFNAMPKGGAVDLTDQELKRAITYMANKSGGSFNPDEAAP
          110      120      130      140      150      160

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||
a130       ADNAASGTASAPADSAPAEAKAEDKGAAAPAVGVGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAADVYMANQSGAKFX

```

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```

a130      |||||
          KKDDWAPRIKKGKETLHKHALEGFNAMPAGGNAGLSDDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

```

g132.seq
1  ATGGAAGCCT TCAAAACCTT AATTGGATT ATTAATATTA TTTCGCTTT
51  GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACCTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CCAACTTcct CAgccGCTCG AccGccGTTG CAGCAACAtt
201 tttcttTGca acctgcAtgg gctatggTgt atattcacac CCACACGACA
251 AAACACGGTT TGGACTTcag caacataCGA CAGACTCAGC AagcACCCAA
301 ACCcgtAAGC AATACCGAAC CTTCTGCCCC TGTTCTCTCAG CAGCAGAAAT
351 AACagtTTTt CAAATgccga caTGgtga

```

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

```

g132.pep
1  MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51  AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

```

m132.seq (partial)
1  ATGGAACCTT TCAAAACCTT AATTGGATT GTTAATTAA TTTCGCTTT
51  GGCCGCTCTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGA...

```

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

```

m132.pep (partial)
1  MEPFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

```

m132/g132
          10      20      30
m132.pep  MEPFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG
          || |||||:|:|||||:|||||
g132      MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSGSGSAQGVFGSAGNANFLSRS
          10      20      30      40      50      60

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

```

a132.seq
1  ATGGAAGCCT TCAAAACCTT AATTGGATT GTTAATATAA TTTCGCTTT
51  GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CTAACCTCCT CAGCCGCTCG ACCGCCGTTG CAGCAACATT
201 TTTCTTTGCA ACCTGCATGg GCTATGGTGT ATATTACAC CCACACGACA
251 AAACACGGTT TGGACTTCAG CAACGTACAA CAAACTCAGC AAGCACCCAA
301 ACCCGTAAGC AATACCGAAC CTTCTGCCCC TGTTCTCTCAG CAGCAGAAAT
351 AACAGTTTTT CAAATGCCGA CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

```

a132.pep
1  MEAFKTLIWI VNIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51  AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QRTTNSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

```

m132/a132 92.1% identity in 38 aa overlap

378

```

      10      20      30
m132.pep  MEPFKTLIWIVNLISALAVFVLVLLQHGKGADAGATFG
           || ||||| |||||:|||||:||||| ||||| |||||
a132      MEAFKTLIWIVNIIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFCSAGNANFLSRS
           10      20      30      40      50      60

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

```

g134.seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCCGATGCGG GTAAAACAC GCTGACCGAA AAATGCTGC
101 TGTTCGCGG CGCGATTCAA AGCGCAGGCA CGGTGAAAGG TAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGÀ TGCAGTTGCA CTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CAGTGGACAG CGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCGATA
401 CGCGGATTGT TACCTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCT
451 TTGGAATCTT TGGACGAAGT GGAAGACATC CTGCAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCTGCGG
601 CACGAGTTCG ACATCATCAA AGGCATAAAC AATCCGAAT TGGAACAACG
651 CTTTCCGTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAATTTAAT CTCGacgaAT TTCTCGccgG CGAACTCAGC
751 CCAGTGTCT TCGGCTCTGC GATTAACAAC TTCGGCATTG AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CACCCGCACC GAAACCGCGC GACGCGACCA
851 TGCGCATGGT CGGGCCGGAC GAGCCGAAAT TTTCCGGATT TATCTTTAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATCG CCTTCTTGCG
951 CGTCTGCTCC GGTAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTAG TAACCTTCAT GTCGCACGAC
1051 CGCGAACTGG CGGAAGAAGC CTACGCCGCG GACATCATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAATTCG GCGACAGCTT CTCCGAAGGC GAACAACCTG
1151 CGTTTACCGG CATCCCATTG TTCGCGCCCG AACTGTTCG CAGCGTCCGC
1201 ATCAAAAACC CGCTGAAAT CAAACAAC TG CAAAAGGTT TGCAACAAC
1251 CGGCGAAGAA GGTGCGGTT CAGTATTCAA ACCGATGAGC GCGCGGATT
1301 TGATTTGGG TCGGTCGCG GTGTGCACT TTGAAGTCGT AACCTCAGCG
1351 CTCGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCGGAATTG
1451 AAAAAGCCAA CGCAGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGGG TTGACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCAACA TTCGGTCAA CTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

```

g134.pep
1  MSQEILDQVR RRRFAIISH PDAGKTTLFE KLLLFSGAIQ SAGTVKGKKT
51  GKFATSDWMD IEKQGISVA SSMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRS
151 LELLDEVEDI LQIRCAPVTW PIGMGKNFKG VYHILNDBIY LFEAGGERLP
201 HEFDIIKGIN NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATMRMVGPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELAEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQBRWPDIV FHETREHSVK L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

```

m134.seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCAG GTAAAACAC GTTGACTGAA AAATCTTGC
101 TGTTCGCGG CGCGATTGAG AGCGCGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACTTCCGA CTGGATGGAA ATCGAGAAGC AGCGCGGCAT

```

```

201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAACCTT TGGACGAAGT GGAAAACATT TTAATAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGAAATTTAT CTCTTTGAAG CTGGCGCGCA ACGCTGCGCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTTAAT CTCGACGAAT TCCTCGCCCG CGAACTCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCAATG ATTGACTGGG CGCCCGCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGAGC GAGCCGAAGT TTTCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG
951 CGTCTGCTCC GGCAAATTCT AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCGGCC TCCAGCGTGG TTACCTTCAT GTCGCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGG
1151 CGTTCACCGG CATCCCATTC TTCCGACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACG CAAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GCGCGCGTGC AGGTGTTCAA ACCGATGAGC GCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAACG AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCTGAATTTG
1451 AAAAAGCCAA CGCGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTGGGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

```

m134.pep
1 MSQEILDQVR RRRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFDATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRNVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYVEAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng)

from *N. gonorrhoeae*:

```

m134/g134
      10      20      30      40      50      60
m134.pep MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
|||||
g134      MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
      10      20      30      40      50      60

      70      80      90      100     110     120
m134.pep IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA
|||||
g134      IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA
      70      80      90      100     110     120

      130     140     150     160     170     180

```

380

m134 . pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVEDILQIRCAPVTWPIGMGNFKG
	130 140 150 160 170 180
m134 . pep	190 200 210 220 230 240
	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134 . pep	250 260 270 280 290 300
	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPEPKFSGFIFK
	250 260 270 280 290 300
m134 . pep	310 320 330 340 350 360
	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELAE EAYAG
	310 320 330 340 350 360
m134 . pep	370 380 390 400 410 420
	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134 . pep	430 440 450 460 470 480
	GAVQVFKPMMSGADLILGAVGVQLQFEVVT SRLANEYGVEAVFDSASIW SARWVSCDDKKKL
g134	GAVQVFKPMMSGADLILGAVGVQLQFEVVT SRLANEYGVEAVFDSASIW SARWVSCDDKKKL
	430 440 450 460 470 480
m134 . pep	490 500 510 520 530
	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134 . seq
1  ATGTCCCAAG  AAATCCTCGA  CCAAGTGCGC  CGCCGCGCGA  CGTTTGCCAT
51  CATCTCCAC  CCTGACGAG  GTAAAACAC  GTTGACTGAA  AACTCTTGC
101  TGTTTTCAGG  TGGGATTCAA  AGCGCGGTA  CGGTAAAAGG  CAAGAAAACC
151  GGCAAATTCG  CCACCTCGA  CTGGATGGAC  ATCGAGAAGC  AGCGCGGCAT
201  TTCCGTGGCA  TCAAGCGTGA  TGCAGTTCGA  CTATAAAGAC  CACACCGTCA
251  ACCTTTTGGA  CACGCCGGA  CACCAAGACT  TCTCCGAAGA  CACCTACCGC
301  GTTTTGACCG  CCGTCGATAG  TGCCTTGATG  GTCATCGACG  CGGCAAAAGG
351  CGTGAAGCG  CAAACCATCA  AACTCTTGAA  CGTCTGCCGC  CTGCGCAATA
401  CGCCGATTGT  TACGTTCATG  AACAAATACG  ACCGCGAAGT  GCGCGATTCC
451  CTGGAATTGC  TGGACGAAGT  GGAAAACATC  CTGCAATCC  GCTGCGCGCC
501  CGTAACCTGG  CCGATCGGCA  TGGGCAAAA  CTTCAAAGGC  GTGTACCACA
551  TCCTGAACGA  CGAAATCTAT  CTCTTTGAAG  CGGGCGGCGA  ACGCTTGCCG
601  CACGAGTTCG  ACATCATCAA  AGGCATCGAT  AATCCCGAAT  TGGAAACAACG
651  CTTTCCGTTA  GAAATACAGC  AGTTGCGCGA  CGAAATCGAA  TTGGTGCAGG
701  CGGCTTCCAA  CGAGTTCAAT  CTCGACGAAT  TCCTCGCCGG  CGAACTCAGC
751  CCCGATTCT  TCGGCTCTGC  GATTAACAAC  TTCGGTATTC  AGGAAATCCT
801  CAATTCAATG  ATTGAATGGG  CGCCCGCGCC  GAAACACGCG  GATGCGACCG
851  TGGCTATGGT  CGAGCCGGAC  GAGCCGAAGT  TTTCCGGATT  TATCTTCAA
901  ATCCAAGCCA  ATATGGACCC  GAAACACGCG  GACCGTATTG  CCTTCTTGGC

```

```
951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT TCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTC TTCGCGCCG AACTGTCCG CAGCGTCCG
1201 ATCAAAACC CGCTGAAAT CAAGCAACTG CAAAAAGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GGC GCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCA GTGAAGTCGT TACCTCGCG
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```
a134.pep
1 MSQEILDQVR RRRTFAIISH PDAGKTLTE KLLLFSGAIQ SAGTVKGKKT
51 GK FATS DWM D IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDI IKGID NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLOFEVVTSR
451 LANEYGEAV FDNASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*
```

m134/a134 98.9% identity in 531 aa overlap

m134.pep	10	20	30	40	50	60
a134	10	20	30	40	50	60
m134.pep	70	80	90	100	110	120
a134	70	80	90	100	110	120
m134.pep	130	140	150	160	170	180
a134	130	140	150	160	170	180
m134.pep	190	200	210	220	230	240
a134	190	200	210	220	230	240
m134.pep	250	260	270	280	290	300
a134	250	260	270	280	290	300
m134.pep	310	320	330	340	350	360
a134	310	320	330	340	350	360

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	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGVQLQFEVVTSLRANEYGVEAVFDSASIWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGVQLQFEVVTSLRANEYGVEAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

```

g135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGACgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCAGTG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCCGC AAACGGCACG GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGTCTGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcCgaaa gcggGGgcag cgttTAtgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

```

g135.pep
1  MKYKRIVFKV GTSSITRSDG SLSRGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHINHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDS LAEAAEHQAD
251 GSFFVPRAKG LRTQKQLAF YSESGGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

```

m135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```

```
m135.pep
1  MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TCQLAALHHA GHELVLVSSG
51  AVAAGFGALC FKKRPVKIAD QKSAAAVGQG LLMEYNTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGAL SVLQRRRAVP IINENDTVSV BELKIGDNDT
151 LSAQVAAIMQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHINHEIIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAGK LRTQKWLAF YSESRGSVYV DEGAEHALS QKSKLIMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLTEF*
```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
g135	MKYKRIVFKVGTSSITRSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
	:					
	70	80	90	100	110	120
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGI VSAQILLSRADFADKRRYQNAGGAL					
g135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGI VSAQILLSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m135.pep	SVLLQRRRAVPIINENDTVSVEELKIGDNDTL SAQVAAMIQADLLVLLTDIDGLYTGNPNS					
g135	SVLLQRRRAIP IINENDTVSVEELKIGDNDTL SAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
	:					
	190	200	210	220	230	240
m135.pep	NPDAVRLDKIEHINHEI IEMAGGSGSANGTGGMLTKI KAATIAAESGVPVYICSSLKPDA					
g135	NPDAVRLDKIEHINHEI IEMAGGSGSANGTGGMLTKI KAATIAAESGVPVYICSSLKPD S					
	190	200	210	220	230	240
	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSES RGSVYVDGEAEHALSEOGKSLLMSGI					
g135	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSES GGSVYVDGEAEHALSEOGKACX					
	250	260	270	280	290	
	:     :					
	310	320	330	340	350	360



m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGAAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```
a135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTCGGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCA3GGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGSCGA CAACGACACA
451 TTGAGTGGCG AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACA GCGGGTATGC TGACTAAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAGAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGCAAAAG GCGAGTCCTG TTCGCCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTCGCTA AGGCGAAAGG CGTGTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTAG
```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```
a135.pep
1  MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TRQLAALHHA GHLEVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNFS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIATESGVVP YICSSLKPDA LAEADNQAD
251 GSFFVPRAKG LRTQKWLAF YSESRGGVYV DEGAHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*
```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNFS					
a135	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNFS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVVPYICSSLKPDA					
a135	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVVPYICSSLKPDA					
	190	200	210	220	230	240

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	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLLMSGI					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSESRGVYVDEGAEHALSEQGKSLLMSGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAEDLLKSRKAKGVFIHRDDWISITP					
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAEDLLKLRKAKGVFIHRDDWISITP					
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

```

g136.seq
1  ATGGAAATCC GGTTCAGAC AGCATTTTTA CGTTTGGTTC AGatgaAAAC
51  AACCGTtca aTTCTtaccg caACACGCCT TGTATTTCCT GccgCTGCCG
101 CACGGACAGG GATCGTTCCT GCCGgtTTTT TCCCTTCCC TCGGACGGT
151 TTGCGGTTTG TTGATGACCG CTGCCAGTA GCGGTAGATG Tctgccagcg
201 cgTAAGGCag tTCGGAcgca agttccgcca gctcgcttc ggTGAATTGC
251 AGgcgataa cgccgtttTC CTCTTCGTGg taaatgccgc ccactgccat
301 cacgGGGTAA AACAGCTCTT CAAACGCTTC ATCATCGGCG GCTTCAAACC
351 AATCGGTCGG CACAATGTCC AAACCGTAAA GATAGGCGTT GCACCAAGTG
401 TAAAAATCGC TGCCGCCCTC GCCGTCGTG TAGAGCCACA AATCGGGCAG
451 CTTTTATCC GACATCGCGG CGGTGTGTT CATCGCCATT GCCAAACCA
501 GCCGTTTCGAT TTCGGAACGT TCGGCGGCGG TAAATTGCGA TTCGTCGCCC
551 AACACTTCGG GCAGCCAGTC GAGCGGTGCC AATTGTGTCG GCCCGCTCAA
601 CAGCGCCGTC ATAAACCTT GAACCTCGTC GCAACGCATC GTGTTGCCTT
651 GTTCGCTTTT GGCATCCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

```

g136.pep
1  MEIRFQTAFL RLVQMKTNAS ILTATRLVFP AAAARTGIVP AGFFPFPADG
51  LRFVDDRLPV AVDVCQVRVQ FGRKFRQLAF GELQADNAVF LFVFNAAHCH
101 HRVKQLFKRF IIGGFKPIGR HNVQTVKIGV APSVKIAAAL AVVVEPQIGQ
151 LFIHRGGCF HRHCQNQPPD FGTFGGKLR FVAQHFGQPV ERCQFVRPAQ
201 QRRHKTLLNV ATHRVALFAF GIQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

```

m136.seq
1  ATGGAAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
51  CGTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTTTC GCCTTCCTTG
101 CGGACGGTTT GCGGTTTGTT GATGACTGCC TGCCAGTAGC GGTAGATATC
151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTCTG
201 TGAATTGCAG ACGGATAGCG CCGTTTTCTT CTCGTCGTA AATACGCCCC
251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC
351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTATA CAGCCACAAA
401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTCCTA TCGCCATTGC
451 CAAAACCAGC CGTTCGATT CGGAACGTC GCGGGCGGTA AATTGCGATT
501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
551 CCGCTCAACA GCGCGGTCAT AAAACCTTGA ACCTCGTCG AACGCATCGT
601 GTTGCTTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCTTTT CAAATGGGTT
701 TTGCGCCCTA TTATCGCCGC AATGCCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

Homology with a predicted ORF from *N. gonorrhoeae*

m136/g136

```

m136.pep      10          20          30          40
               METNASILLTATRLVFSA12AARTGIVPACFFAFAPDGLRFVDDCLPV
               |:|||||
g136           MEIRFQTAFRLRVQMKTNASILTATRLVFPAA12AARTGIVPAGFFPPPADGLRFVDRLPV
               10       20       30       40       50       60

               50       60       70       80       90       100
m136.pep      AVDIQRCIRQLGFQRQLAFCELTDSAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR
               |||: | :||: | :||| |||:|:|||:|:|: | :||| |||||
g136           ADVDCQRVRQFGRKFRQLAFGELQADNAVLFVVNAAHCHGVKQLFKRFIIGGFKPIGR
               70       80       90       100      110      120

               110      120      130      140      150      160
m136.pep      HNIQTVKISIAPCVKIAA12AVFVIQPQIGOFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR
               |||:|||||:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
g136           HNVTQTKIGIVAPSVKIAAALAVVVEPQIQQLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR
               130      140      150      160      170      180

               170      180      190      200      210      220
m136.pep      FVAQHFGQPVERCQFVRPAQQRHKTLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH
               |||||
g136           FVAQHFGQPVERCQFVRPAQQRHKTLNLVATHRVALFAFGIQX
               190      200      210      220

               230      240
m136.pep      HFPPQMGMFAPYYRRNAVX

```

```

a136.seq
1  ATGGAACAA  ACGCTTCAAT  TCTTACCGCA  ACACGCCTTG  TATTTTCTGC
51  CGTGCCCGCA  CGGACAGGGA  TCGTTCTCTGC  CTGTTTTCCT  GCCTTCCCTG
101 CGGACGGTTT  GCGGCTTGTT  TCGTACCGCC  TGCCAGTAGC  GGTAGATATC
151 CGCCAATGCA  TAAGGCAACT  CGGATTCCAG  TTCCGCCAGC  TCGCCTTCTG
201 TGAATTGCAG  ACGGATAGTG  CCGTTGTCCT  CTTCGTCGTA  AATACCGCCC
251 AATGCCATGA  TGGGATAAAA  CAATCTCTCA  AACGCTTCAT  CATCGACGGC
301 TTCAACCAAA  TCGGTCCGCA  CAATATCCAA  ACCGTAAGA  TAAGCATAGC
351 ACCATGTGTA  AAAATCGCTG  CCGCGCTCTT  CGTTTTCATA  GAGCCACAAC
401 TCGGGCAGTT  TTTTATCCGA  CATCGCGGCG  GTTGTTTCCA  TCGCCATTGC
451 CAAAACCAGC  CGTTCGATTT  CGGAACGTTT  GCGGCGGTA  AATTGCGATT
501 CGTCGCCCAA  CACTTCGGGC  AGCCAGTCTA  GCGGTGTCAA  TTTGTCCGGC
551 CGGCTCAACA  GCGCGTCAT  AAAACCTTGA  ACCTCGTCGC  AAGCATCTGT
601 GTTGCTTTGT  TCGCTTTTGG  CATCAACAAC  TTGCTCAAC  CGCGCTTTGG
651 ATGCTTCGGT  AAATTTTCGG  GAATCCATCA  TTTTCTTTT  CCAATGGGTT
701 TTGCGCCCTA  TTATAGTGGA  TTAATTTTAA  ATCAGGACAA  GCGGACGAAG
751 CCGCAGACAG  TACAATAAGT  ACGGCAAGCG  GAGGCAACGC  CGTACTGGTT
801 TAAATTTAAT  CCACTATATC  CGGCAATATG  CGTCTGA

```

a136.pep

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```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKEPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTG  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQRRRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFFP  PMGFAPYYSG  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

	10	20	30	40	50	60
m136.pep	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ					
	:					
a136	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLPVAVDIRQCIRQLGFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m136.pep	FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV					
	:					
a136	FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m136.pep	KIAAAVFVFIQPIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ					
	:					
a136	KIAAAVFVFIQPIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m136.pep	FVRPAQRRHKTNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFFPMGFAPYYRR					
	:					
a136	FVRPAQRRHKTNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFFPMGFAPYYSG					
	190	200	210	220	230	240
m136.pep	NAVX					
a136	LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC  ATCACcaaTT  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCCGC  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTTA
101 CCTTTCTCGG  CAGAAAGCGC  ATCGCGCAAG  GCTTGTCCGT  TTTTACCAAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGG  GTGTAGTTAT  TGCCATATGG  TTGTTCAGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAACCTA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATTACCG  ACATTAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCGCA
501 TTACGAAGAT  GCCGAAGCCG  CCGCGCACAA  TCCGCTTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCGGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCCGCTT  TATTGCCGAA  TTGCGCGGCC  AACCCGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGGTTGAGCG  TCCCAGATGAT
801 TGTTTTGGGT  ATCGTCGGCT  TTGTCCGGTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence &lt;SEQ ID 530; ORF 137.ng&gt;:

g137.pep

m137.seq

This corresponds to the amino acid sequence <SEO ID 532; ORF 137>:

m137.pep

```

1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINGELWG
151 RVTDINAFWA MGFPQARYE AEAAAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGFIRFRIE FARQPDYILG
251 LLTLGLSMGO WLSVPMIVLG IVGFVRFGMK KOH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

m137/g137

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESLDD	FTLWG			
g137	MIIHHQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESLDD	FTLWG			
	10	20	30	40	50	60
m137.pep	ILGVILGGRIGYVLFYKFS	DYLAHPLDIFK	VWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF		
g137	ILGVILGGRIGYVLFYKFS	DYLAHPLDIFK	VWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF		
	70	80	90	100	110	120
m137.pep	ILGVILGGRIGYVLFYKFS	DYLAHPLDIFK	VWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF		
g137	ILGVILGGRIGYVLFYKFS	DYLAHPLDIFK	VWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF		
	70	80	90	100	110	120
m137.pep	LKLMDTVAPL	VPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW				
g137	LKLMDTVAPL	VPLGLASGRIGNFINGELWGRITDINAFWAMGFPQAHYEDAEAAAHNPLW				
	130	140	150	160	170	180
m137.pep	LKLMDTVAPL	VPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW				
g137	LKLMDTVAPL	VPLGLASGRIGNFINGELWGRITDINAFWAMGFPQAHYEDAEAAAHNPLW				
	130	140	150	160	170	180
m137.pep	AEWLQQYGM	LPFRHPSOLYQFALEGICLFTVIWLF	SKKORSTGOVASLFLGGYGI	FRFIA		
g137	AEWLQQYGM	LPFRHPSOLYQFALEGICLFTVIWLF	SKKORSTGOVASLFLGGYGI	FRFIA		

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```

|||||
g137      AEWLQQYGM LPRHPSQLYQFALEGICLFAVVWLFSSKKPRPTGQTAALFLGGYGIVFRFIAE
          190      200      210      220      230      240

          250      260      270      280
m137.pep  FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX
          |||||
g137      FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 533>:

```

a137.seq
1   ATGATTACCC ATCCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGGCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTCTCTCG CAGAAGGCGC ATCGCGCAAG GCTTGTCCGT TTTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATATGG TTGTTCGGTC GCAAACACGG
351 CATCGGCTTC CTCAAACCTGA TGGACACGGT CGCACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGCGCA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTGG GCAGAAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCGCGCTC GTTTGGCTGT TCTCTAAAAA
651 ACAGCGGCCG ACCGGACAAG TCGCCTCACT CTTCCTCGGC GGCTACGGCA
701 TATTCGCTT CATTGCCGAA TTTGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 534; ORF 137.a>:

```

a137.pep
1   MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTWG ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINGELWG
151 RVTDINAFWA MGFPOARYED LEAAAHNPLW AEWLQQYGM LPRHPSQLYQF
201 ALEGICLFAV VWLFSKKQRP TGQVASLFLG GYGIFRFIAE FARQPDDYLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

m137/a137 98.2% identity in 283 aa overlap

```

          10      20      30      40      50      60
m137.pep  MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTWG
          |||||
a137      MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTWG
          10      20      30      40      50      60

          70      80      90      100     110     120
m137.pep  ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFGRKHGIGF
          |||||
a137      ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFGRKHGIGF
          70      80      90      100     110     120

          130     140     150     160     170     180
m137.pep  LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPOARYEDAEAAAHNPLW
          |||||
a137      LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPOARYEDLEAAAHNPLW
          130     140     150     160     170     180

          190     200     210     220     230     240
m137.pep  AEWLQQYGM LPRHPSQLYQFALEGICLFTVIWLFSSKKQRTGQVASLFLGGYGIFRFIAE
          |||||
a137      AEWLQQYGM LPRHPSQLYQFALEGICLFAVVWLFSSKKQRTGQVASLFLGGYGIFRFIAE

```

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	190	200	210	220	230	240
	250	260	270	280		
m137.pep	FAROPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX					
a137						
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

g138.seq

```

1  ATGGAGTTTG AAAACATTAT TTCCGCCGCGc gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACAtcc gccgGTTTTC CGGTTCCGGTC GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTTGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCTGA AGCcgcgcgc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCCGTAT CGGGTCGATG ATTTTAGGCA GAGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

g138.pep

```

1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGFEVQGM RVTDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIAKAKL LVDTPEQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAQVM DKTGNLLTKL TPKRIDGLIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

m138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGGTTTTC CGGTTCCGGTC GCCGTCATCA
101 AATACGCGCG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCTGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCCGTAT CGGTTTCATG ATTTTGGGCG GTGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

m138.pep

```

1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```

### Homology with a predicted ORF from *N. gonorrhoeae*

m138/g138

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

1	ATGGAGTCTG	AAAACATTAT	TTCCGCCGCC	GACAAGGCGC	GTATCCTTGC
51	CGAAGCGCTG	CCTTACATCC	GCCG GTTTTC	CGGTTCG GTC	GCGGTCA TCA
101	AATACGCGCG	CAACCGGATG	ACCGAACTTC	CCTTGA AAGA	AGGGTTTGCG
151	CGCGATGTCT	TGCTGCTGAA	CGTGTCGGC	ATTCAATCCG	TCATCGTTCA
201	CGGCGGCGGG	CGCAGATCA	ATGCGATGCT	TGAAAAAGTC	GGCAAAAAGG
251	GTGAGTTTGT	CCAAGGAATG	CGCGTTACCG	ACAAAGAGGC	GATGGATATT
301	GTCGAAATGT	TGTTGGGCGG	CGATGTC AAT	AAAGAACTCG	TGTCGATGAT
351	TAACATCATG	GGCGGACACG	GCGTCGGCGT	AAGCGAATGC	GACGACCATT
401	TCA TTAAAGC	GAAGAAACTT	TTGATCGATA	GCCCCGAACA	GAATGGCGTG
451	GACATCGGAC	AGGTCGGTAC	GGTGGAAAGC	ATCGATACCG	GTTTGGTTAA
501	AGGGCTGATA	GACAGCTGGT	GCATTCCCGT	CGTCGCCCCC	GTCGGCGTAG
551	GTGAAA AAG	GCAAGCGTTC	AACATCAACG	CCGATT TTGT	AGCAGGCAAA
601	TTGGCGGAAG	AATTGAACAAGC	GCAAAA AACTC	TTGATGATGA	CGAATATCGC
651	CGGTGTGATG	GACAAAACGG	GCAATCTGCT	GACCAA AACTC	ACGCCGAAAC
701	GGATTGATGA	ACTGATTGCC	GACGGCACGC	TGATG GCGG	TATGCTGCCG
751	AAAATCGCTT	CTGCGGTGCA	GACGCCCGCT	AACGGCGTGA	AAGCCACGCA
801	TATCATCGAC	GGCAGGTGCG	CCAACGCGCT	TTTGCTGGAA	ATCTTTACCG
851	ATGCCGTGAT	CGGTTCGATG	ATTTTGGGCG	GTGGGGAAGA	TGCGCTGA



This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRVPNALLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA RDVLLKLVG					
a138	MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA RDVLLKLVG					
	10	20	30	40	50	60
m138.pep	IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI VEMVLGGHVN KEIVSMINTY					
a138	IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI VEMVLGGHVN KEIVSMINTY					
	70	80	90	100	110	120
m138.pep	GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV DIGQVGTVES IDTGLVKGLI ERGCI PVVAP					
a138	GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV DIGQVGTVES IDTGLVKGLI ERGCI PVVAP					
	130	140	150	160	170	180
m138.pep	VGVGEKGEAF NINADLVAGK LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA					
a138	VGVGEKGEAF NINADLVAGK LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA					
	190	200	210	220	230	240
m138.pep	DGTLYGGMLPK IASAVEAAV NGVKATHIID GRVPNALLE IFTDAGIGSM ILGGGEDAX					
a138	DGTLYGGMLPK IASAVEAAV NGVKATHIID GRVPNALLE IFTDAGIGSM ILGGGEDAX					
	250	260	270	280	290	299
m138.pep						
a138						
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAggc ggcggcggag
101 gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201 AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCTGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301 ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351 CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401 GTATCGTCTGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAACTG
451 TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAAATTACA
501 AAAACTATAC GGCCTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
51  NSRTIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101 IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPEL
151 YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
1  ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGACTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCGAC TTCAATGCAG GCGGTACCGG TATCGGCAGC
151 AACAGCAGAG CAACAACAGC GAAATCAGCA GCAGTATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTCCA AACCCAAATG ACGCATLACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTACG AAAAACTATA
501 CCGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.pep
1  MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
51  NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETFQTMQ THYKNLINK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE
151 LYGRKEHGYN ENYEKLYGVY AEGSA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m139/g139

	10	20	30	40	50	60
m139.pep	MRTTPTFPTKTFKPTAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA					
g139	MRTTSTFPTKTFKPAAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATIAESA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRI CIPETFQTMQTHYKNLINK					
g139	AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIKAP-RICI PETFQTMQTNINKMINLK					
	70	80	90	100	110	
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX					
g139	PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

```
a139.seq
1  ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCGAC TTCAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACAACAGC GAAATCAGCA GCAATATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTACA AACCCAAATG ACGCATACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTAC. AAAAACTATA
501 CCGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

```
a139.pep
1  MRTTPTFPTK TFKPAANALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
```

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```

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETLQTQM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSI SFPE
151 LYGRKEHGYN ENYXKLYGVY AEGSA*

```

m139/a139 97.1% identity in 175 aa overlap

```

              10      20      30      40      50      60
m139.pep    MRTPTFFPTKTFKPTAMALAVATTL SACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a139         MRTPTFFPTKTFKPAAMALAVATTL SACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
              10      20      30      40      50      60

              70      80      90     100     110     120
m139.pep    AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFTQTMTHYKNLINLK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a139         AISYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETLQTQMTTHXKNLINLK
              70      80      90     100     110     120

              130     140     150     160     170
m139.pep    PAIEAGYTGRGVEVGIVDTGESVSGSISFP ELYGRKEHGYNENYKLYGVYAEGSAX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a139         PAIEAGYTGRGVEVGIVDTGESVSGSISFP ELYGRKEHGYNENYXKLYGVYAEGSAX
              130     140     150     160     170

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

```

g140.seq
1   Atgtcggcac gCGGCAAGGG GGCAGgctat ctcAACAGTA CCGGACGACa
51  TGTTCCTTC CTGAGTGCCG CCAAAATCGG GCAGGATTAT TCTTCTTCA
101 AAAATATCAA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GCAGTGAAGG CGACACGCCG TCCTATTATG TCCGTCGCGG
201 CAATCGGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GGCGGCAGCA ATCTGGAAAA CCTGATGGTC
301 GAGCTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGTGCGCCGAC CGCACAGATA TGCCGGGCAT CCGCTACGG CGCACAACCT
401 TCCGCACAGC GGCAGCCGTA CAGCATGCGA ATACCGCCGA CGGCGTACGc
451 aTCTTcaacA GTCTCGCCGC TAccgTCTat GccgACAGTG CCGCCGCCCA
501 TGccgATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGGTAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT CGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 TATCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATAGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTA GTCTGTTTGC AGGCATACGG CACGATGTGG GCGATATCGG
801 CATCTCAAA GGCCTGTTCT CctaCGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGATGAA TATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG TGGTGTCAAC GTTCCGTTTG CCGCAACGGG
951 AGATTTGACG GTTGAAGGCG GTCTGCGCCA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCagt GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
1051 GAAGGCACAC TGGTGCGACT CGCGGTCTG AAAGTGTGCG AACCTTGAG
1101 CGATAAAGCC GTCCTGTCTG CGACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CGCGGTAACG GGCGGCTTTA CCGGCGCGGC TGCAGCAACC
1201 GGCAAGACGG GTGCACGCAA TATGCCGCAC ACCCGCCGGG TTGCCGGTCT
1251 GGGGGTGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACACCGG TTCCAACAG TACGCAACC ACAGCGGACA AATCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 548; ORF 140.ng&gt;:

```

g140.pep
1   MSARGKGAGY LNSTGRHVPF LSAAKIGQDY SFFKNIKTG GLLASLDSVE
51  KTAGSEGDTP SYVVRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAVAD RTDMPGIRLR RTTFRTAAAV QHANTADGVR
151 IFNSLAATVY ADSAAHADMD QGRRLKAVSD GLDHNGTGLR VIAQTQDDGG
201 TWEQGGVEGK MRGSTQTIGI AAKTGENTTA AATLGIGRST WSENSANAKT

```

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```

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRHDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAAT
401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV
451 GYRF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

```

m140.seq
1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG
51 TGTTCCTTTC CTGAGTGCCG CCAAATCCGG GCAGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GCAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GCGGCGAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTTAC GGCAGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CCGGTGTACGC
451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCAACA GGACGGTGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGACG CTACAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CCGTGTC AAC GTTCCGTTTG CCGCAACGGG
951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTGCGCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
1051 GAAGGCACGC TGGTCGGAAT CGCGGCTCTG AAGCTGTCCG AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGCGCGG CGTGGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAGAAGCG GGGCAGCACA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT
1251 GGGCGCGGAT GTCGAATTCT GCAACGCGTG GAACGCGCTG GCACGTTACA
1301 GCTACGCCGG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

```

m140.pep
1 MSARGKGAGY LNSTGRRVPF LSAKIGQDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDTL SYVVRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNSLAATVY ADSTAHAADM QGRRLKAVSD GLDHNGTGLR VIAQTQDDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

```

m140/g140
10 20 30 40 50 60
m140.pep MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g140 MSARGKGAGYLNSTGRRHVPFLSAKIGQDYSFFKNIKTDGGLLASLDSVEKTAGSEGDTP
10 20 30 40 50 60
70 80 90 100 110 120

```

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m140.pep	SYVVRGNAARTASAAAHSA	PAGLKHAVEQGGSNLENLM	VELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAHSA	PAGLKHAVEQGGSNLENLM	VELDASESSATPETVETAVAD
	70	80	90 100 110 120
m140.pep	RTDMPGIRPYGATPRAAAVQ	HANAADGVRIFNSLAATVYAD	STA AHADMQGRRLLKAVSD
g140	RTDMPGIRLRRTTPTAAAVQ	HANTADGVRIFNSLAATVYAD	SA AHADMQGRRLLKAVSD
	130	140	150 160 170 180
m140.pep	GLDHNGTGLRVIAQTQQDGG	TWEQGGVEGKMRGSTQT	VGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQQDGG	TWEQGGVEGKMRGSTQT	IGIAAKTGENTTAAATLIGRST
	190	200	210 220 230 240
m140.pep	WSENSANAKTDSISL	FAGIRHDAGDIGYLKGLFSY	GRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISL	FAGIRHDVGDIGYLKGLFSY	GRYKNSISRSTGADEYAEGSVNGTL
	250	260	270 280 290 300
m140.pep	MQLGALGGVNVPPAATGDL	TVEGGLRVDLLKQDAFAEK	GSALGWSGNSLTEGTLVGLAGL
g140	MQLGALGGVNVPPAATGDL	TVEGGLRHDLLKQDAFAEK	GSALGWSGNSLTEGTLVGLAGL
	310	320	330 340 350 360
m140.pep	KLSQPLSDKAVLFATAG	VERDLNGRDYTEVTGGFTG	ATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAG	VERDLNGRDYAVTGGFTG	AAAAATGKTGARNMPHTRRVLGLVD
	370	380	390 400 410 420
m140.pep	VEFGNGWNLARYSYAG	SKQYGNHSGRVGVGYRFX	
g140	VEFGNGWNLARYSYTG	SKQYGNHSGQIGVGYRFX	
	430	440	450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140.seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCCTTC CTGAGTGCCG CCAAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCGCGC CCCGCCGGTC
251 TGAACACAGC CGTAGAACAG GCGGCAGCA ATCTGGA AAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCGGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCCA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCAACA GGACGGTGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCAAAA CCGGCGAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAC AGCATCAGCC
851 GCAGCACC GG TCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
901 ATGACAGCTG GCGCACTGGG CGGTGTCAAC GTTCCGTTG CCGCAACGGG

```

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```

951 AGATTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AACAGGATG
1001 CATTGCGCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTGCG AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGCTGG TTCCGGTCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTT GCACGTTACA
1301 GCTACGCCGG TTCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

```

a140.pep
1 MSAGGKGAGY LNRTGQRPVF LSAKIGRDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDITL SYYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRLKAVSD GLDHNATGLR VIAQTQDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
a140	MSAGGKGAGYLNRTGQRPVFLSAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
	10	20	30	40	50	60
m140.pep	SYYVRRGNAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYYVRRGNAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	SYYVRRGNAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYYVRRGNAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRLKAVSD					
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNNLAATVYADSTAAHADMQGRRLKAVSD					
	130	140	150	160	170	180
m140.pep	GLDHNGTGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
m140.pep	GLDHNGTGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
m140.pep	WSSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	WSSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
a140	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
	310	320	330	340	350	360
m140.pep	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
a140	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
	310	320	330	340	350	360
m140.pep	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
	370	380	390	400	410	420
m140.pep	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

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	370	380	390	400	410	420
	430	440	450			
m140.ppep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
a140	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAAccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGGGCGGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TCGCGAGGCC TTCTTTGGGT
301 CCGGTGTTCC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT AC CGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACGCGCGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTTga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTGa tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTt t gGCAATATC TCGTCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATT TGTGCAAACC ATCGAAGGCA CTCGCGCCTT
801 TGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACC GAAGCA
901 GGCTTCGGCG CGGACTTGGG TCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACC GCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GCGGCGCGGG
1251 CCGGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACCTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTCG ATTT CAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCGGCG GCGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCCT GCCGAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pep

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFQVKGGA GGGYAQVLP EDINLHFTGD FHAIGAANL LAAMLNHIY
151 QGNELNIDPK RVLWRRVDM NDRQLRNIID GMGKPDVDM RPDGFDITVA
201 SEVMAVFCLE KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAID NQPNNFGFAY DVELGIDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPCMAK TOYSLSDNAK
501 LLGCEPGEFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDE
551 HGVHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAATCG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TCGCGGAACC TTCTCTGGGG
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GCGGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCGGTTGA CGGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAAACC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGCCTTCGGC CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAATGCCC
951 CCTTGCCCGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCGACGCG CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCTT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CCGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTTG ATTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGG TGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCGGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGT CCGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHYKA KINPAEAFKL
51  POKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFGVKGGAA GGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDVGM RPDGFDTIVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIDDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVIHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

	10	20	30	40	50	60
m141.pep	MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKLPQKQGRLLIV					
g141	MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKLPQKQGRLLIV					
	10	20	30	40	50	60



400

	70	80	90	100	110	120
m141.pep	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLP					
	:					
g141	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m141.pep	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
	:					
g141	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
	130	140	150	160	170	180
	190	200	210	220	230	240
m141.pep	GMGKPDVGVMRPGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	:					
g141	GMGKPDVGVMRPGFDITVASEVMAVFCLAKDISDLKERFGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	:					
g141	AHGAMAALLKDAIKPNLVQTTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGAEKFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	:					
g141	GFGADLGAEKFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAEIAMIEKACAEHGVESL TEVWGKGAGGAD					
	:					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSDAEIAMIEKACAEHGVESL TEVWGKGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
	:					
g141	LARKVVNAIDNQPNNGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	:					
g141	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
	:					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

```

al41.seq
1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```

```

201 GCGGGGCGAA GGTAACCA CCGTAACCAT CGGTTTGCGG SACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TCGCGGAGCC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGCGCGCGCA GGCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAACTG CTGCGCGCA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCAAA CGCGTGCTGT GCGGCGCGT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAAAC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGTTCGCGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTGCGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGCG GTGGAACGCG CCAACCTCGG CGAAGAAAAA
1051 TTAGACGCTT TGAAAAAGG TTGCCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTTCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGCGCGCGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACTCG TTTCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGAT CCCAAAAGT GTACGGCGCG GAAGATGTTG ATTTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAACTGGGC TTGGACAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVDM NDRQLRNIID GMGKPVDGM RPDGEDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WKGKGAGGAD LARKVVNAIE SQTNNFGFAY JVELGIKDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVIHGLF+

```

m141/a141 99.5% identity in 558 aa overlap

```

m141.pep      10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKLPQKQGRILIV
|||||
a141          10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKLPQKQGRILIV

m141.pep      70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGGAAGGGYAQVLPM
|||||
a141          70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGGAAGGGYAQVLPM

m141.pep     130     140     150     160     170     180
EDINLHFTGDFHAIGAANNLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID
|||||
a141          130     140     150     160     170     180
EDINLHFTGDFHAIGAANNLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID

```

402

	190	200	210	220	230	240
m141.pep	GMGKPV DGV MRPDGFDITVASEVMAVFC LAKDISDLKERLGNILVAYAKD GSPVYAKDLK					
a141	GMGKPV DGV MRPDGFDITVASEVMAVFC LAKDISDLKERLGNILVAYAKD GSPVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTI EGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTI EGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGA EKFCDIKCR LAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGA EKFCDIKCR LAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNR FVSDADAELAMIEKACA EHGVEVSLTEVWGKG GAGGAD					
a141	LLKHISNLKNVFGLPVVVALNR FVSDADAELAMIEKACA EHGVEVSLTEVWGKG GAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAATGTTC
151 GGCAACATCC TGATGTTCGT CCGCCAGCAT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATeggaATG AttegCGCAC TCCGGTTTAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC CGTCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1  MRADFMFADN MPVQVRORAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMF
51  GNILMFVRQH IDAEAAVFRQ DRNDSRTPVY AQHHGRRLVG NRRNRHCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQOF*

```

This corresponds to the amino acid sequence <SEO ID 562; ORF 142>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng)

from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 563>:

```

a142.seq
1  ATGCGTGC GG  ATTTTCATGTT  TGCCGACAAT  ATGCCCGTGC  AGGTGCGCCA
51  ACGCGCCCTC  TATTTCAAGT  TGTCCCGGTTT  TGCCGCGATG  CCAGATGTGG
101 TAGGCAAAAG  GCTCTTCGGG  GCACAGGCGCG  CTCAGCCCGG  CAAAATGTTC
151 GGCAACATCC  TGATGTTCGT  CCGCCAGCGT  ATTGATGCAG  AGAGTGCCGT
201 TTTCCGACAG  GATCGGAATG  ATTCGCGCAC  TCCGGTTGAT  GCACAGCATC
251 ACGGTGCGGG  GCTCGTCCGT  AACCGGCGCA  ACCGCGGTCA  TTGTAAATGCC
301 GTAACGCCCT  GCCGCACCGT  CTGTCGTGAT  GACATGAACG  CCTGCCGCAC
351 AGGATGCCAT  CGCATCAAG  AACGAAGTTT  GAAAAGTTT  TCGCAAAATCC
401 GCCATTTTTC  CCGTTTAAAC  TGTCCCTTAT  ATAAGAATGC  TGCACACAAG
451 GCACCCCCCA  TGTGCAGCAG  TTCTGATTCA  AAAAGCCGTC  GGTCTGGACAT
501 TTCCGCGCGT  TACGGCGTAT  TACGAGTTCA  ACGCATCCTC  GATTTTGGCA
551 AGTTCTGCCA  ACAGTCTTTT  AAGCAGCAGC  ATTTTCTCGC  GCGCCAGCAC
601 TTCCTCGATA  GCGTCGTAAC  GCTCGTCCAC  TTCTTCGCGG  ATTTTCTCAT
651 ACAGGCTTTC  GCCCTCGGCA  GTACAGCTTCA  GAAAAACACG  TCGTGTGTGCG
701 TTGGAAGGTT  TCAGGCGGAC  AACCAAACCC  CGTTTTTCAA  GCGGGGTTCG
751 GATACCGGTC  AGGCTTGGGC  GCAAAATGCA  CGCCTGATTC  GGCCAAATCT

```

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801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC  
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG  
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep  
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF  
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTFVD AQHHGRRLVR NRRNRRHCNA  
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK  
 151 APPMCSSSDS KSRRSDISAR YGVLVRQIRL DFGKFCQQVF KQHFLLAAQH  
 201 FLDSVVTLVH FFADFLIQLL ALGSQKQKNT SLVVGRFQAD NQTRFFKAGQ  
 251 DTGQAGAQNA RLIRQILKVQ RAVFRQKTDN PELLIGNIRL IQNRPELGHQ  
 301 GFPCLYQTDI DRRMF\*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF					
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTFVDAQHHGRRLVGNRRDRRCNAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTFVDAQHHGRRLVGNRRDRRCNAVTPCRTVCRDDMNACRTGCH					
	70	80	90	100	110	120
	130	140	150	159		
m142.pep	RITERSLKIFLQIRHFSPLNCPYKNAAHKASPHVQQFX					
a142	RITERSLKSFLOIRHFSPLNCPYKNAAHKAPPMCSSSDSKSRRSDISARYGVLVRQIRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a142	DFGKFCQQVFKQHFLLAAQHFLDSVVTLVHFFADFLIQLLALGSQKQKNTSLVVGRFQAD					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq  
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAG  
 51 CTCGCAGATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT  
 101 TGGGCTGTTT TTTCATCCTG CCGCGCTGG CCGGGATGCT GGTTCAGCCG  
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG  
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA  
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG  
 301 GCCTTGTCCT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA  
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CCGCGATATG GTCAACGAGG  
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAA' GTTCTTAGC GAATACGGAC  
 451 GCGGTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC  
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCCTGGTC GTAGCATTCT  
 551 ATGTGGGTGC GGCCTTACTG ATTATTACCA GTGCGTTTAC AATCTCCAAA  
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT  
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC  
 701 CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTTCTG CTGGTTTCGCC  
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGACG AAAACGCTCTG  
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT  
 851 ACGGCGTTTT GCGGCGGGTG TAGTCGGTGG CCGCGGTGAT TTGTTCTGTT  
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGCGGGGTT ATTTCCGCTG  
 951 TTTGGCTTTG GCGGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC  
 1001 AATACGCACT CATCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC  
 1051 ATTATCACTT ATCCGCTGAC GATTTGCGCC AACGCTTGT CGGGCAAAACA  
 1101 CATGGATACT TATTTGGGCC TGTttaacgg ctctgtCTGT ATGCcgcaaa  
 1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

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1201 CAGGCAACCA TGTTCCTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT  
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep  
 1 MLSFGYLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP  
 51 IVGYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA  
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGD VNEEQKSYAY GIQSFLANTD  
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK  
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFVTV TPVQFFCWFA  
 251 FRYMWYSAG AIAENVWHTT DASSVGHQEA GNRYGVLAIV \*SVAAVICSF  
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNYALILS YILIGIAWAG  
 351 IITYPLTIVA NALSGKHMGT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH  
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq  
 1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG  
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT  
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAGCCG  
 151 ATTGTGGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCGG  
 201 CCGTCTGCCG TATCTGCTTT ATGGCAGCGT GATTGCGGTT ATTGTGATGA  
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG  
 301 GCTTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTGCTCAA  
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCACGAGG  
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAA  
 451 GCGGTCGTGG CGGCGATTCT GCCGTTGTG TTTGCGTATA TCGGTTTGCG  
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGCTC GTGGCGTTTT  
 551 ATGTGGGTGC GCGGTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAA  
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT  
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC  
 701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCGCC  
 751 TTCCAATATA TGTGGACTTA CTCGCGAGGC GCGATTGCGG AAAACGCTCTG  
 801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT  
 851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CGGCGGTGAT TTGTTCTGTT  
 901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGCGGGGTT ATTTCGGCTG  
 951 TTTGGCTTTG GCGCGGCTCG GCTTTTCTC CGTTTCTTC ATCGGCAACC  
 1001 AATACGCGCT GGTGTGTGCT TATACCTTAA TCGGCATCGC TTGGGCGGGC  
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA  
 1101 TATGGGCACT TACTTGGGCT TGTTTAACGG CTCTATCTGT ATGCCTCAA  
 1151 TCGTCGCTTC GCTGTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG  
 1201 CAGGCCACTA TGTCTTGGT AGGGGCGGTC GTCCTGCTGC TGGGCGCGTT  
 1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep  
 1 MLSFGELGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP  
 51 IVGHYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA  
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGD VNEEQKGYAY GIQSFLANTG  
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK  
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFVTV TLVQFFCWFA  
 251 FQYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAIV QSVAAVICSF  
 301 VLAQVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG  
 351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL  
 401 QATMFLVGGV VLLLGAFSVF LIKETHGGV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

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m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSFGYLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
	KPRLGGRRLPYLLYGTLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGGRRLPYLLYGTLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKGVVPQTIV
g143	QPFKMMVGDVNEEQKSYAYGIQSFLANTDAVVAAILPFVFAYIGLANTAEGKGVVPQTIV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAAPKVFWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
	TLVQFFCWFAFYMWYTSAGAIENVWHTTDASSVGQYQAGNRYGVLAQVAVVICSF
g143	TPVQFFCWFAFRYMWYTSAGAIENVWHTTDASSVGHQYQAGNRYGVLAQVAVVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNQYALILSYILIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVVLGAFSVC
g143	NALSGKHMDTYLGLFNGSVCMQIVASLLSFVLPMLGGHQATMFLVAGAVLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

a143.seq

1	ATGCTCAGTT	TCGGCTTTCT	CGGCGTTCAG	ACGGCCTTTA	CCCTGCAAAG
51	CTCGCAGATG	AGCCGCATCT	TCCAGACGCT	CGGTGCCGAT	CCGCACAGCC
101	TCGGCTGGTT	CTTTATCCTG	CCGCCGCTGG	CGGGGATGCT	GGTGCAGCCG
151	ATTGTGCGCC	ATTACTCCGA	CCGCACTTGG	AAGCCGCGTT	TGGGCGGCGG
201	CCGTCTGCCG	TATCTGCTTT	ATGGCACGCT	GATTGCGGTT	ATTGTGATGA
251	TTTTTGATGCC	GAACTOGGGC	AGCTTCGGTT	TCGGCTATGC	GTCGCTGGCG
301	GCTTTGTCTGT	TCGGCGCGCT	GATGATTGCG	CTGTTAGACG	TGTCGTCAAA
351	TATGGCGATG	CAGCCGTTTA	AGATGATGGT	CGGCGACATG	GTCAACGAGG
401	AGCAGAAAGG	CTACGCCTAC	GGGATTCAAA	GTTTCTTAGC	GAATACGGGC
451	GCGGTGCTGG	CGGCGATTCT	GCCGTTTGTG	TTTGCCTATA	TCGGTTTGGC
501	GAACACCGCC	GAGAAAGGCG	TTGTGCCGCA	GACCGTGGTC	GTGGCGTTTT
551	ATGTGGGTGC	GCGGTGCTG	GTGATTACCA	GCGCGTTTAC	GATTTTCAAA
601	GTGAAGGAAT	ACAATCCGGA	AACCTACGCC	CGTTACCACG	GCATCGATGT
651	CGCCGCGAAT	CAGGAAAAAG	CCAACTGGAT	CGAACTCTTG	AAAACCGCGC
701	CTAAGGCGTT	TTGGACGGTT	ACTTTGGTGC	AATTCTTCTG	CTGGTTTCGCC

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751 TTCCAAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT
851 ACGGCGTTTT GCGGCGCGTG CAGTCGGTTG CGGCGGTGAT TTGTTCTGTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTTCGGCTG
951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTACGG CTCTATCTGT ATGCCGCAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGCGCTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  MLSFGLGVQ TAFTLOSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSDRTW KPRLGRRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
101 ALSFGLMIA LLDVSSNMAM QPFKMMVGDM VNEEQGYAY GIQSFLANTG
151 AVVAAILPEV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWYTSAG AIAENVWHTT DASSVGYPEA GNWYGVLA AVQSVAVICSF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGFLNGSIC MPQIVASLLS FVLFPMGLGL
401 QATMFLVGGV VLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
a143	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
	10	20	30	40	50	60
m143.pep	70	80	90	100	110	120
a143	KPRLGRRRLPYLLYGTLIIVIMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	130	140	150	160	170	180
a143	QPFKMMVGDMVNEEQGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTA EKGVPQTVV					
	130	140	150	160	170	180
m143.pep	190	200	210	220	230	240
a143	VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	250	260	270	280	290	300
a143	TLVQFFCWFAFQYMWYTSAG AIAENVWHTT DASSVGYPEA GNWYGVLA AVQSVAVICSF					
	250	260	270	280	290	300
m143.pep	310	320	330	340	350	360
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	370	380	390	400	410	420
a143	NALSGKHMGT YLGFLNGSIC MPQIVASLLS FVLFPMGLGL QATMFLVGGV VLLGAFSVF					



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a143      |||||
           NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLOATMFLVGGVLLLGAFSVF
           370      380      390      400      410      420

           430
m143.pep  LIKETHGGVX
           |||||
a143      LIKETHGGVX
           430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTG GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCGTtTT
351 CAACGCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTGGatattT
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGTtaccT ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGC CGGACAT
551 ATTCGGCCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFVSLADGV
51  RENPVVSFDD AASYADNPFFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGyFLPLGRG RPAYRYLSRH
151 RARRHGVPRD AAHLAAGRG PARCGSAYSA GRtYSGRCRK TARLNGFRFP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTG GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCGGTTT
351 CAACGCGGTG GCGGCAGACG GCGGTTCCGT GGTGCTGCGC AGCCGCGTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGg ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TAaCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFVSLADGV
51  RENLVVSFDD AASYADNPFFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFGFGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAHLL AAGRGPARG SAYSAGRtYA
201 GRCRKARLN GFRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
g144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFSVLADGVRENPFVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
g144	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m144.pep	AADGRSVVLRSLATVGRRLSQRFQFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL					
g144	AAD-----GRRLSQRFQ--YFLPLGRGRPAYRYSRHRARRHGVRPDAHLL					
		130	140	150	160	
	190	200	210	219		
m144.pep	AAGRGPARGSAYSAGRTYAGRCRKRTARLNGFRRPRSIX					
g144	AAGRGPARGSAYSAGRTYSGRCRKRTARLNGFRRPRSIX					
	170	180	190	200		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

a144.seq

1	ATGAGCGATA	CCCCCGCTAC	CCGCGATTTC	GGCCTGATCG	ACGGGCGTGC
51	CGTAACCGGC	TATGTGCTGT	CCAACCGGCG	TGGTACGCGT	GTCTGCGTGC
101	TGGACTTGGG	CGGGATTGTG	CAGGAATTTT	CCGTTTGGC	AGACGGCGTG
151	CGCGAAAACC	TCGTGGTGTC	GTTGACGAT	GCGGCTTCCT	ATGCGGACAA
201	TCCGTTTCAG	ATTAACAAGC	AGATAGGGCG	CGTGGCCGGA	CGCATCCGCG
251	GTGCGGCGTT	CGACATCAAC	GGCAGGACTT	ACCGCGTGGA	GGCCAACGAA
301	GGCAGGAACG	CGCTGCACGG	CGGTTGCGAC	GGGCTGGCCG	TTACCCGTTT
351	CAACGCGGTG	GCGGCAGACG	GCCGTTGCGT	GGTGTGCGC	AGCCGCGCTG.
401	CAACAGTCGG	CCGACGGTTA	TCCCAACGAT	TTGGATTGG	ATATTTCTTA
451	CCGCTTGGAC	GAGGACGACC	GGCTTACCGT	TACCTATCGC	GCCACGCGCG
501	TGGGCGACAC	GGTGTTCGAC	CCGACGCTGC	ACATTTACTG	GCGGCTGGAC
551	GCGGGCGCTG	ACGATGCGGT	TCTGCATATT	CCGCAGGGCG	GACATATTCC
601	GGCCGATGCC	GAAAACTGC	CCGTCTCAAC	GGTTTCAGAC	GACCTCGAAG
651	TATTGA				

This corresponds to the amino acid sequence &lt;SEQ ID 576; ORF 144.a&gt;:

a144.pep

1	MSDTPATRDF	GLIDGRAVTG	YVLSNRRGTR	VCVLDLGGIV	QEFSVLADGV
51	RENLVVSFDD	AASYADNPFQ	INKQIGRVAG	RIRGAADFID	GRTYRVEANE
101	GRNALHGGSH	GLAVTRFNAV	AADGRSVVLR	SRLXTVGRR	SQRFQFGYFL
151	PLGRGRPAYR	YLSRHRARRH	CVRPDAHLL	AAGRGPARGC	SAYSAGRTYS
201	GRCKRTARLN	GFRRPRSI*			

m144/a144 99.1% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
a144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					

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```

|||||
a144      AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
              70      80      90      100     110     120

              130      140      150      160      170      180
m144.pep  AADGRSVVLRSLRATVGRRLSQRFGFYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
|||||
a144      AADGRSVVLRSLRXTVGRRLSQRFGFYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
              130      140      150      160      170      180

              190      200      210      219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCRKTARLNGFRRPRSIX
|||||
a144      AAGRGPARGCSAYSAGRTYSGRCRKTARLNGFRRPRSIX
              190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1  ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51  AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA ctTCCCCGACT GTCCGTCCCG CGCcttTGA GGCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 TCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCCTCC TCGCGGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTATGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.pep
1  MKQIPLRLQ VVIDHDKVEQ YGLDFMPCL RQPPLDNFPT VRPAPFEARG
51  KHVERRRQDK DTDSFRQ RVA NLRRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCFQ KSLLRDKRFK LFFGNKVIMY AVCFAFTRRA RMRHGNAGT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51  AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCCGACT GTCCGTCCCG CGTCCGTTGA GGCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCCGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCCG CGTATTCCAA AAAAGCTTCC TCGCGGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1  MAQILLRSRQ VVIDHDKVKQ YGLDFMPCL RQPPLDNFPT VRPASVEARG
51  KYVERRRQDK DADGFGQ RVA NLRRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSFLRDKRLK LFFGNKVIMY AVCFAFTRRA RVRHGNAGT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVV	IDHDKVKQYGLLD	FMPCLRQPP	LDNFPTVRPAS	VEARGKYVERRRQDK	
g146	10	20	30	40	50	60
	MKQIPLRLLOVV	IDHDKVEQYGLF	DFMPCLRQPP	LDNFPTVRPAP	FEARGKHVERRRQDK	
m146.pep	70	80	90	100	110	120
	DADGFGQVRVAN	LRRLNVDFQNH	VIACRRQRIHT	LRACAVIVAKY	VGVFQKSFLRDKRLK	
g146	70	80	90	100	110	120
	DTDSFRQVRVAN	LRRLNVDFQNH	VIACRRQRIHAL	RACAVIVAEYVC	VFQKSLLRDKRFK	
m146.pep	130	140	150	160	170	180
	LFFGNKVIMYAV	CFATRRARRVR	HGNAQTMVVC	QQPRHQGFAR	AGSGRNDKDVAF	SIS
g146	130	140	150	160	170	180
	LFFGNKVIMYAV	CFATRRARRMR	HGNAQTMVVC	QQPRHQGFAR	AGSGRNDKDVAF	SIS
m146.pep	190	200	210			
	GHIFYLYIFQPI	VSQWTPSFLF	ADAHILPLLF	FX		
g146	190	200	210			
	GHIFYLYIFQPI	VSQRTPYFIF	ADAHILPLLF	FX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```
a146.seq
1  ATGGCGCAAA TCCTCTCCG CCCGCGCCAA GTCATCATTG ACCACGACAA
51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCTT CGACAGCCTC
101 CTTTGATAAA CTTCCCGACT GTCCGTCCCG CGTCCGTTGA GACGCGCAGC
151 AAGCACATCG AAAGACGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTC CAAAATCAG
251 TCATAACCTG CCGCCGCCAA CGCATTCACA CCCTCCGCGC TTGTGCCGTA
301 ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGACG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCCG
501 AAGCGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

```
a146.pep
1  MAQILLRPRQ VIIDHEKIEQ YGLDFMPCL RQPPLDNFPT VRPASVETRS
51  KHIERRRQDK DADGFGQRI S NLSRALNVDF QNHVITCRQ RIHTLRACAV
101 IVAEHVRVFQ KSLLRCKRLK LFFGNKVIMY AVCFATRRRT RVRHGNAT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPGF
201 LFADAHILPL LF*
```

m146/a146 90.6% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVV	IDHDKVKQYGLLD	FMPCLRQPP	LDNFPTVRPAS	VEARGKYVERRRQDK	
a146	10	20	30	40	50	60
	MAQILLRPRQVI	IDHDKIEQYGLF	DFMPCLRQPP	LDNFPTVRPAS	VETRSKHIERRQDK	
	70	80	90	100	110	120

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```

m146.pep  DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSLRDKRLK
           |||||::|| |||||::|||::|||::|||::|||::|||::|||::|||::|||
a146       DADGFGQRIISNLSRALNVDFQNHVITCRRQRIHTLRACAVIVAEHVRVVFQKSLRDKRLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m146.pep  LFFGNKVIMYAVCFAETRRARRVRHGAQTVMVCQPRHQRFARAGSGRNDKDVAFSIS
           |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
a146       LFFGNKVIMYAVCFAETRRARRVRHGAQTVMVCQPRHQRFARAGSGRNDKDVAFSIS
           130     140     150     160     170     180

           190     200     210
m146.pep  GHIFYLYIFQPIVSQWTPSFLFADAHILPLLEFX
           |||||::|||::|||::|||::|||::|||::|||::|||
a146       GHIFYLYIFQPIVSQRTPGFLFADAHILPLLEFX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC AACTCAAAC CCATTGTTTT
51 ATCAATTCTT TTAATCAACA CACCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGGCTGCT GCACACTTCG ACCGCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTCGCC AAAAAAGCCG CAACTTGGG GACGCTTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAGTAT TGAACCATCA
351 CGGCGAAACG GGCATATGCG CGGACTTTTC TCCCGATCAC GCCATTATGG
401 TAGATACCGC CTGTTCGCAA CAGGTTGAAA TCCTGCGCG GCGGTTACG
451 CTCTTGTA CA GCTCGGcaa tgtggcgg GCTGtcaat gttgccgatg
501 gAAAAAtccc ccaaaaAAtg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLK?IVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51 RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDTALSQ QVEILRGPVT
151 LLYSSGNVAG AGQCCRWNKP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTTG GAAACGGTCA GCGTCGTCGG
51 CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGACACT TCGACCGCCT
101 CCGACAAAAT CATCTCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GCGGACGCTT TAGACGCGT ACCGGGCATC CACGCTTCGC AATACGGCGG
201 CGGCGCGTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAAG
251 TGT'TGAACCA TCACGCGCAA ACAGGCGATA TGGCGGATTT TTCGCCCAGT
301 CACGCCATTA TGGTAGATAC CGC'TTGTG CAACAGGICG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCTGAAAA CGGCGTATCG
451 GGCRAACTCG GATTGCGTTT GAGCAGCGGC AATCTGGAAA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAAA CTTTGTATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGGTTA CCGCAATCTG
601 AAACGCCTGC CCGACAGCCA CGCCGATTG CAAACGGGCA GCATCGGGCT
651 GTCTTGGGTT GCGCAAAAAG GTTTTATCGG CGTAGCGTAC AGCGACCGTC
701 GCGACCAATA TGGTCTGCCT GCCACAGCC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCCACGAC GACGATAATG CACACGCACA CACCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGCTACGAAC TCCGTGCCGA
951 ATGGAAGCAA CCGTTCCCGG GTTTTGAAGC CCGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAAGCAG GCGATGCAGT CGAAAACTTT
1051 TTAAACAACC AAACGCAAAA CGCCCGCATC GAGTTGCGCC ACCAACCCAT

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```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCAGAC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACAGC CACAACACAA ACTCAGCCTG ACCGCTCCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC GCACTTCTAC GCGCGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTGGGCTTCC ACCTGAAAGC CTCGTGACC
1951 GACCGTATCG ATGCCAATTT GGACTACTAC CGCGTGTTCG CCCAAAACAA
2001 ACTCGCCGCG TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAACTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGGCG GTGAACGTGA
2201 AGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNEVL HTEGLYRKSQ DYAVPRYRNL
201 KRLPDSHADS QTSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PEPGFALRV HLNRRNDYRD EKAGDAVENF
351 FNNQTONARI ELRHQPIGRL KGSWGVQYLQ QKSSALSASIS EAVKQPMLLD
401 NKVQHYSFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPQHKLSL TASHQERLPS TOELYAHGKH
501 VATNTFEVGN KHLNKRSSNN IELALGYEGD RWQYNLALYR NRGNYIYAO
551 TLNDGRGPKS IEDDSEMKLV RYNQSGADFY GAEGEYFKP TPRYRIGVSG
601 DYVRGRLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

                                10      20      30
m147.pep                      PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
                                |:| | | | | | | | | | | | | | | | | | | | | |
g147      MRREAKMAQITLKPVL SILLINTPLLAQA HETEQSVGLETVSVVGKSR PRATSGLLHTS
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m147.pep  TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g147      TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m147.pep  GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKI PEKMPENGVS
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g147      GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWNK NPPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```

a147.seq
1  ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCAAGCG CATGGAAC TG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTC CG
151 CGCGCCACTT CGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGCGGAC ACCTTGCAGC AAAAAGCCGT CAACTTGGGT GATGCTTAG
251 ACGGCGTACC GGGCATTCA TGCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGGCGAAACG GCGGACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTCGCAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGATCA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 AAAAAATCCC GAAAAAATGC CTGAAAACGG CGTATCGGGC GAACCTGGAT
551 TCGGTTTGAG CAGCGGCAAT CTGGAAAAAC TCACGTCGGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACTT TGTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATACAGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGG
1001 TAGACCTGCG CAACAAACGC TACGAATCC GCGCCGAATG GAAGCAACCG
1051 TTCCCGGTTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACTTTTTT AACAACCAAA
1151 CGCAAAACGC CGGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACAGCTT
1351 GAAGCGGCGC TACGCGTGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAAACCGC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAACT CAGCCTGACC GCCTCCCATC AGGAACGCCT
1551 GCGCTCAACG CAAGAGCTGT ACGCACACGG CAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GAAGCGGCGC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCCGGCGAC TATGTACGAG
1901 GCGGTCTGAA AAACCTGCCT TCCCTACCGG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCGTTCCGGC
2001 TCGCGCCTC GCGTCCACC TGAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTTGGA CTACTACCGC GTGTTGCGCC AAAACAACT CGCCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAA GCCGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```

a147.pep
1  MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVRGOTGRR IKVLNHHGET GDMADFSPDH AIMVDSALSQ OVEILRGVPT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSF ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPRYRNLK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNAIE LRHQPIGRK
401 GSWGVOYLGQ KSSALSATSE AVKQPMLLDN KVQHYSFEGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYYNHPL PDLGAHRQTA RSFALSGNWX
501 FTPQHKLST ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

```

415

601 YNQSADDFYG AEGEIYFKPT PRYRIGVSGD YVRGR LKNLP SLPGREDAYG  
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLOYR VFAQNKLARY  
701 ETRTPGHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP  
751 QMGRSFTGGV NVKF\*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLTVSVVGKSRPRATSGL	LHTS
a147	MRREAKMAQTT	LKPIVLSILLINTPLLSQA	HGTEQSVGLETVSVVGKSRPRATSGL	LHTS		
	10	20	30	40	50	60
m147.pep		40	50	60	70	80
		TASDKIISGDTLRQKAVNLGDALDGV	PGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET			
a147		TASDKIISGDTLRQKAVNLGDALDGV	PGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET			
		70	80	90	100	110
m147.pep						
a147						
m147.pep		100	110	120	130	140
		GDMADFS	PDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENG	VSG	
a147		GDMADFS	PDHAIMVDSALSQQVEILRGPVTL	LYSSGNVAGLVDVADGKIPEKMPENG	VSG	
		130	140	150	160	170
m147.pep						
a147						
m147.pep		160	170	180	190	200
		ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHAD	SQ		
a147		ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHAD	SQ		
		190	200	210	220	230
m147.pep						
a147						
m147.pep		220	230	240	250	260
		TGSIGLSWVG	EKGFIGVAYS	DRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHL		
a147		TGSIGLSWVG	EKGFIGAAYS	DRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHL		
		250	260	270	280	290
m147.pep						
a147						
m147.pep		280	290	300	310	320
		LTEEDIDYDN	PGLSCGFHDDNAHAH	THSGRPWIDLNRKRYELRAEWKQFFPGFEALRVH		
a147		LTEEDIDYDN	PGLSCGFHDDDAHAH	AHNGKPWIDLNRKRYELRAEWKQFFPGFEALRVH		
		310	320	330	340	350
m147.pep						
a147						
m147.pep		340	350	360	370	380
		LNRNDYRHDEKAGDAVENFFN	QTONARIELRHQPIGRLKGSWG	VQYLQKSSALS	SAISE	
a147		LNRNDYRHDEKAGDAVENFFN	QTONARIELRHQPIGRLKGSWG	VQYLQKSSALS	SATSE	
		370	380	390	400	410
m147.pep						
a147						
m147.pep		400	410	420	430	440
		AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYQDKALIDRENYN	HPL		
a147		AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYN	HPL		
		430	440	450	460	470
m147.pep						
a147						
m147.pep		460	470	480	490	500
		PDLGAHRQTARSFALSGN	WYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK			
a147		PDLGAHRQTARSFALSGN	WYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK			
		490	500	510	520	530
m147.pep						
a147						
m147.pep		520	530	540	550	560
		HLNKERSNNIELALGYEGDRWQYNLALYRN	RFGNYIYAQTLNDGRGPKSIEDDSEMKLVR			
a147		HLNKERSNNIELALGYEGDRWQYNLALYRN	RFGNYIYAQTLNDGRGPKSIEDDSEMKLVR			



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	550	560	570	580	590	600
m147.pep	580	590	600	610	620	630
	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQ					
	610	620	630	640	650	660
m147.pep	640	650	660	670	680	690
	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
m147.pep	700	710	720	730		
	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSETGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSETGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1   ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGctgg ttcaTCCCGA
51  AgctATgagt gtcggcgCGC TTGccgAcaa AATCCGCAAA AtcgaAAact
101 gGCCGCAAAA AGgcaTCTTA TTCCACGACA TCACGCCCGT CCTGCAAAGT
151 GCGGAATACT TCCGCCTTTT GGTGATTTG CTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGCTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGtcg gctTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTAcg cgcTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGa tgccgTCAAA CCCGTTTCGC
401 GCGTCTGCT GGTGATGAT TTGGTTGCCA CGGGCGGCAC AATGCTTGCC
451 GGGTGGAAAC TGATCCGCAA ACTCGGCGGG GAAATGTGCG AAgcgcgcgC
501 CATTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGCGCAAGT
551 GCGCGCCCTT ATTTACCCCTG CTTCAAAACG AAGGCTGCAT GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1   MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKGIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK
101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK PGRVLLVDD LVATGGTMLA
151 GLELIRKLGG EIVEAAAIL EFTDLQGGKNI RASGAPLFTL LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1   ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGCTGG TTCATCCCGA
51  AGCTATGAGT GTCGGCGCGC TTGCCGACAA AATCCGCAAA ATCGAAAAC
101 GGCCGCAAAA AGGCATCTTA TTCCACGACA TCACGCCCGT CCTTCAAAGC
151 GCGGAATACT TCCGCCTTTT GGTGATTTA TTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGTTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGTCG GTTTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTACG CGCTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGA TGCCGTCAAA CTCGTTTCGC
401 GCGTCTGCT GGTGATGAT TTGATTGCCA CGGGCGGCAC GATGCTTGCC
451 GGAATGGAAC TGATCCGCAA ACTCGGCGGA GAAATGTGCG AAGCCGCCGC
501 CATTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGTGCAAGCG
551 GCGCGCCCTT ATTTACCCCTG CTTCAAAACG AAGGCTGTAT GAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1   MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKGIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK

```

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101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA  
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLVATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCCGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAAA	CTCGGTTCCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAGC	TGATCGGCAA	ACTCGGCGGG	GAAATGTGCG	AAGCCGCCGC
501	CATTTTGAA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGGCCCTT	ATTACCCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LNVGFPVIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m148.pep  LVYRYMDQKIDIVAGLDARGFIIIGALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a148      LVYRYMDQKIDIVAGLDARGFIIIGALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
          70      80      90      100     110     120

          130     140     150     160     170     180
m148.pep  AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGSEIVEAAAILEFTDLQGGKNI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a148      AVEIHTDAVKLGSRVLLVDDLVATGGTMLAGLELIRKLGSEIVEAAAILEFTDLQGGKNI
          130     140     150     160     170     180

          190     200
m148.pep  RASGAPLFTLLQNEGCMKGX
          ||||||||||||||||||
a148      RASGAPLFTLLQNEGCMKGX
          190     200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1  ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGA AAAAAC
101 AAAAAGCCTC CATCCGTAC GACAAAGCAT TGATTGATCG AGAAACTAC
151 TACAACCAGC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAA cgCCTGCCGT CAACGCaagA actGtACgca
301 cacggcAAGC ACgtcgccac CAACACCTTT GAagtcggca acaaACACCT
351 CAACAAAGAG Cgttccaaca atatcgAACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGAtT CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggagcC GGCCCCAAAT CCATCgaaga
501 cgacagcgga ATGaagcTCG TGCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACgGcgcgga aggcgaaatc tACTTcaaaC CGAcACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCTT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCcettcaTC GCACAAGCCG
701 ACCAAAACGC CCCCCGCATT ccggtGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGT
801 CGCCCAAAAC AAATCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CGGTGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGTTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAAt gGGCCGAGC TTtgccgGcG
1001 gcgtaAACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1  MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFPPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGDWRQYNL AAYRNRFNGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLFGR EDPYGKRPF I AQADQNAPRI PAARLGFHLK
251 TSLTDRIDAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1  ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATCGG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGA AAAAAC
101 AAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGAAACTAC
151 TACAACCACC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGCAAAAC ACgtcgccac CAACACCTTT GAAGTCGGCA ACAAAACCTT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACCTAC

```

m149.pep

1	MLLDNKVQHY	SFFGVEQANW	DNFTLEGGVR	VEKQKASIQY	DKALIDRENY
51	YHNHPLDLGA	HRQTSARFAL	SGNWFYTPQH	KLSLTASHQE	RLPSTQBELA
101	HGHVIAVNTF	EVQNKHNLKE	RSNNIELQSG	YEGDRWQYNL	ALYRNRFNGY
151	IYAQTLNDGR	GPKSIEDDSE	MKLVRYNQSG	ADFYGAEGEI	YFKPTPRYRI
201	GVSGDYVRGR	LKNPLPSLGR	EDAYGNRPFI	AQDDONAPRV	PAARLGPHLK
251	ASLTDRIDAN	LDYYRVFAQN	KLARYETRPS	GHHMLNLGAN	YRRNTRYGEW
301	NWYVKDANLL	NOSVYAHSSF	LSDTOMGRTP	FTGGVNVKFK	

Homology with a predicted ORF from *N.gonorrhoeae*

from *N. gonorrhoeae*:

m149/g149

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDRENNYHNPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENNYQNPLPDLGA					
	10	20	30	40	50	60
m149.pep	HRQTARSPFALSGNWFYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTTFEVGNKHLNKE					
g149	HRQTARSPFALSGNWFYTPHHKLSLTASHQERLPSTQELYAHGKHVATNTTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	RSNNIELALGYEGDRWQYNIALYRNRFRGNYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
g149	RSNNIELALGYKGRWQYNLAAYRNRFRGNYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
	130	140	150	160	170	180
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGRELAYGNRPFFIAQDDQNAPRV					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDPYGKRPFIAQADQNAPRI					
	190	200	210	220	230	240
m149.pep	PAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW					
g149	PAARLGFHLKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	310	320	330	340		

420

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX  
310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq  
1 ATGTCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTTCG GTGTAGAACA  
51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC  
101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAACTAC  
151 TACAACCATC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC  
201 ATTCGCACTT TCGGGCAACT GGTATTTCAC GCCACAACAC AAACCTCAGCC  
251 TGACCGCCTC CCATCAGGAA CGCTGCCGT CAACGCAAGA GCTGTACGCA  
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT  
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG  
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC  
451 ATTTACGCCA AAACCTTAAA CGACGGACGC GGCCCAAT CCATCGAAGA  
501 CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGT GCGGACTTCT  
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC  
601 GCGGTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT  
651 ACCCGGCAGG GAAGACGCCT ACGCAACCG CCCACTCATT GCCCAAGCCG  
701 ACCAAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA  
751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT  
801 CGCCAAAAC AAACCTCGCC GCTACGAAAC GCGCACGCCG GGACACCATA  
851 TGCTCAACCT CGGCGCAAAC TACCGCGCA ATACGCGCTA TGGCGAGTGG  
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA  
951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACGGCG  
1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep  
1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY  
51 YNHPLPDLGA HRQTARFAL SGNWYFTPOH KLSLTASHQE RLPSTQELYA  
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY  
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI  
201 GVSGDYVRGR LKNLPSLPGR ZDAYGNRPLI AQADONAPRV PAARLGVHLK  
251 ASLTDRIAN LDYRVFAQN KLARYETRT PGHMLNLGAN YRRNTRYGEW  
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF\*

m149/a149 98.8% identity in 339 aa overlap

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYQYDKALIDRENYNHPLPDLGA					
a149	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYQYDKALIDRENYNHPLPDLGA					
	10	20	30	40	50	60
m149.pep	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	130	140	150	160	170	180
m149.pep	RSNNIELALCYEGDRWQYNLALYRNRFNGNYIAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
a149	RSNNIELALCYEGDRWQYNLALYRNRFNGNYIAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	190	200	210	220	230	240
m149.pep	ADFYGAEGEYIFKPTPRYRIGVSGDYVRGRRLKNLPSLPFGREDAYGNRPFIQADONAPRV					
a149	ADFYGAEGEYIFKPTPRYRIGVSGDYVRGRRLKNLPSLPFGREDAYGNRPFIQADONAPRV					
	250	260	270	280	290	300
m149.pep	PAARLGFHLKASLTDRIANLDYRVFAQNKLARYETRTPGHMLNLGANYYRRNTRYGEW					

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||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a149 PAARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW
      250      260      270      280      290      300

      310      320      330      340
m149.pep NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
      310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 601>:

g149-1.seq

```

1  ATGGCACAAA TCACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51  CACACCCCTC CTCGCCAAG CGCATGAAAC TGAGCAATCG GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCGAC TTCGGGGCTG
151 CTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACTTTGCG
201 CCAAAAGGCC GTCAACTTGG GCGACGCTTT GGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGGCATCCG CTCCTGTTAT TCGCGGTCAA
301 ACGGGCAGAC GGATTAAAGT ATTGAACCAT CACGGCGAAA CGGGCGATAT
351 GCGGGACTTT TCTCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTGCG
401 AACAGGTTGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGGAT GGA AAAATCC CCGAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGaagccgG ATTGCGTTTG AGCAGCGGCA
551 ATTTAGAAAA ACTGACATCC GCAGGCATCA ATATCGGACT GGGCAAAAAC
601 TTCGTGCTGC ATACCGAAGG CTTGTACCGC AAATCGGGCG ATTACGCCGT
651 ACCGGCTTAC CGCAATCTGA AACGCCTGCC CGACAGCCAT GCCGATTGCG
701 AAACGGGCGA CATCGGGCTG TCTTGGGTGG GCGAAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACCGTCG CGACCGCTAC GGCCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATCA
851 ACAAAACGCTA TTTGACGCTT TATCGCACT TGTGACCGCA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG GCGACGGTGC
951 ACACGCACAC ACCCACAACG GCAAAACCGTG GATAGACCTG CGCAACAAC
1001 GCTACGAAC TCGCGCCGAA TGGAGCAGC CATTCGCCG TTTTGAAGCC
1051 CTGCGCGTAC ATCTGAACCG CAATGACTAC CACCACGACG AAAAAGCAGG
1101 CGATGCAGTA GAAAATTCTT TCAACAACAA AACACACAAC GCCCGTATCG
1151 AGTTGCGCCA CCAACCCATA GGCGCTCTGA AAGCAGCTG GGGCGTGCAA
1201 TATTTGGGAC AAAAATCCAG CGCGCTTTCC GCCATTCCCG AAACCGTCCA
1251 ACAACCGATG TTGATTGACA ACAATGTCCG CCATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATTGGGAC AACTTCACGC TTGAAGGCGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT CCGGTACGAC AAAGCATTGA TTGATCGAGA
1401 AAACCTACTA AACACGCCCC TGCCCGACCT CGCGCGCGAC CGCCAAACCG
1451 CCCGCTCGTT CGCACTTTTC GGCACCTGGT ATTTACGCCC ACACCACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCGCTCAA CGCAAGAACT
1551 GTACGCACAC GGCAAGCAGC TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGCGGACC GCTGGCAATA CAATCTGGCA GCCTACCGCA ACCGATTCCG
1701 CAACTACATT TACGCCCAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGTGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGT GTTTCGGGCG ACTATGTACG AGGCGCTCTG AAAAACCTGC
1901 CGTCCCTACC CGGCAGGGAA GATCCCTACG GCAAACGTCC CTTTATCGCA
1951 CAAGCCGACC AAAACGCCCC CCGCATTCCG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAACC TCGCTAACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG TACGCCCGGA
2101 CACCATATGC TCAACCTCGG TGCAAACTAC CGCGCAATA CGCGCTATGG
2151 CGAGTGGAA TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCCCTC TCTGATACGC CGCAAAATGG CCGCAGCTTT
2251 ACCGCGGCG TAAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 602; ORF 149-1.ng>:

g149-1.pep

```

1  MAQITLKPIV LSILLINTPL LAQAHETEQS VGLTVSVVG KSRPRATSGL
51  LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDRAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSGEAGLRL SSGNLEKLT AGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFYI
251 AAYSDDRRDR GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNFGLSCG FHDGDGAHAH THNGKPWIDL RNKRYELRAE WKQFPFGFEA

```

```

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLAGH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFNGYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DPYKRPPIA
651 QADQNAPIRIP AARLGFHLKT SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.00q

```

1 ATGGCACAAA CTACACTCAA ACCCATTTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGG
101 AAACGGTCAG CGTCGTCCGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTTGG
201 CCACAAAAGCC GTCAACTTGG GCGACGCTTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GGCGGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCCG
401 AACAGGTCGA AATCCTGCGC GGGCCSGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCTGA TGTGCGCAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAA GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC GCCAATCTGA AACGCGTGCC CGACAGCCAC CGCGATTCCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTACGCTACA GCGACCGTCG CGACCAATAT GGTCTGCTCG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAACGCTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACCT CCGTGCCGAA TGGAAAGCAAC CGTTCCCGCG TTTTGAAGCC
1051 CTGGCGGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCACTC GAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTGCTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTATACAA AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTAA
1251 ACAACCGATG CTGCTTGACA ACAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAACCTGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTACT AACCAACCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCGGCTCATT CGCACTTTTC GGCAACTGGT ATTTACGACC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAACACG TCGCCACCAA CACCTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGGCG ACTATGTACG AGGCGCTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCCTAC GCAACCGTCC TTTTCATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTCCG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAAATTT GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACTAC CGCGCAATA CGCGCTATGG
2151 CGAGTGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAGC CAGCTTTCTC TCTGATACGC CGCAAAATGG CCGCAGCTTT
2251 ACCGGCGCGC TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pap

```

1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAINVDT ALSQQVEILR GPVTLTLYSSG
151 NVAGLVDVAD GKIPKMPEN GVSSELGLRL SSGNLEKLTG GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGERGFTG
251 VAYSDDRQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQPPPGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS AISEAVKOPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLAGH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

```

551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA  
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGREG DAYGNRPFIA  
651 QDDQNAPRVP AARLGFLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG  
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
751 TGGVNVKF\*

m149-1/g149-1 96.2% identity in 758 aa overlap

m149-1.pep	10	20	30	40	50	60
g149-1	10	20	30	40	50	60
m149-1.pep	70	80	90	100	110	120
g149-1	70	80	90	100	110	120
m149-1.pep	130	140	150	160	170	180
g149-1	130	140	150	160	170	180
m149-1.pep	190	200	210	220	230	240
g149-1	190	200	210	220	230	240
m149-1.pep	250	260	270	280	290	300
g149-1	250	260	270	280	290	300
m149-1.pep	310	320	330	340	350	360
g149-1	310	320	330	340	350	360
m149-1.pep	370	380	390	400	410	420
g149-1	370	380	390	400	410	420
m149-1.pep	430	440	450	460	470	480
g149-1	430	440	450	460	470	480
m149-1.pep	490	500	510	520	530	540
g149-1	490	500	510	520	530	540
m149-1.pep	550	560	570	580	590	600
g149-1	550	560	570	580	590	600
m149-1.pep	610	620	630	640	650	660
g149-1	610	620	630	640	650	660



	670	680	690	700	710	720
m149-1.pep	AARLGFHLKASLTDRIDANLDY	YRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN				
g149-1	AARLGFHLKASLTDRIDANLDY	YRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN				
	670	680	690	700	710	720
	730	740	750	759		
m149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

a149-1.seq

1	ATGGCACAAA	CTACACTCAA	ACCCATTGTT	TTATCAATTC	TTTAAATCAA
51	CACACCCCTC	CTCTCCCAAG	CGCATGGAAC	TGAGCAATCA	GTGGGCTTGG
101	AAACGGTCAG	CGTCGTCGGC	AAAAGCCGTC	CGCGCGCCAC	TTCCGGGCTG
151	CTGCACACTT	CTACCGCCTC	CGACAAAATC	ATCAGCGGCG	ACACCTTGCG
201	ACAAAAGCC	GTCAACTTGG	GTGATGCTTT	AGACGGCGTA	CCGGGCATTC
251	ATGCCTCGCA	ATACGGCGGC	GGCGCATCCG	CTCCCGTTAT	TCGGCGTCAA
301	ACAGGCAGAC	GGATTAAAGT	GTTGAACCAT	CACGGCGAAA	CGGGCGACAT
351	GGCGGACTTC	TCTCCAGACC	ATGCAATCAT	GGTGACAGC	GCCTTGTCGC
401	AACAGGTCGA	AATCCTGCGC	GGTCCGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGCTGGTCGA	TGTTGCCGAT	GGCAAAATCC	CCGAAAAAAT
501	GCCTGAAAC	GGCGTATCGG	GCGAACTCGG	ATTGCGTTTG	AGCAGCGGCA
551	ATCTGAAAA	ACTCAGCTCC	GGCGGCATCA	ATATCGGTTT	GGGCAAAAC
601	TTTGTATTGC	ACACGGAAGG	GCTGTACCGC	AAATCGGGGG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCCTGCC	CGACAGCCAC	CGCGATTTCG
701	AAACGGGAG	CATCGGGCTG	TCTTGGGTTG	GCGAAAAAGG	CTTTATCGGC
751	GCAGCATACA	GCGACCGTCG	CGACCAATAT	GGTCTGCCTG	CCCACAGCCA
801	CGAATACGAT	GATTGCCACG	CCGACATCAT	CTGGCAAAAG	AGTTTGATTA
851	ACAAACGCTA	TTTGCGAGTT	TATCCGCACC	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTGCGGC	TTTCACGACG	ACGATGATGC
951	ACACGCCCAT	CCCCACAACG	GCAAACCTTG	GATAGACCTG	CGCAACAAC
1001	GCTACGAAC	CCGCGCCGAA	TGGAGCAAC	CGTTCGCCGG	TTTTGAAGCC
1051	CTGCGCGTAC	ACCTGAACCG	CAACGACTAC	CGCCACGACG	AAAAAGCAGG
1101	CGATGCAGTA	GAAAACTTTT	TTAACAACCA	AACGCAAAAC	GCCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAG	AAAAATCCAG	TGCTTTATCT	GCCACATCCG	AAGCGGTCAA
1251	ACAACCGATG	CTGCTTGACA	ATAAAGTGCA	ACATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAACTGGGAC	AACTTCACGC	TTGAAGCGCG	CGTACGCGTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGCTACGAC	AAAGCATTGA	TTGATCGGGA
1401	AAACTACTAC	AACCATCCCC	TGCCCGACCT	CGGCGCGCAC	CGCCAAACCG
1451	CCCGCTCAAT	CGCACTTTCC	GGCAACTGGT	ATTTCACGCC	ACAACACAAA
1501	CTCAGCCTGA	CGGCCTCCCA	TCAGGAACGC	CTGCCGTCAA	CGCAAGAGCT
1551	GTACGCACAC	GGCAAACACG	TCGCCACCAA	CACCTTTGAA	GTCCGGCAACA
1601	AACACCTCAA	CAAGAGCGGT	TCCAACAATA	TGCAACTCGC	GCTGGGCTAC
1651	GAGGGCGACC	GCTGGCAATA	CAATCTGGCA	CTCTACCGCA	ACCGCTTCGG
1701	CAACTACATT	TACGCCCAAA	CCTTAAACGA	CGGACGCGGC	CCCAATCCCA
1751	TCGAAGACGA	CAGCGAAATG	AAGCTCGTGC	GCTACAACCA	ATCCGGTGCG
1801	GACTTCTACG	GCGCGGAAGG	CGAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCATCGGC	GTTTCCGGCG	ACTATGTACG	AGGCCGTCTG	AAAAACCTGC
1901	CTTCCCTACC	CGGCAGGGAA	GACGCCTACG	GCAACGCCCC	ACTCATTGCC
1951	CAAGCCGACC	AAAACGCCCC	TCGCGTTCCG	GCTGCGCGCC	TCGGCGTCCA
2001	CCTGAAAGCC	TCGCTGACCG	ACCGCATCGA	TGCCAATTTG	GACTACTACC
2051	GCGTGTTTCG	CCAAAACAAA	CTCGCCCGCT	ACGAAACCGC	CACGCCCGGA
2101	CACCATATGC	TCAACCTCGG	CGCAAATAC	CGCCGCAATA	CGCGCTATGG
2151	CGAGTGGAAT	TGGTACGTCA	AAGCCGACAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCACAG	CAGCTTCCTC	TCTGATACGC	CGCAATGGG	CCGCAGCTTT
2251	ACCGCGCGCG	TGAACGTGAA	GTTTTAA		

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

a149-1.pep

1	MAQTLKPIV	LSILLINTPL	LSQAHGTEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDGV	PGIHASQYGG	GASAPVIRGQ
101	TGRRIKVLNH	HGETGDMADF	SPDHAIMVDS	ALSQQVEILR	GPVTLLYSSG
151	NVAGLVVDAD	GKIEPKMPEN	GVSGELGLRL	SSGNLEKLTS	GGINIGLGKN
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSH	ADSQTGSIGL	SWVGEKFIG
251	AAYSDDRDQY	GLPAHSHEYD	DCHADIIWQK	SLINKRYLQL	YPHLLTEEDI
301	DYDNPGLSGC	FHDDDDAHAA	AHNKGPWIDL	RNKRYELRAE	WKQPPFGFEA

351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRKKGSGWVQ  
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVVRV  
451 EKQKASIRYD KALIDRENY NHELPLDLGAH RQTARSFALS GNWYFTPQHK  
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY  
551 EGDWRQYNLA LYRNRFGNYI YAGTLNDGRG PKSIEDDSEM KLVRYNQSGA  
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPLIA  
651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTEG  
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
751 TGGVNVKF\*

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGPVTLTYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGPVTLTYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSTGSGIGL					
m149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSTGSGIGL					
	190	200	210	220	230	240
	250	260	270	280	290	300
a149-1.pep	SWVGEKGFTGAAYSDRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
m149-1	SWVGEKGFTGAAYSDRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a149-1.pep	DYDNPGLSCGFHDDDDAHAAHNGKWPIDLRNKRYELRAEWKQPFPGFEALRVHLNRNDY					
m149-1	DYDNPGLSCGFHDDDDAHAAHNGKWPIDLRNKRYELRAEWKQPFPGFEALRVHLNRNDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRKKGSGWVQYLGQKSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRKKGSGWVQYLGQKSSALSATSEAVKQPM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVVRVEKQKASIRYDKALIDRENYNHPDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVVRVEKQKASIRYDKALIDRENYNHPDLGAH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

426

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a149-1.pep  DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRKLNLPSPGREDAYGNRPLIAQADQNAPRV
m149-1       DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRKLNLPSPGREDAYGNRPFIAQDDQNAPRV
              610      620      630      640      650      660

a149-1.pep  AARLGVLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
m149-1       AARLGVLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              670      680      690      700      710      720

a149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
m149-1       WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              730      740      750

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

```

g150.seq (partial)
1  ..TACTGCAAGG CAGACCCCTT TCCGCGCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGTA
101 GCGGTTCCGA TTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCTGCGG GTTGCCTCCG
251 CACTGTTATC CCATTTTCGAA CTCACGCAAA ACACCCCGC CTTTGTCAAA
301 GGTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAAATCGC CGGCCTGTG
451 CGCCCGCTTG CGCCGCGCCT GTATTGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCGTTTC GAACACGAAG
551 GCGCGCCAG GCGGGCGGCG GCATCGGTT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGTGCGCCT GTTTGCCGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTGG CAATGGCTGC AGGAAGCGCG
951 GCATATCTAT GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCGG GGCATTGCGA CGAAGACGGC
1051 GCAGAAGGAT ATTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

```

g150.pep (partial)
1  ..YKADPFPA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAGGKTL P VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQQRAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDF L HRYDFAWSR DQEEKIYVQD
301 KIREQAEGWL QWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

```

m150.seq
1  ATGCAGAA CAATCCGCC ATTACCGCCT CTGCGGCCCG AAATCAGCA
51  GCTCTGTGCG GGGCTGGACG CGGCACAATG GCGGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGCAGA ACCTTTTCC GTAACCGTCC TTCCGCCTC
201 GCAAACCGCG AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCGGCGCG CATCCAAGTC AGTCGCGCGG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGCGGAACG CCGCCTGCTG CTGGTTACCT CCACCAAGG
351 CGAAGGCGAA CCGCGGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAAACTCC AATTGCGCT ACTGGGTTG

```

m150.pgp

1	1	MQNTNPPLPP	LPPEITQLLS	GLDAAQWAWL	SGYAWAKAGN	GASAGLPAQO
51		TALPAAEPFS	VTVLSASQTG	NAKSVDKAA	DSLEAAGIOV	SRAELKDYKA
101		KNIAGERLLL	LVTSTQGEGE	PPKEAVVLHK	LLNGKKAPKL	DKLQFAVLGL
151		GDSSYPNFCQ	AGKDFDRRFE	ELGAKRLLER	VDADLFTFAS	ANAWTDNIAA
201		LLKEEAANKR	ATPAPQTTPP	AGLQATPDGR	YCKAAFFPAA	LLANQKIDAT
251		QSDKDVRIIE	LTDSGSDLHY	LPGLDALGVWF	DNDPALVREI	LDLLGLDIPAT
301		EIQAGGKMMP	VARALSSHFE	LTQNTPAFVK	GYAAFAHYEE	LDKIIDNAV
351		LQDFVQNTPI	VDVLHRFPAS	LTAEQFIRLL	RPLAPRLYSI	SSAQAEVGDE
401		VHLTVGVVRF	EHEGRARTGG	ASGFLADRLE	EDGTVRVFVE	RNDGFRLEPED
451		SRKPIVMIGS	GTGVAPFFRA	VQQRAAENAE	GKNWLI FGNP	HFARDFLYQT
501		EWQFAKDFG	LHYDFAWSR	DQEEKIYVQD	KIREQAEDGLW	QWLQEGAHYI
551		VCDDAAKMAK	DEAAALLDVI	I GAGHLDEEG	AEEYLDMLRE	EKKRYORDVY*

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

	210	220	230	240	250	260
m150.pep	LLKEEAAKNRATPAQTTPPAGLQ	TAPDGRGYCKA	AFPFAALLANQKITARQSDKDVRIE			
g150			YCKADFPFAALLANQKITARQSDKDVRIE			
			10	20	30	
	270	280	290	300	310	320
m150.pep	IDLSGSDLHYLPGDALGVWFNDNPALVREILDLLGIDPATEIQAGGKMMPVARALSSHFE					
	:					
g150	IDLSGSDLHYLPGDALGVWFNDNPALVGEILDLLGINPATEIQAGGKTLPVASALLSHFE					
	40	50	60	70	80	90
	330	340	350	360	370	380
m150.pep	LTQNTPAFVKGYAAFAHAYEELDKIIADNAVLODFVONTPIVDVLHRFPASLTAEOFIRL					



1701 GGATGTGATT ATCGGGGCAG GACATTTCGA CGAAGAGGCC GCAGAAGAAT  
1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTATTATGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep  
1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ  
51 TALPTAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA  
101 KNIAGERRLL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL  
151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA  
201 LLKEEAAKNR ATPAPQTTPP AGLQTAPDGR YCKADPFPA LLANQKITAR  
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDQAT  
301 EIQAGGKTLP VASALLSHFE LTQNTPAFVK GYAPFADDDE LDRIAADNAV  
351 LQGFVQSTPI ADVLHRRPAK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE  
401 VHLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED  
451 SRKPIVMIGS GTGVAPFRAF VQORAAENAE GKNWLFNGNP HFARDFLYQT  
501 EWQQFAKDF LHRDYFAWSR DQEEKIYVQD KIREQAEGW QWLQEGAHY  
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG ABEYLDMLRE EKRYQRDVY\*

m150/a150 94.8% identity in 599 aa overlap

m150.pep	10	20	30	40	50	60
	MQNTNPPLPPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPAEPFS	NAKSVADKAA	DSLEAAGIQV	SRAELKDYKA	
a150	10	20	30	40	50	60
	MQNTNPPLPPMPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPAEPFS	NAKSVADKAA	DSLEAAGIQV	SRAELKDYKA	
m150.pep	70	80	90	100	110	120
	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	LVTSTQGEGE				
a150	70	80	90	100	110	120
	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	LVTSTQGEGE				
m150.pep	130	140	150	160	170	180
	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRFEEL	GAKRLLER				
a150	130	140	150	160	170	180
	PPEEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCRAGKDFDKRFEEL	GAKRLLER				
m150.pep	190	200	210	220	230	240
	VDADLDFTASANAWTDNIAALLKEEAAKNRATPAPQTTPPAGLQTAPDGR	YCKADPFPA				
a150	190	200	210	220	230	240
	VDADLDFAAADGWTDNIAALLKEEAAKNRATPAPQTTPPAGLQTAPDGR	YCKADPFPA				
m150.pep	250	260	270	280	290	300
	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LDLLGIDPAT				
a150	250	260	270	280	290	300
	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LDLLGIDQAT				
m150.pep	310	320	330	340	350	360
	EIQAGGKMPVARLSSHFELTQNTPAFVKGYAAFAHYEELDKIIADNAV	LQGFVQNTPI				
a150	310	320	330	340	350	360
	EIQAGGKTLPVASALLSHFELTQNTPAFVKGYAPFADDDELDRIAADNAV	LQGFVQSTPI				
m150.pep	370	380	390	400	410	420
	VDVLHRRFPASLTAEQFIRLLRPLAPRLYSISSQAEVGDEVHDTVGVVRF	EHEGRARTGG				
a150	370	380	390	400	410	420
	ADVLHRRFPASLTAEQFIRLLRPLAPRLYSISSQAEVGDEVHDTVGVVRF	EHEGRARAGG				
m150.pep	430	440	450	460	470	480
	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVAPFRAF	VQORAAENAE				
a150	430	440	450	460	470	480
	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVAPFRAF	VQORAAENAE				
m150.pep	490	500	510	520	530	540
	GKNWLIFGNPHFARDFLYQTEWQQFAKDFLHRDYFAWSRDQEEKIYVQD	KIREQAEGW				

g151.seq

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.ppe

1	MKQIRNIAII	AHVDHGKTTL	VDQLLRQSGT	FRANQQVDER	VMSDNDLEKE
51	RGITILAKNT	AIDYEGCHIN	IVDTPGHADF	GGEVERVLGM	VDCVVLLVDA
101	QEGPMPQTRF	VTKKALALGL	KPIVVINKID	KPSARPSWVI	DQTFELFDNL
151	GATDEQLDFP	IVYASGLSGF	AKLEETDESS	DMRPLFDITL	KYTPAPSGSA
201	DEPLQLQISO	LDYDNYTGRl	GIGRILNGRI	KPGQTVAVMN	HEQIOAQORI
251	NQLLGFKGLE	RVPLEEAEAG	<u>DIVIISGIED</u>	IGIGVTITDK	DNPKGLPMLS
301	VDEPTLTMDF	MVNTSPLAGT	EGKFVTSRQI	RDRLQKELLT	NVALRVBDTA
351	DADVFRVSGR	GELHLTILLE	NMRREGYELA	VGKPRVVYRD	IDGQKCBPYE
401	NLTVDVPPDN	QGAAMEELGR	RRGELTNMEL	DGNRGTRLEY	HIPARGKLI
451	QGEFMTLTRG	VGLMSHVDD	YAPVKPDMPG	RHNGVLVSQE	OGEAVAYALW

501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD  
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMRYL SELERRRHFK  
 601 KLD\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
51  AACACATTG GTCGACCAAC TGCTGCGCCA ATCOGGCACA TTCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAATCGAC AAGCCGTCCG
401 CTCGTCCGAG CTGGGTATC GACCAAACTT TCGAGCTGTT CGACAATTG
451 GGCGCGACCG ACGAGCAGT GGATTTCCCG ATGTGTTACG CTCAGGGTT
501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACGAG CGCGAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCCCT GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTGGA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGCG GACATCGTGA TTATTCCGG TATCGAAGAC ATCGGTATCG
851 CCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
951 GGCGGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TGCGCGTGA AGATACCGCC
1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCCGC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGCGGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTGCTGGT GTCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA
1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAAA
1801 AAGCTGGATT GA

```

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFDL YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
g151	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVVLVDAQEGPMPQTRFVTKKALALGL					
g151	70	80	90	100	110	120
	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVVLVDAQEGPMPQTRFVTKKALALGL					
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFEFLDNLGATDEQLDFFIVYASGLSGFAKLEETDESN					
g151	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFEFLDNLGATDEQLDFFIVYASGLSGFAKLEETDESS					
m151.pep	190	200	210	220	230	240
	DMRPLFDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRIILNGRIKPGQTVAVMN					
g151	190	200	210	220	230	240
	DMRPLFDTILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRIILNGRIKPGQTVAVMN					
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPGLPMLS					
g151	250	260	270	280	290	300
	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPGLPMLS					
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
g151	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
m151.pep	430	440	450	460	470	480
	RRGELTNMESDNGRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	430	440	450	460	470	480
	RRGELTNMESDNGRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK					
g151	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK					
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					

433

m151.pep      KLDX  
 ||||  
 g151          KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq  
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA  
 51 AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA  
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA  
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA  
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGGCGAAG  
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGT GGTGGACGCG  
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGGC  
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAATCGAC AAACCGTCCG  
 401 CCCGTCGAG CTGGGTCATC GACCAAACTT TCGAGCTGTT CGACAACCTG  
 451 GCGCGGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT  
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC  
 551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG  
 601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTCGACTACG ACAACTACAC  
 651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC  
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCTC  
 751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC  
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATGAAGAC ATCGGCATCG  
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCTGCC GATGTTGAGC  
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT  
 951 GGCAGGTACG GAAGGCAAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC  
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGCTGGA AGTACCGCC  
 1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GCGGAGCTGC ACCTGACCAT  
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGCGAAAC  
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA  
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA  
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG  
 1301 GACGACCCG CCTCGAATAC CATATCCAG CGCGCGGCTT GATCGGCTTC  
 1351 CAAGGCGAAT TTATGACCTT GACGCGCGGG GTCGGGCTGA TGAGCCACGT  
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG  
 1451 GCGTGCTGGT GTCCCAAGAG CAGGCGGAGG CAGTCGCTTA CGCCTTGTGG  
 1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA  
 1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA  
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC  
 1651 GAAGCCGTTT GCCTGACCAC GCCGATTAG CTGACGCTGG AAGGTGCGGT  
 1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCAGCCG CAATCCATCC  
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCGC CCATTTCAAA  
 1801 AAGCTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep  
 1 MKQIRNIAII AHVDHGKTTI VDQLLRSGT FRANCOVDER VMDSNDLEKE  
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA  
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL  
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYT?APSGSA  
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQIAQGRI  
 251 NQLLGFKGLE RVPLEAEAG DIVIISGIED IGIGVTITDK DNPKGPLMLS  
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLCHELLT NVALRVEDTA  
 351 DADVFRVSGR GELHLLILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE  
 401 NLTVDVPPDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF  
 451 QGEFMTLTRG VGLMSHVFDY YAPVKPDMPG RHNGVLVSQE QGEAVAYALW  
 501 NLEDGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD  
 551 EAVRLTTPIK LTLEGAVEFI DDDELVEITP QSIRLRKRYL SELERRRHFK  
 601 KLD\*

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

m151.pep	NKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151	NKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
a151	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
a151	KPIVVINKIDKPSARPSWVIDCTFELFDNLGATDEQLDFFIVYASGLSGFAKLEETDES
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
a151	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
a151	HDQQIAQGRINQLLGFEGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
a151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLQKELLTNVALRVEDTADADVFRVSGR
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
a151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
a151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
a151	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMI-GIHSRDNDLVVNPLKGKK
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
a151	LTNIRASGTDEAVRLTPIKLTLEGAVEFIDDELVEITPOSIRLRKRYLSELERRRHFK
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAaaca aaACCaaagt ctgGGacttc cCaccgcc ttTTCactG
51  GctgcttgCC gCATCCetgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGGCTCG GGCTGCTCGT CCTTTTCCTG

```

g152.pep

```

1  MKNKTKVWDF  PTRLFHWLLA  ASLPFMWYSA  KAGGDMLOWH  TRVGLLVFL
51  LVFRLCWGIW  GSDTARFSRF  VRGWAGIRGY  LKNGI PEHIQ  PGHNPLGALM
101 VVALAAAVSF QVGTGLFAAN ENTFTSTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVSAVH IAAVAYRIF KKKNLVLRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

m152.seq

1	ATGAAAAACA	AAACCAAAGT	CTGGGACCTC	CCCACCCGCC	TTTTCCACTG
51	GCTGCTTGCC	GC GTCCCTGC	CCTTTATGTG	GTATAGCGCG	AAAGCCCGCG
101	GC GATATGCT	GCAATGGCAG	AGCGCGCTCG	GGCTGTTCGT	CCTTTTCTGT
151	CTCGATTTTC	GCCTCTGCTG	GGCGATTTGG	GGCAGCGATA	CGCCCGCTTT
201	TTCCCGTTTC	GTCCAAGGCT	GGG CAGGCAT	ACGCGGCTAT	CTGAAAAACG
251	GTATTTCCCGA	ACACATCCAG	CCCGACACA	ACCCTTGGG	CGCACTGATG
301	GTCTGTGCGC	TTTTTGCCCG	CGTGTCTCTT	CAAGTACGCA	CCGGGCTTTT
351	TGCCCGCGAT	GA AAACACCT	CTAGCACCAA	CGGTCCGCTC	AACCAATTGG
401	TTCCCGAACA	TACGGCGAGC	CTTATGCGGA	AAATCCACCT	CAACTTTTTC
451	AAGCTGCTCG	CCGTTTTTTTC	TGCAATCCAC	ATCGCCGCCG	TCGCCGCATA
501	CCGCGTATTC	AAAAAGAAAA	ACCTCATCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCAGGCAA	AGCCGCGCTT
601	GCCCGCCGAT	TATCGGTTGC	CTCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCTCGA				

m152.ppt

```

1  MKNKTKVWDL PTRLFWLLA ASLPFMWYSA KAGGDMLOWH TRVGLFVLFL
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVFS QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHNLFF
151 KKLAVFSIAH IAAVAAAYRV KKKNLILPMI TGPKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAIILL*

```

Homology with a predicted ORF from *N.gonorrhoeae*

m152/g152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPT	RLFWHLLAASLP	FMWYSAKAGGDM	LQWHTRVGLFVL	FLLVFRLCWGIW	
g152	MKNKTKVWDFPT	RLFWHLLAASLP	FMWYSAKAGGDM	LQWHTRVGLLVL	FLLVFRLCWGIW	
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GS	TARFSRFVQGW	AGIRGYLKNGI	PEHIQPGHNPL	GALMVVALLAAV	SFQVGTGLFAAD
g152	GS	TARFSRFVRGW	AGIRGYLKNGI	PEHIQPGHNPL	GALMVVALLAAV	SFQVGTGLFAAN
	70	80	90	100	110	120

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	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AIHIAA VAAAYRVFKKKNLILPMI					
	:     :     :     :     :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFS AVHIAA VAAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	:			
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
1  ATGAAAAACA AAACCAAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151 CTCGTATTCC GCCTCTGCTG GGCATTTCG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCGGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCTCGA ACACGTCCAA CCGGACACA ACCCCTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCGCG CGTGTCTTTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCGGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTTCG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451 AACTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAAGAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGCAA AGCCGCGCTT
601 GCCGCCGAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFLEFL
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAYSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFS AVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAIILLS*
  
```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	:     :     :     :     :					
a152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKTGGDMLQWHTRVGLFLEFLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAYSFQVGTGLFAAD					
	:     :     :     :     :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAYSFQVGTGLFAAD					
	70	80	90	100	110	120

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AIHIAA VAAAYRVFKKKNLILPMI					
	:     :     :     :     :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AVHIAA VAAAYRVFKKKNLVLPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	:			
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

g153.seq  
 1 atgggggtttg cttacAgat gacgtatatc gaggtCGGga taccggaggc  
 51 ggcatccgtc ctttCgctGC CCGAGATgat ggcctgatG GTGTTtCagg  
 101 attATGGTTT TttggcCGAA GTGATGTTTG TGctgaCTTT cGGCGcgcCG  
 151 GTTCTGTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA  
 201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA  
 251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTCT GGTGGCGTAT  
 301 ATCAAGCTCT CGTCTGTGGC AAAGGTTGCG TTCGGGCGG CGTTTTATCT  
 351 GATGTTCCGC CTGTCGGTTA TGCTGATTGG GACTTCGGTA TCGGTTCCCC  
 401 AGCATTGGGT GTATTTCCAA ATCGGGCGGC TGACGGGGAA TAATGCGGTT  
 451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTTccg  
 501 cgacAGTgcc gaatcccCCT GCGGGGTGTg cgCGCgggaA CTgtacggcg  
 551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCTgac ggcggcggTT  
 601 GTTTTGATT TCCctgCcaa TATCctgccc attaTGAttt cgtccaATCc  
 651 tgcggccacg GAGGcCAACA CCATCTTTAG CCGCATCGCT TATATGTGGG  
 701 ACCagggcga CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG  
 751 GTGCCGCTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CCGCGGCACG  
 801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA  
 851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT  
 901 TTGATGTGTT CGTTCcAcac TTATGCCGCG CCGGTCATTc CCGGCAGTGC  
 951 GGCAGTCTAT TTCTGCCTGG TCGTGATTtT GACGATGCTG TCCGCCTATT  
 1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CCGCATTGCT  
 1051 TTCAACGAAA CGGAAAATA TGACTGA

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

g153.pep  
 1 MGPAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMEVLTFGAP  
 51 VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY  
 101 IKLSSVAKVR FGPAFYLMFA LSVNLIRTSV SVPQHVVYFQ IGRLTGNNAV  
 151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYGGRPKSLs ISSAFLTAAY  
 201 VLVFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL  
 251 VPVLKIAAMS VLIAARFAL PAGAKKLSHL YRITEAVGRW SMIDIFVII  
 301 LMCSFHTYAA RVIPGSAAYV FCLVILITML SAYYFDPRL L WDKRASDGIA  
 351 FNETBKDY\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

m153.seq  
 1 ATGGCGTTTG CTTACGGTAT GACGTATAIC GAGGTCGGGA TACCGGGTGC  
 51 GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG  
 101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG  
 151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA  
 201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA  
 251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT  
 301 ATCAAGCTCT CGTCTGTGGC AGAGGTTGCG TTCGGGCGCG CGTTTTATCT  
 351 GATGTTCCGC CTGTCAGTTA TGCTGATTGG GACTTCGGTA TCGGTTCCCC  
 401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT  
 451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG  
 501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CCGTGCGGAA CTGTACCGCC  
 551 GACGCGCGAA AAGTCTGAGT ATTTGCTCGG CGTTTCTGAC GCGCGCGGTT  
 601 ATTTTGATT TCCCTGCCAA TATCCTGCCG ATTATGATT CTGCCAATCC  
 651 TGCCGCGACG GAGGTCAATA CCAFCCTTAA CCGCATCGCT TATATGTGGG  
 701 ACAGAGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG  
 751 GTGCCGCTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG  
 801 CTTCGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA  
 851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT  
 901 TTGATGTGTT CGTTCACAC TTATGCCGCG CCGGTCATTc CCGGCAGTGC  
 951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT  
 1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CCGCATTGCT  
 1051 TTCAATGAAA CGGAAAACA TGACTGA

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

m153.pep  
 1 MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMEVLTFGAP  
 51 VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY

101 IKLSSVAEVR FGPAPYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNAV  
 151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL ISSAFLTAAV  
 201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL  
 251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII  
 301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL LWDKRASDGIA  
 351 FNTEKHDX

m153 / g153 96.1% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFPQDYGFLAEVVFVLTFGAPVLFLLCLYV					
g153	MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFPQDYGFLAEVVFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMVDVFFVSTLVAYIKLSSVAEVRFGPAPYLMFA					
g153	YAALIRKQAYPALRLATRVMLRQAMVDVFFVSTLVAYIKLSSVAKVRFGPAPYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVFPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
g153	LSVMLIRTSVSVFPQHWVYFQIGRLTGNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
g153	LYGGRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
g153	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKLSHLRYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNTEKHDX					
g153	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNTEKYDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

a153.seq

1 ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC  
 51 GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG  
 101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACCTT CGGCGCGCCG  
 151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA  
 201 ACAGGCGTAT CCTGCGCTGC GTTGGCAAC GCGTGTGATG GTGCGCTTGA  
 251 GACAGGCGAT GATGCTGGAT GTGTTTTTGG TTTCCACTTT GGTGGCGTAT  
 301 ATCAAGCTCT CGTCTGTGGC AGAGGTTCCG TTCGGATCGG CGTTTTATCT  
 351 GATGTTCCGG CTGTCGGTTA TGCTGATTCG GACTTCGGTA TCGGTTCCCG  
 401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT  
 451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCGCTGCC TGTATTCCG  
 501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CCGTGCGGAA CTGTACCGCC  
 551 GACGGCCGAA AAGTCTGAGT ATTTCGTCGG CGTTTCTGAC GCGGCGGTT  
 601 ATTTTGTATT TCCTGCCAA TATCCTGCCG ATTATGATT CGTCCAATCC  
 651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG  
 701 ACGAGGGCGA CAGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG  
 751 GTCCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG  
 801 CTTCGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA

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851  CCGAAGCGGT  CGGCCGCTGG  TCGATGATTG  ATATTTTGT  GATTATTATT
901  TTGATGTGTT  CGTTCACAC  TTATGCCGCG  CGCGTCATTC  CGGSCAGTGC
951  GGCAGTCTAT  TTCTGCCTGG  TCGTGATTCT  GACGATGCTG  TCCGCCTATT
1001 ATTCGACCC  GCGCTGCTT  TGGGACAAAC  GCGCTTCAGA  CGGCATTGCT
1051 TTCAATGAAA  CGGAAAAACA  TGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI  EVGIPGAASV  LSLPEMMRLM  VFQDYGFLAE  VMFVLTFGAP
51  VLFLLCLYV  YAALIRKQAY  PALRLATRV  VRLRQAMMVD  VFFVSTLVAY
101  IKLSSVAEVR  FGSAYFLMFA  LSVMLIRTSV  SVPQHWVYFQ  IGRLTGDNV
151  QTASEGKTCC  SRCLYFRDSA  ESPCGVCGAE  LYRRRPKSL  ISSAFLTA
201  ILYFPANILP  IMISSNPAAT  EVNTILNGIA  YMWDEGDR  AAVIFSASIL
251  VPVLKIAAMS  VLIASARFAL  PTGAKKLSH  YRITEAVGRW  SMIDIFVIII
301  LMCSFHTYAA  RVIPGSAAVY  FCLVVILTML  SAYYFDPRL  WDKRASDGI
351  FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLYRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
a153	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA  ACAGCCCTCC  TCCAAACGGA  CACGCTCAAG  CACGCGTCCG
51  CAAAAACAAC  accttctct  CCGCCGTCTG  GCTGGTCCCG  CTGATCGCGC
101  TGATTGCCGG  CGGCTGGCTT  TGGGTTAAGG  AAATCCGCAA  CAGGGGGCCT
151  GTGGTTACGC  TCTTGATGGA  CAGCGCGGAA  GGCATCGAAG  TCAACAATAC
201  GGTCATTAAG  GTATTGAGCA  TCGATGTCGG  ACGCGTTACC  CGAATCAAAC
251  TGCGCGACGA  CCAAAAAGGC  GTGGAAGTTA  CTGCCCAACT  CAATGCGGAC
301  GTATCCGGCC  TCATCCGCAG  CGATACCCAG  TTTTGGGTGG  TCAAGCCGCG
351  TATCGACCAA  AGCGGcgtAA  CCGGTTTGGG  TACGCTGCTT  TCGGGTTCGT

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTATC TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCCACAG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCCGGCG CGATTTTATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCT GTcgaATACA AAGGGCTgaA
951 TGTcggCATG GTTTCGGATG TCCCTTATTT TGACCGCAAt gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagcctTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAACAACAA
1101 ATTCCAGACG GCCTTAAACA AAGGCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGCG GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGTCTGCTCG CGAACTCAA GTCCGCATC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACCTG AAGAGTTGC GCATAACCTT CCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAAAgacg TtcaACCGT CATTAACACT TTGAaAGAAa
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAGAccc tATCCCGAAa
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pep
1  MTDNSPPPNNG HAQARVRKNN TFLSAVVLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAB GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTPG KSGEAKDVFO
151 VQDIPPVTAI GQSGRLRLNI GKNDRIILNVN SPVLYENFMV QGIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGGK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVAEIN
451 GSLAEELKSA KSANAALSSI DKLVGNPQTQ NIPNELNQLT KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSKDPPIPK
551 GSR*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

m154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CAGGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTATCAAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTGG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTATC TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCCACAG CAGCGGCATC AAACCTCAATT CCGCCCTCT CTGCTGCCCTG
751 CTGTCCGGCG CGATTTTATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGACG TCCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAACAACAA
1101 ATTTCCAGACG GCCTTAAACA AAGGCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTCCGCA

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1201 TCACCTAAGC TGGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGCG
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCCAAT CGCCTATCTA CGCGCACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAAC TTAAGACG TTCAACCGT GATTAATACT TTGAAAGAAA
1601 AACCCACGC GCTGATTTT AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

m154.pep

```

1 MTDNSPPPNHQAQVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51 VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ
151 VQDIPPVTAI GQSGRLRLNI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETGSGI KLSAPLPLAL
251 LSGAISFDSF KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAEIN
451 GSLABLKSTL KSANAALSSI DKLVGKPTQ NIPNBLNQL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNHQAQVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	MTDNSPPPNHQAQVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
m154.pep	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
m154.pep	130	140	150	160	170	180
	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI GQSGRLRLNI GKNDRIILNVN					
g154	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI GQSGRLRLNI GKNDRIILNVN					
m154.pep	190	200	210	220	230	240
	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETGSGI					
g154	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETGSGI					
m154.pep	250	260	270	280	290	300
	KLSAPLPLAL LSGAISFDSF KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ					
g154	KLSAPLPLAL LSGAISFDSF KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ					
m154.pep	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
m154.pep	370	380	390	400	410	420
	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					

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	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDLQVKLADLLDKFDKLPLOKTVAEIENGSLAELKSTLKSANAALSSIDKLVGKPKQTQ					
g154	GGLDDLQVKLADLLDKFNNLPLOKTVAEIENGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
g154	NSSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154 . seq
1   ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCT GGAAGCGGCG ATCAATATCG
701 AAACCAACAG CAGCGGCATC AAATCAATT CCGCCCCTCT CCCTGCCCTG
751 CTGTCCGGCG CGATTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCCGATG TTCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCGCTT CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CCGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTAAAAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCACACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1   MTDNSPPNG HAQARVRKNN TFLSAVWLV LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVEQ

```

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151 VQDIPPVTAI GQSGRLRLNLI GKNDRLNVN SPVLYENFMV GQVESAHFDP  
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL  
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ  
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS  
351 RLEINAEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA  
401 SPKLRPHTVY AGDTVATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN  
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT KEKRLTLQGV  
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK  
551 GSR\*

## m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPN	GHAQARVR	KNNFTLSA	VWLVLPLI	ALIAAGGW	LWVKEIRN
a154	MTDNSPPPN	GHAQARVR	KNNFTLSA	VWLVLPLI	ALIAAGGW	LWVKEIRN
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVI	KVLSIDVG	RVTRIKLR	DDQKGVET	QAQLNADV	SGLIRSDT
a154	GIEVNNTVI	KVLSIDVG	RVTRIKLR	DDQKGVET	QAQLNADV	SGLIRSDT
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGT	LLSGSYIA	FTPGKSDE	AKDVQVQD	IIPPVTAI	GQSGRLRL
a154	SGVTGLGT	LLSGSYIA	FTPGKSDE	AKDVQVQD	IIPPVTAI	GQSGRLRL
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFM	VGQVESAH	FDPSDQSV	HYTIFIQSP	NDKLIHSA	SASRFWLE
a154	SPVLYENFM	VGQVESAH	FDPSDQSV	HYTIFIQSP	NDKLIHSA	SASRFWLE
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLP	PALLSGAI	SFDSPKTK	NSKNVKS	EDSFTLYD	SRSEVANL
a154	KLNSAPLP	PALLSGAI	SFDSPKTK	NSKNVKS	EDSFTLYD	SRSEVANL
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVG	SPVEYKGL	NVGVVSDV	PYFDRNDS	LHLFENGW	IPVRIRIE
a154	SVRGLTVG	SPVEYKGL	NVGVVSDV	PYFDRNDS	LHLFENGW	IPVRIRIE
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQQF	QTALNKGL	TATISSNN	LLTGSKMIE	LNDQPSAS	PKLRPHTV
a154	KEHWKQQF	QTALNKGL	TATISSNN	LLTGSKMIE	LNDQPSAS	PKLRPHTV
	370	380	390	400	410	420
m154.pep	430	440	450	460	470	480
	GGLDDLQV	KLADLLDK	FDKLPLDK	TVAELNGS	LAEKSTLK	SANAALSS
a154	GGLDDLQV	KLADLLDK	FDKLPLDK	TVAELNGS	LAEKSTLK	SANAALSS
	430	440	450	460	470	480
m154.pep	490	500	510	520	530	540
	NIPNELNQ	TLKELRTL	QGVSPQSP	PIYGDVQN	TLQSLDKT	LKDVQPV
a154	NIPNELNQ	TLKELRTL	QGVSPQSP	PIYGDVQN	TLQSLDKT	LKDVQPV
	490	500	510	520	530	540

444

```

                    550
m154.pep      NSSSKDPIPKGSRX
               |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1   atGAAaatcg GtataCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTtggaCGA TGCCCGTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGC GCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCTCGC ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGCGGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTATATCG CGCGAAATG AAGCTCTTTG CGAACACGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCAAGCT
801 GATTACCAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGGcgacg gcgaaATCAC
1101 CTTCCCGCCT CCGcgaTtc aggtTTCcg cgggcccGAG CAAAcgcgct
1151 ctgaAAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tgttCCctg
1201 tggAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgetgtgGgt
1251 cggCgcggtc gcacccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGTAC CATGTCTGTT GgaacgTCAG CCACTCGCTG
1351 TCACACCCG TGatgtcggt aaccaaCgcc atctccGGCA tcatgtcggt
1401 cggCGCGCTG CTGCAAAATCG GTCAGGGcaa cgggttcggt TCgctGCTGT
1451 CGTTTGTTC CATCCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1   MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTI V SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFA
151 RFFTQGITAA GKVPQAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFLQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKpAPKLITK EMVESMKSGS VIVDLAATGG NCELTRPGE
301 SVTGNVVKII GYTDMANRLA QSSQLYATN LVNLTKLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLM SVTNA ISGIMVVGAL LQIQGNGFV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMFK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1   ATGAAAATCG GTATCCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCG GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGTGCAGGT TTGGCGGCAA GTTGGACGA TGCCCGTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAACTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

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445

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301 TTGGTCGAAG CTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCGGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGAGG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCATTCGG GGCAAACCCG CGCCCAAGCT
801 GATTACCAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGCAGCGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCGCTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCTT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTAAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGAAAAA AACTCGCGCC CGCCGTCATC GCCCGCTCT TGGTACTGTG
1251 GGTGCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCTG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGGCA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAAG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLFAEQAQEV
251 DIIITTAAP GKPAKLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YVYVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
          10      20      30      40      50      60
m155.pep  MKIGIPRESLSGETRVACTPATVALLGKLGFFETVVESGAGLAASLDDAAYQTAGATVADK
          |||||||
g155       MKIGIPRESLSGETRVACTPATVALLGKLGFFETVVESGAGLAASLDDAAYQTAGATVADK
          10      20      30      40      50      60

          70      80      90     100     110     120
m155.pep  AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
          |||:|||||
g155       AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
          70      80      90     100     110     120

          130     140     150     160     170     180
m155.pep  ISRAQALDALSSMANISGYRAVIEAANAAGFRFFTGQITAAGKVPVPAQVLVIGAGVAGLAA
          |||||||
g155       ISRAQALDALSSMANISGYRAVIEAANAAGFRFFTGQITAAGKVPVPAQVLVIGAGVAGLAA

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	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFAEQAKEVDIIITTAAPGKPAKPLITKEMVESNKSQSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAAPGKPAKPLITKEMVESNKSQSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYIDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYIDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPPIQVSAQPPQTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVVGA					
g155	VTRDGEITFPPPIQVSAQPPQTPSEKAAAPAKPEPKPVPLWKKLAPAAIAAVLVLVVGA					
	360	370	380	390	400	410
	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAAATCG GTATCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGCATACCC
201 TTTAATTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCGC ATTTGCGCGC GCGAGGCTTT GGACGNTTGT TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGCG
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCGTGAAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGGCGAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCAA ACAGGGCGAA
901 TTGTTTCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGACAGT CTTCCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTAAAGC CCGAACAAAG ACGGCGAAAT CAGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCAAGC CCGAACCGAA ACCCGTTCCT

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1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGGCGCGC GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTCGCTGC
1451 TGTCGTTTGT TGCCATCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAAP GKPAKXXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKVPV
401 LWKKLAPAXI AAVLVLWVGA VAPAAFLNHF IVFVLACVIG YYVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQNGF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

	10	20	30	40	50	60
m155.pep	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m155.pep	AAVWVCPLIYKVNAPSEDELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPR					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m155.pep	ISRAQALDALSSMANISGYRAVIEAANAFAFRFTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFAFRXFTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLF AEQAKEVDIIITTAAPGKPAKPLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLF AEQAKEVDIIITTAAPGKPAKXXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPIQVSAQPQQTPEKAVPAKPEPKVPVPLWKKLAPAVIAAVLVLWVGA					
a155	VTRDGEITFPPIQVSAQPQQTPEKAAPAAKPEPKVPVPLWKKLAPAXIAAVLVLWVGA					
	370	380	390	400	410	420





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g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCGCGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCAGCCGC
201 CGTTTTCGCG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTGTG
351 CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51  HAAQONGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LRLAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVAAAX*

m156/a156  90.6% identity in 127 aa overlap

           10      20      30      40      50      60
m156.pep  MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
           |||||
a156      MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
           10      20      30      40      50      60

           70      80      90      100     110     120
m156.pep  FAPFAAAVLTAHATGNAAQSTINTLACLFILRLAFIWCYIADKAAMRSLMWAGGFACTV
           |||||
a156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGFVCTV
           70      80      90      100     110     120

m156.pep  GLFVAAAX
           |||||
a156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgccctgcgc cgccaattgC gCgGgcggcg
51  ttcgcAAATg GGcgagacg tGCGggCGGC GGCGgCgata Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCGGCGCA Aaactctatc tgcettATAT CGAACCCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTGGGCATA GACCGCGAAG
401 GCTACCGTTT GGGGCAGGCA GCGGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTTGCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLKRYI KRGRKIGVYW
 51 PMGKELRLGG FVRAAQKRGK KLYLPYIEPH TRRMWFTYPY ERGMERERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPREAHDLF LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
 51 TTCGCAAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGCG GGAAATCGG CGTGATTGG
151 CCGATGGGCA AGGAATTGCG TTGGACGGC TTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGGGCGGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTGCGA AAAAGCGTGT
351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCCGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GGCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTCAGGC AAAAACCGTG GCGTGGGCT TTGCCTGCCA
501 GTTGTGGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGGACGGT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAATV KINHLKRYI KKGRKIGVYW
 51 PMGKELRLDG FVRAAQKRGK ELYLPYIEPR SRRMWFTYPY ADGVKQERKR
101 GRAKLHVPQF AGRKKRVHDL NLLVPVVGVM DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMGRDVRAAAATVKINHLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAEKLYLPYIEPRSRMWFTYPYADGVKQERKRGRAKLHVPQFAGRKKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRMWFTYPYPERGEMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	NLLVPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCCG
 51 CGCGCAGATG GGGCATCAAG GGCGGTGGC GGCGGGGCAA ACCATTAACC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTTATC TGCCTTATAT CGAACC GCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCCTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACC GCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

## a157.pep

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGO TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFCQFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSOMGRDVR	AAATVKINHLLKRYIKKGRKIGVYW	PMGKELRLDG			
a157	MRNEEKHALRRELRRARAQM	GHQGRLAAGQTINRLLKRYIKRGRKIGVYW	PMGKELRLDG			
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAE	LYLPYIEPRSRMWFTYPYPADGVKQERK	GRAKLHVPQFAGRKR	RVHDL		
a157	FVRAAQKRGAKLYLPYIEPRSRMWFTYP	PESGME	RERIRGRAKLNVPQFAGRKIRVHGL			
	70	80	90	100	110	120
m157.pep	NLLLV	PVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTV	GVGFACQLVDRLPVEA	HDRS		
a157	SVLLVPLVGI	DREGYRLGQAGGYDATLAAMKYRLQAKTV	GVGFACQFVDRLPREPHDLL			
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

## g158.seq

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGCT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACCTATCCG CATATCcgac TTTCGCTCGT TTCTTCGGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCTT TACGGGCGCG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACC GGTCTCTAAAT
601 ACATGGGCGG TTTTAGatgc GCAGGGAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG  
 851 TATTTTGGGA TTTTATTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG  
 901 AATACCAAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep  
 1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTTRQLNLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEV PQGVLRVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DELVDNDITE  
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR  
 301 NTK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq  
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAG  
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG  
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC  
 151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGCGC CGCAATATTT  
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA  
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG GTTGAGCGT GGATTCCGCG  
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA  
 351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCCGAA GGCTATATCA  
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC  
 451 GATTCCGGGC TCGGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT  
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG  
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT  
 601 ACATGGGCGG TTTTAGATGC GCAGGGAAT CCCTATAAGA TTTCACCGCA  
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT  
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA  
 751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC  
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG  
 851 TATTTTGGGA TTTTATTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep  
 1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTTRQLSLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEI PQGVLSVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DELVDNDIAE  
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
g158	MKTNSEELTVFVQVVESGSFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRAQRILQEMAAAETEMLAHVHEIPQGVLSVDSAMPMVLHLLAPLAAKFNERYP					
g158	EEGAQYFRRAQRILQEMAAAETEMLAHVHEVPQGVLRVDSAMPMVLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

m158.pep	130	140	150	160	170	180
	HIRLSLVSSGGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158						
	HIRLSLVSSGGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
m158.pep	190	200	210	220	230	240
	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGGEILRSLCLSGCGIVCLS					
g158	: : :					: : :
	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
m158.pep	250	260	270	280	290	300
	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNLNCGX					
g158						
	DFLVDNDITEGKLIPLFAEQTSNKTHPFNAVYYSDKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

```

a158.seq
1  ATGAAAACCA ATTCAGAAGA ACTGACCCTA TTTGTTCAAG TGGTGGAAAG
51  CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCAGTGGCA AATTCCTGCC
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
151 AACC GCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAGAAATC GGCAGCGCGT GAAACCGAAA
251 TGCTGGCAGT GCACGAAATC CCGCAAGGCG TGTTGCGCGT GGGATCCGCG
301 ATGCCGATGG TGCTGCATCT GCTGCGCGCG CTGGCAGCAA AATTCACGCA
351 ACGCTATCCG CATATCCGAC TTTGCTCGT TTCTCCGAA GGCTATATCA
401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
451 GATTCGGGCG TGCCTGCACG CATCTGTTT GACAGCCGCT TCCGCGTAAT
501 CGCCAGTCTCT GAATACCTGG CAAACACGCG CACGCGCAAT CTACAGAGG
551 AGCTTGCCGG CCACCAATGT TTAGCTTCA CCGAACCGGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGATGT CGAGGAAATC CCCTATACGA TTTACCCGCA
651 CTTTACGCGC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
701 GCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA
751 GGAAAGTTAA TTCCCTGCTC CGCGGAACAA ACCTCCAATC AAACGCACCC
801 CTTTAAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
851 TATTTTTTGA TTTTTTAGTG GAGGAACCTG GAACAATCT CTGTGGATAA

```

**a158.pep**

1	MKTNSEELTV	FVQVVEGSF	SRAAEQLMAA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRR	QRILEMMAA	ETEMLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSE	GYNLIERKV	DTALRAGELD
151	DSGLRARHLF	DSRFRVYASP	EYLAKHRTSQ	STEECAGHCQ	LGFTPEGSLN
201	TGAVLDAQGN	PKYKSPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYSDKAVNL	RLRVFLDFLV	EELGNLNCG*

	10	20	30	40	50	60
m158.pep	MKTN	SEELTVFVQV	VGSGSFSRAAEQL	AMANS	SAVSRIVKR	LEEKLGVNLLNRTTRQLSLT
a158	MKTN	SEELTVFVQV	VGSGSFSRAAEQL	AMANS	SAVSRIVKR	LEEKLGVNLLNRTTRQLSLT
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYF	RRRAQRILQEM	AAAE	ETMLAV	HEIPQGVLSV	DAMS
a158	EEGAQYF	RRRAQRILQEM	AAAE	ETMLAV	HEIPQGVLRV	DAMS
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSDKTHPEFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSNKTTHPEFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1   ATGGAcattc  tGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCGCGTCC  GGTCGGCACG  GGCGATATTG  TATTTTCCC
201 GCGGGCTTG  GGTATGTGT  TGAGCCACGA  CGGAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGCTGG  ATATGAGCCT  GTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTTCATGTC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTC  CGTGGTCAAC  GCATTACCGT  CCGTCCTGCT
501 GGTGCTTATC  CTGCGGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAATCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGTTGTC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGCACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAC  CCCGATTCG  GTTTTGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTGCG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng> :

```

g160.pep
1   MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYOTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVDN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAARN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSFGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1   ATGGACATTC  TGGACAAACT  GGTCGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGAACGCGCA  AGGATTGGTA  CACATTGTTA  CATCGGCGAG  CCGCTATCTC
151 TGCATCGACG  GCGAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCAGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCC  GTTTCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTETCGTC

```

m160.pap

1	MDILDKLVDF	AQLTGSVDVQ	CLLGGQWSVR	HETLQREGLV	HIVTSGSGYL
51	CIDGETSPRP	VSTGDIVFFP	RGLGHVLSHD	GKCGESLQPD	MRQHGAFIVK
101	QCGNGQDMSL	FCARFRYDTH	ADLMNGLPET	VFLNINAHPSL	QYVVSMLQLE
151	SKKPLTGTVS	<u>MVNALSSVLL</u>	VLILRAYLEQ	DKDVELSGVL	KGWQDKRLGH
201	LQKGVIDKPE	DEWNVDKMVA	AANMSRAQLM	RRFKSRVGLS	PHAFVNHIRL
251	QKGALLKKK	PDSVLVSVALS	VGFSQSETHF	KAFKRQYHVS	PGQYRKEGGQ
301	K*				

### Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50	60
m160.pep		MDILDKLVDFAQLTGSVDVQCLLGQWSVRHETLQREGLVHIVTSGSGYLCIDGETSPRP					
		:					
g160		MDILDKLVDLAQLTGSADVQCLLGQW---HETLQREGLVHIVTAGSGYLCIDGETSPRP					
		10	20	30	40	50	
		70	80	90	100	110	120
m160.pep		VSTGDIVFFPRGLGHVLSHDGKCGESLQPDMRQHGAFIVKQCNGQDMSLFCARFRYDTH					
g160		VSTGDIVFFPRGLGHVLSHDGKYGESLQPDIRQNGTFMVKQCNGLDMSLFCARFRYDTH					
		60	70	80	90	100	110
		130	140	150	160	170	180
m160.pep		ADLMNGLPETVFLNIAHPSLQYVVSMQLQESKKPLTGTVSMVNALSSVLLVLILRAYLEQ					
g160		ADLMNGLPETVFLNIAHPSLQYVVSMQLQESKKPLTGTVSVVNALPSVLLVLILRAYLEQ					
		120	130	140	150	160	170
		190	200	210	220	230	240
m160.pep		DKDVELSGVLKGWQDKRLGHLIQKVIDKPEDEWNVDKMVAANMSRAQLMRRFKSRVGLS					
g160		DKDVELSGVLKGWQDKRLGHLIQKVIDKPEDEWNIDKMVAANMSRAQLMRRFKSQVGLS					
		180	190	200	210	220	230
		250	260	270	280	290	300
m160.pep		PHAFVNHIRLQKGALLLKKNPDSVLSVALSVGFQSETHFGKAFKRQYHVS PGQYRKEGGQ					
g160		PHAFVNHIRLQKGALLLKKTPDSVLEVALSVGFQSETHFGKAFKRQYHVS PGQYRKEGGQ					
		240	250	260	270	280	290
m160.pep	KX						
g160	KX						

```

a160.seq
      1  ATGGACATTC  TGGACAAACT  GGTGCATTTG  GCCCAATTGA  CGGGCAGTGT
     51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT

```



456

```
101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAATATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGC GGCA ACGGACAGGA TATGAGCCTG TTTTGC GCGCC GTTCCGCTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTGGG TTTTGTGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCAAT ACCGGAAGA AGGCGGGCAA
901 AAATAA
```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```
a160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*
```

m160/a160 100.0% identity in 301 aa overlap

```
10 20 30 40 50 60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
a160 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
10 20 30 40 50 60

70 80 90 100 110 120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
a160 VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
70 80 90 100 110 120

130 140 150 160 170 180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
a160 ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
130 140 150 160 170 180

190 200 210 220 230 240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
a160 DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
190 200 210 220 230 240

250 260 270 280 290 300
m160.pep PHAFVNHIRL QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
a160 PHAFVNHIRL QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
250 260 270 280 290 300

m160.pep KX
a160 KX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTtTg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTGAGGAA
451 CCGCGCGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAATGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTGTCGgt ttgggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tgggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAeg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTtTCTg ggcgaagagc ttttctggCA
801 GGAAATATCT GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMFLS
51  TVTLGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGCGTGT
301 ACCCTGAGTT ACACCTCGTC GATTTTtTg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTGAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAATGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTGTCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCCT GTCCTTTCCA TCGGCAETTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATCACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTtTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATATCT GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLS
51  TVALGAAAVL RRDXTFTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE

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458

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSCIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLFSTVALGAAAVL					
	:     :     :     :     :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMLFSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKHNLRSMVGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
	:     :     :     :     :					
g161	RRDTFRTPHWKHNLRSMVGTGAMLLLFYAVTHLPLTTGVTLSYTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGCFAGVLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	:     :     :     :     :					
g161	RISVYTQAVLLLGCFAGVLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSCIGVSALIAQLSMTRAYKVGDKFT					
	:     :     :     :     :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	:     :     :     :     :					
g161	VASLSYMTVVFSALSAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

```

a161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTA TGAACGTAT' TATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGEACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCCTT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCTGTAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGTGCTG CTCCTTGGTT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTATCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCTT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCG TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTCCTG GCCGAAGAGC TTTTCTGGCA
801 GGAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA

```

459

851 TCCGCCCCAC TGCCTTCAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA  
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep  
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLS  
51 TVALGAAAVL RRDFTERTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV  
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE  
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT  
201 LTGWHTLSFP SAVYLSICGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV  
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR  
301 \*

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	10	20	30	40	50	60
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
m161.pep	RISVYTQAVLLLGFGAGVVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGAGVVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGAGVVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGAGVVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
m161.pep	VASLSYMTVVSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	VASLSYMTVVSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq  
1 ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT  
51 TTAAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAGAAG  
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTTt  
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT  
201 AGGACGGGAT GAAGATGT3C CGGAATTCGG CTTCTGTCTG TGGCTGGCGA  
251 TGCTGTTTGC GGCCGGGATG GCGTGGGCC TGATGTTTT CGGCGTGGCA  
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA  
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTCACG  
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTGGACGGT GCTTTATTGG CGGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTC
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACCG CTGCTTTTTC
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCTGTGTTTT TGAACCTCT GCCGACTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCTG TGGAAAGGCT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGACAGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACGAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATAIGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

```

g163.pep
1  MVILTTLEFFV  CVLVVLVLTV  PDQVQMWLDR  AKEVIFTEFS  WFYVLTFEISF
51  LGFLLILSVS  GLGNIRLGRD  EDVPEFGFLS  WLAMLFAGM  GVGLMFFGVA
101 EPLMHYFSDI  TVGAPEHRQQ  QALLHTVFHW  GVHAWSVYGT  IALALAYFGF
151 RYKLPLALRS  CFYPLLKEKI  SGRFGDAIDI  MALLATFFGI  ITTLGFGASQ
201 LGAGLOEMGW  IAENSPGVQV  LIIAAVMSLA  VVSAISGVGK  GVKVLSEINL
251 GLAEFLLFFV  LAADPTVYLL  SAFGDNIGNY  LGNLVRLSLK  TYAYEREHKP
301 WFESWTVLYW  AWWCSWAFV  GLFIARISKG  RTIREFVFGV  LLIPGLEFVL
351 WFTVFGNTAI  WLNDGVAGGM  LEKMTSSPET  LLFKFFNYLP  LPELTSIVSL
401 LVISLFFVTS  ADSGIYVINN  ITSRDKGLSA  PRWOAVMWGV  LMSAVAVLLM
451 RSGGLGNLQS  MTLIVSLFFA  LLMLIMCFSL  WKGLSADKKY  FETRVNPTSV
501 FWTGGKWKER  LVRIMSQTQE  QDILKFLKHT  ASPAMHELQR  ELSEEYGLSV
551 RVDKMFHQDE  PAIEFVIRKE  TMRDFMYGIK  SVGQDVSDQL  INDGKLEPHIR
601 HQTTYKPYAY  FFDGRVGYDV  QYMNKDELIA  DILKNYERYL  MLLDDVGQEL
651 MAHEQVELAE  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

```

m163.seq
1  ATGGTTATTT  TGACGACTTT  GTTTTTTGTG  TGTGTTTGG  TGGTATTGGT
51  TTTAACCCTG  CCGGATCAGG  TGCAGATGTG  GCTCGATCGG  GCAAAAGAAG
101 TCATTTTTAC  CGASTTCAGC  TGGTTTTATG  TTTAACGTT  TCCATTTTT
151 CTGGGTTTCC  TGCTGATACT  CTCGGTCAGC  AGTTTGGGAA  ACATCAGGCT
201 CGGACGGGAT  GAAGATGTGC  CGGAATTCGG  CTTCCTGTCG  TGGCTGGCGA
251 TGCTGTTTGC  GGCGGGATG  GGCGTGGGTC  TGATGTTTT  CGGCGTGGCA
301 GAGCCGTTGA  TGCATTATTT  TTCGGACATT  ACGGCCGCGA  CGCCGGAACA
351 CAGGCAGCAG  CAGGCATTGC  TGCACACGGT  GTTCCATTGG  GCGGTTACAG
401 CTTGGTCGGT  GTACGGTACG  ATTGCATTGG  CTTTGGCTTA  TTTCCGTTTC
451 CGCTACAAGC  TGCCGCTTGC  CCTGCGTTCT  TGTTTTTACC  CCCTGTTGAA
501 AGAAAAAATT  TCCGAAGGT  TCGGCGATGC  CATTGATATT  ATGGCGTTGC
551 TTGCTACTTT  TTTCGGCATC  ATCACCACAT  TGGGGTTCGG  GGCTTCGCAA
601 CTGGGCGCCG  GATTGCAGGA  AATGGGCTGG  ATTGCCGAAA  ACAGCTTCAG

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTGTGTT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTTCG GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTAAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCGGTTTGTG GGTGTTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGGGGGTT TTGCTCATCC CCGGCTGTGT CGGCGTTTGT
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTCG
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTATATG
1251 CCGTGAACAA ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCGGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTCGCGA TAAGAAATAT TTTGAGACCC GGGTTAACC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTCCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGSTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLT VPDQVQMWLDRAKEVIFTEFSW FYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGR GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSW FYVLTFSIFLGFLILSVS					
g163	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSW FYVLTFSIFLGFLILSVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
	190 200 210 220 230 240
m163.pep	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLLIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLLIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
	250 260 270 280 290 300
m163.pep	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRSLKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRSLKTYAYEREHKP
	250 260 270 280 290 300
	310 320 330 340 350 360
m163.pep	WFESWTVLYWAWWCWAPFVGLFIARISKGRITREFFVGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCWAPFVGLFIARISKGRITREFFVGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
	370 380 390 400 410 420
m163.pep	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
	430 440 450 460 470 480
m163.pep	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
	490 500 510 520 530 540
m163.pep	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVIRIMSQTQEODILKFLKHTASAMHELQR
	490 500 510 520 530 540
	550 560 570 580 590 600
m163.pep	ELSEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSQDLINDGKLPHIR
g163	ELSEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSQDLINDGKLPHIR
	550 560 570 580 590 600
	610 620 630 640 650 660
m163.pep	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

a163.seq	1	ATGGTTATTT	TGACGACTTT	GTTTTTTGTG	TGTGTTTGG	TGGTATTGGT
	51	TTTAACCGTG	CCGATCAGG	TGCAGATGTG	GCTCGATCGG	GCAAAAGAAG
	101	TCATTTTAC	CGAGTTCAGC	TGGTTTATG	TTTAAACGTT	TTCCATTTT
	151	CTGGGTTTCC	TGCTGATACT	CTCGGTCAGC	AGTTTGGGAA	ACATCAGGCT

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201 CCGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCCG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCCT TTTTGTGCT GTTTTTTGT TGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGAAATC
851 TGGTGCGCCT CAGTTTAAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCITTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACTTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCGTA TGTTTTCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTACGCTG TGGAAAGGAT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CCGGTCGATA AGATGTTTCA TCAGGACGAG CCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 TACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAACATG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

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This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLEPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIOW IAENSFSVOV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFEWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCPSL WKGLSADKKY FETRVNPTSV
501 FWTGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTPYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQVEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCLVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a163       MVILTTLFFVCLVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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|||||
a163      SLGNIRLGRDEVPFEGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
              70          80          90          100          110          120

              130          140          150          160          170          180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
              |||||||
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
              130          140          150          160          170          180

              190          200          210          220          230          240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              |||||||
a163      MALLATFFGIITTLGFGASQLGAGLQEIOWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              190          200          210          220          230          240

              250          260          270          280          290          300
m163.pep  GVKVLSRLNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              |||||||
a163      GVKVLSRLNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              250          260          270          280          290          300

              310          320          330          340          350          360
m163.pep  WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
              |||||||
a163      WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
              310          320          330          340          350          360

              370          380          390          400          410          420
m163.pep  WLNDGVAGGMLEKMTSSPETLLKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              |||||||
a163      WLNDGVAGGVLEKMTSSPETLLKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              370          380          390          400          410          420

              430          440          450          460          470          480
m163.pep  ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL
              |||||||
a163      ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL
              430          440          450          460          470          480

              490          500          510          520          530          540
m163.pep  WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKOTASPMHELQR
              |||||||
a163      WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKHTASPMHELQR
              490          500          510          520          530          540

              550          560          570          580          590          600
m163.pep  ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              |||||||
a163      ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              550          560          570          580          590          600

              610          620          630          640          650          660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              |||||||
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              610          620          630          640          650          660

m163.pep  X
          |
a163      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGGCGC TTCCTGTTTCG CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTTGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTCCG
201 CCGCTTCCCC GAAAAACCGC ACTTGGGCGC CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTCTg cegatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTCAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCGCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGGCGA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCATTTCG TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GGCCTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTTCG
1151 GCGAGGACGA aatccgcgc caccTGCCTA CCGTGTGCGC AAATTTCAAA
1201 ATCCCAAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGRQPR INDLAHIYT SGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKRD LIISKQONVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGCGGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251 TACCGATGAA CACATTTTGG AAAAAACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGGCTT AAGGCGCAAA CGCCCGTCGA AAAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCGGCT TCCCCGAAAA ACCCGACTTG GGCGGCCAAC CCCGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCCTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGTGCGCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCGG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAAATCC TTGGTATTTC AGATGGTTCA
851 ACCGCATTCT CCGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA

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951  CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051  GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GCGGAAGTGG GCGAAGTGAT
1101  CGTCAGGGGC GGTTCGCTGA TCGGGGGCTA CCTCAATATG CCTGCCGCCA
1151  CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201  ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251  TATTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301  ACAAATCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351  TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401  TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451  TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501  ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKEGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRD R FIVFLPMFHS FTLTAMVLLP IYMACS IILV KSVFPFSNVL
251 KQTLKRA TV FLGVP AIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFP R AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGE LIVRG GSVMRGYLNM PAATDETIVN GWLKTGFVFT
401 IDEDFIFIV DRKKDLIISK GQNVYPREIE EEIYKLDAVE AA AVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGVKLRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
g164      MNTFLKNSEYAYILNDCKARFLFASAGLSK
          10      20      30

          120     130     140     150     160     170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90

          180     190     200     210     220     230
m164.pep  SGTTGHPKGALISYANLFANLNGIERIFKISKRD R FIVFLPMFHSFTLTAMVLLPIYMAC
g164      SGTTGHPKGALISYANLFANLNGIERIFKISKRD R FIVFLPMFHSFTLTAMVLLPIYMAC
          100     110     120     130     140     150

          240     250     260     270     280     290
m164.pep  SIILVKSVPFSPSNVLKQTLKRA TVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP
g164      SIILVKSVPFSPSNVLKQALLKRA TVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          160     170     180     190     200     210

          300     310     320     330     340     350
m164.pep  LAEQTILDFKAKFPRAKLEGYGLSEASPVVAVNTPERQKARSVG I PLPGLEAKAVDEEL
g164      LAEQTILDFKAKFPRAKLEGYGLSEASPVVAVNTPERQKARSVG I PLPGLEAKAVDEEL
          220     230     240     250     260     270

          360     370     380     390     400     410

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m164.pep  VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          |||||||
g164      VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          |||||||
g164      LIISKQNVYPREIEEEIHKLDAAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          |||||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTTC AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GCGCGGCTTG AAGCGCAGAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCGGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCGGATATAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTTC
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA
951 GTGACTGAGC GAAGCCTCGC CGTCTGTCGC CGTCAATACG CCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGG AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTG AGTGCCGCGC GCGCAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGCTA CCTCAATATG CTGCGGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTGTTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTTC GACCGCAAAA AAGATTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCGC TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKN NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPDL GRQPRINDLA HIIYTSGTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQALLKRATV FLGVPPIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIIV DRKKDLISK GQNVYPREIE EEIYKLDAAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRLRTV LANFKIPKQI HFKDGLPRNA

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468

501 TGKVLKRVLK EQFDGNK\*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNI					
a164	10	20	30	40	50	60
	MNRTYANFYEMLTAAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNI					
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	70	80	90	100	110	120
	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTS					
a164	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTS					
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKRDRIIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKRDRIIVFLPMFHSFTLTAMVLLPIYMACSIILV					
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKRRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	250	260	270	280	290	300
	KSVFPFSNVLKQALLKRRATVFLGVPAIYTAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLEGLSEASPVVAVNTPERQKARSVGIPPLGLEAKAVDEELVEVPR					
a164	310	320	330	340	350	360
	ILDFKAKFPRAKLEGLSEASPVVAVNTPERQKARSVGIPPLGLEVKAVDEELVEVPR					
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNM?AATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLIISK					
a164	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNM?AATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLIISK					
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLK EQFDGNKX					
a164	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLK EQFDGNKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCGCGCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTTT CCTCGGCGCG GCGGCGGCGC CACTGACCCT GCTGCAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CctGTGGgC gAaTTGcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALLLQK
251 SGIPGKGYG GLPVSGLFFR NSNPETAEOH NAKVYQASV GAPFMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACCGCGGCA CGGGGCATTC CGCGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGGC GCAGCTCACC CTCCGTACCC
701 GCTTCTCTTT CCTCGGCGCG GCGGCGGCGC CGTGACCCT GCTGCAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

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470

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK  
 251 SGIPEGKGYG GFPVSGLFFR NSNPETAEQH NAKVYQASV GAPPMSPVPHL  
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA  
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	MAEATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
m165.pep	70	80	90	100	110	120
	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
m165.pep	130	140	150	160	170	180
	HCSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDNRNKISDWAPLIMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
m165.pep	190	200	210	220	230	240
	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDGQTLRTRFLFLGA					
g165	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
m165.pep	250	260	270	280	290	300
	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAXVYQASVGAPPMSPVPHL					
g165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAXVYQASVGAPPMSPVPHL					
	250	260	270	280	290	300
m165.pep	310	320	330	340	350	
	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTGCTCA	AAGAACTCGA	ACCGTCTTGG	GAAATCACCC
101	TGATTGAACG	CTTGAAGAT	GTGGCGTTGG	AATCGTCAAA	CGCGTGAAC
151	AACGCCGGCA	CGGGGCATTC	CGCGCTGTGC	GAATTGAACT	ATGCGCCGTT
201	GGGTGCAAAT	GGGATTATCG	ATCCGGCGCG	CGCCCTCAAT	ATTGCCGAAC
251	AGTTTCATGT	CAGCCGCCAG	TTTGGGCGCA	CGTTGGTCGC	GGAAGGCAAG
301	TTGGAAGACA	ATTCTTCAT	CAATGCCGTG	CCGCATATGT	CTTGGTGAT
351	GAATGAAGAC	CATTGTTCTT	ATCTTCAAAA	ACGTTATGAC	GCCTTTAAAA
401	CCCAAAAAT	TTTGGAAAAT	ATGGAATTTT	CCACCGATCG	GAACAAAATT
451	TCCGATTGGG	CTCCGCTGAT	GATGCCCGGC	CGGGACGAAA	ACCAACCCGT
501	CGCCGCCAAC	TACTCCGCCG	AAGGCACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAAAT	GGTGAAATAT	TTGCAGGGCA	AGGGCGTAAA	AACCGAGTTC

```

601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGGCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCACCTATG GATTTGCCGC
1001 TGTCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAATACTA CCCCGAGGCA AACCCGACG
1151 ACTGGGAAT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGT GCAGTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGAT TGCTGGGCGC GTCGCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAAGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTGTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GPFVSGLFFR NSNPETAQH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGS LM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQI IKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

m165.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSW	EITLIERLED	VALESSNAWN	NAGTGHSALC
a165	MAEATDVVLVGGGIMSATLG	VLLKELEPSW	EITLIERLED	VALESSNAWN	NAGTGHSALC
m165.pep	ELNYAPLGANGI	IIDPARALN	IAEQFHVSRQ	FWATLVAEGK	LEDNSFINAVPHMSLVMNED
a165	ELNYAPLGANGI	IIDPARALN	IAEQFHVSRQ	FWATLVAEGK	LEDNSFINAVPHMSLVMNED
m165.pep	HCSYLQKRYDA	FKTQKLFEN	MEFSTDRNKI	SDWAPLMMRG	RDNQPVAA N YSAEGTDVDF
a165	HCSYLQKRYDA	FKTQKLFEN	MEFSTDRNKI	SDWAPLMMRG	RDNQPVAA N YSAEGTDVDF
m165.pep	GRLTRQMVKY	LQKGVKTEF	NRHVEDIKRE	SDGAWVLKTA	DTRNPDGQLT LRTRFLFLGA
a165	GRLTRQMVKY	LQKGVKTEF	NRHVEDIKRE	SDGAWVLKTA	DTRNPDGQLT LRTRFLFLGA
m165.pep	GGGALTLLQK	SGIPEGKGYG	GPFVSGLFFR	NSNPETAQH	NAKVYQASV GAPPMSPVPHL
a165	GGGALTLLQK	SGIPEGKGYG	GPFVSGLFFR	NSNPETAQH	NAKVYQASV GAPPMSPVPHL



472

```

          310      320      330      340      350
m165.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK
          |||||
a165      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPJTKYLLG
          310      320      330      340      350      360

a165      ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
          370      380      390      400      410      420

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGCGCGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGCTTGG  GAAATCACCC
101  TGATTGAACG  CTTGGAagat  gTGGCGTTGG  AATCGTCAA  cCGGTGAAC
151  AACGcCGgca  CGGGGCATT  CCGCTGTGc  GAATTGAACT  AtgcgccGCT
201  GGGtgcggac  ggcgtcatCA  ATCCGGCGCg  cgCCCTGAAT  ATTGCCGAAC
251  AGTTTCATGT  CAGCCGCCAG  TTTTGGGcga  cgctggTCGC  GGAAGGCAAG
301  TTGGAAGACA  ATTCTTCAT  CAATGCCGTG  CCGCATATGT  CTTGGTGAT
351  GAACGAAGAC  CACTGCCGTT  ACCTGCAAAA  ACGCTATGAT  GTGTTAAAA
401  CGCAGAACT  TTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451  TCCGATTGGG  CtccgCTGAT  TATGCGCGCG  CGGGACGAAA  ACCAACCCGT
501  CCGCGCAAC  TATTCGCCG  AAGGCACGGA  TGTCGATTTC  GGACGGCTGA
551  CGCGCCAGAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601  AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651  CAAACCGGCC  GATACCGCA  ACCCAGACTG  GCAGCTCACC  CTCCGCACCC
701  GCTTCTCTTT  CCTCGGCGG  GCGCGCGCG  CACTGACCTT  GCTGCAAAAA
751  TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTACCCG  TGTCCGGCCT
801  GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACACAC  AACGCCAAAG
851  TGTACGGGCA  GGCCTCCGTC  GCGCGCGCG  CGATGTCCGT  CCCGCACCTC
901  GACACACGCA  ACGTAGACGG  CAAACGACAC  CTTAIGTTTC  GTCCTTACGC
951  AGGTTTCCGT  TCCAACITCC  TCAAGCAAGG  CTCGTTTATG  GATTTGCCGC
1001  TGTCCATCCA  TATGGACAAC  CTCTATCCCT  TGCTGCGCGC  CGGCTGGGCG
1051  AATATGCCCG  TGACCAATA  CCTGCTGGGC  GAATTGCGTA  AAACCAAGA
1101  AGAACGCTtt  gCCTCCCTGC  TGgaatacta  cccGaggcag  acccGACGAc
1151  tggctactcat  cagcgaggnc  acGCGTcata  tcattanata  tgactCgaaa
1201  ctgcgcgtgc  tgcagttgta  cgagattgtg  ccaCGGacg  ctgcgtcgcg
1251  cattctggag  cgtcgcggcg  catcacgctn  tgcgctgata  tccgctgatg
1301  acactgctcc  gaGCGcgccc  gtcttggaag  gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NACTGHSALC  ELNYAPLGAD  GVINPARALN  IAEQFHVSRQ  FWATLVAEGK
101  LEONSFINAV  PHMSLMNED  HCRYLQKRYD  VFKTQKLFEN  MEFSTDNRKI
151  SDWAPLIMRG  RDENPQVAAN  YSAEGTDVDF  GRLTRQMVKY  LQGGKGVKTEF
201  NRHVEDIKRE  SDGAWVLKTA  DTRNPDWQLT  LRTRFLFLGA  GGGALTLLQK
251  SGIPEKGYG  GLPVSGLFFR  NSNPETAEOH  NAKVYQASV  GAPPMSVPHL
301  DTRNVDGKRH  LMFPGPYAGFR  SNFLKQGSFM  DLPLSIHMDN  LYPMLRAGWA
351  NMPLTKYLLG  ELRKTKEERF  ASLLEYPRQ  TRRLVLITQX  TRHIIYDSK
401  LRVQLYEIV  PRDARSRILE  RRGASRXALI  SADDTAPSAP  VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

n165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGCGCGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGCTTGG  GAAATCACCC
101  TGATTGAACG  CTTGGAAGAT  GTGGCGTTGG  AATCGTCAA  cCGGTGAAC
151  AACGCCGCA  CGGGGCATT  CCGCTGTGc  GAATTGAACT  ATGCGCCGT
201  GGGTGCAAA  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATTGCCGAAC
251  AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGCTGGTCGC  GGAAGGCAAG
301  TTGGAAGACA  ATTCTTCAT  CAATGCCGTG  CCGCATATGT  CTTGGTGAT
351  GAATGAAGAC  CATTGTCTT  ATCTTCAAAA  ACGTTATGAC  GCGTTAAAA
401  CCCAAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451  TCCGATTGGG  CTCCGCTGAT  GATGCGCGCG  CGGGACGAAA  ACCAACCCGT
501  CCGCGCAAC  TACTCCGCCG  AAGGTACGGA  TGTCGATTTC  GGACGGCTGA
551  CGCGCCAAAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601  AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651  CAAACCGGCC  GATACCGCA  ACCCGACGG  GCAGCTCACC  CTCCGTACCC
701  GCTTCTCTTT  CCTCGGCGCG  GCGCGCGCG  CGCTGACCTT  GCTGCAAAAA
751  TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTCCCG  TGTCCGGCCT
801  GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACACAC  AACGCCAAAG

```

```

851 TGTACGGGCA GGCTTCCGTC GGC GCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTCGCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGAGCA AACCCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGAIGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

ml65-1.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEKG
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDENKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGS LM DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKRD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

ml65-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
ml65-1.pep	MAEATDVVLVGGGIMSATLGVLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
g165-1	MAEATDVVLVGGGIMSATLGVLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
ml65-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEKGLEDNSFINAVPHMSLVMNED					
g165-1	ELNYAPLGADGVINPARALNIAEQFHVSRQFWATLVAEKGLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
ml65-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDENKISDWAPLMMRGDRDENQPVAA N YSAEGTDVDF					
g165-1	HCRYLQKRYDVFKTQKLFENMEFSTDENKISDWAPLMRGRDENQPVAA N YSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
ml65-1.pep	GRLTRQMVKYLQKGKVKTEFNHRHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165-1	GRLTRQMVKYLQKGKVKTEFNHRHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
ml65-1.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
g165-1	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	360
ml65-1.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG					
g165-1	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRACWANMPLTKYLLG					
	310	320	330	340	350	360
	370	380	390	400	410	420
ml65-1.pep	ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKRDSEKGGVLQFGTEIVAHADGS					
g165-1	ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKRDSEKGGVLQFGTEIVAHADGS					
	370	380	390	400	410	
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHOCFFERAPSWEDRLKELVPGYGIKLNENPERADEIIA  
:  
| | |  
g165-1 ILERRGASRXALISADDTAPSAPVLESVX  
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq  
1 ATGCGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC  
51 GACCTTGGGC GTTTTGTCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC  
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC  
151 AACGCCGGCA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGTT  
201 GGTGCAAAAT GGGATTATCG ATCCGCGCGG CGCCCTCAAT ATTGCCGAAC  
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTTCG GGAAGGCAAG  
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT  
351 GAATGAAGAC CATTTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA  
401 CCCAAAAACT TTTTGAATAAT ATGGAATTTT CCACCGATCG GAACAAAAAT  
451 TCCGATTGGG CTCGCGTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT  
501 CGCCGCCAAC TACTCCGCGG AAGGCACGGA TGTCGATTTG GGACGGCTGA  
551 CGCGCCAAAT GGTGAATAT TTGAGGGCA AGGCGTAAA AACCGAGTTC  
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT  
651 CAAAACCGCG GATACCCGCA ACCCGACGCG GCAGCTCACC CTCCGTACCC  
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA  
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGGCT  
801 GTTCTTCCGC AACAGCAACC CCGAAACCGG CGAACAACAC AACGCCAAAG  
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCG CGATGTCCGT CCCGCACCTC  
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTG GGCCTTACGC  
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTATG GATTGCGCG  
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG  
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA  
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACT CCGGAGGCA AACCCGACG  
1151 ACTGGAACT CATCACCGCA GGGCAACGCG TTCAATCAT TAAAAAGAC  
1201 TCCGAAAAAG CGGGCGTGTT GCAGTTGGT ACGGAGATTG TCGCACACCG  
1251 CGACGGCTCG CTCGCGCAT TGCTGGGCGG GTCGCGGGG GCATCGACCG  
1301 CCGTGGCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC  
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA  
1401 GTTGAACGAA AACCCGAAA GGSCGGATGA AATTATCGCC TATACCGCA  
1451 AAGTGTGGA TATTTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep  
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN  
51 NAGTGHSAIC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK  
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI  
151 SDWAPLMMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF  
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLOK  
251 SGIPEGKGYG GFFVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL  
301 DTRNVDGKRH LMEFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA  
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKID  
401 SEKGVVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFFERT  
451 PSWEGRLKEL VPGYGIKLINE NPERADEIIA YTAKVLDI\*

a165-1/m165-1 99.4% identity in 486 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSAIC		
m165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSAIC		
	10	20	30	40	50	60
a165-1.pep	ELNYAPLGANGI	IIDPARALNIAEQFHVSRO	FWATLVAEGKLEDNS	FINAVPHMSLVMNED		
m165-1	ELNYAPLGANGI	IIDPARALNIAEQFHVSRO	FWATLVAEGKLEDNS	FINAVPHMSLVMNED		
	70	80	90	100	110	120
a165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAANYSAEGTDVDF			
m165-1	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAANYSAEGTDVDF			
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAANYSAEGTDVDF			
m165-1	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAANYSAEGTDVDF			
	190	200	210	220	230	240

475

a165-1.pep GRLTRQMVKYLOGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA  
|||||  
m165-1 GRLTRQMVKYLOGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA  
190 200 210 220 230 240

a165-1.pep GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL  
|||||  
m165-1 GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL  
250 260 270 280 290 300

a165-1.pep DTRNVGDKRRLMFGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG  
|||||  
m165-1 DTRNVGDKRRLMFGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG  
310 320 330 340 350 360

a165-1.pep ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLOFGTEIVAHADGS  
|||||  
m165-1 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLOFGTEIVAHADGS  
370 380 390 400 410 420

a165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNNPERADEIIA  
|||||  
m165-1 LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA  
430 440 450 460 470 480

a165-1.pep 489  
YTAKVLDIX  
|||||  
m165-1 YTAKVLDIX

**a165-1/p33940**

sp|P33940|YOJH\_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION  
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID:o372#5; similar to [SwissProt Accession Number  
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical  
to 490 residues of YOJH\_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct  
identical to GB: ECOHU49\_33  
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548  
Score = 458 bits (1167), Expect = e-128  
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

Query: 3 EATDVVLVGGGIMSATLGVLKLELEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62  
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL  
Sbjct: 30 QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAOESSNGWNNAGTGHSALMEL 89

Query: 63 NYAPLGGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLED-NSFINAVPHMSLVNMEDH 121  
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+  
Sbjct: 90 NYTPQNADSGISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDFG 181  
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G  
Sbjct: 150 VNFLRARYAALQQSSLFGRMRYSEDHAQIKEWAPLVMEGRDPQQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLOGKG-VKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240  
+TRQ++ LQ K + + V +KR D W + AD +N Q  
Sbjct: 210 EITRQLIASLQKKSNSLSLQSSSEVRALKRNDNTWTVTVDLKNGTAG-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL 300  
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+  
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVGDKRRLMFGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360  
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+  
Sbjct: 329 DTRVLDGKRVVLFPGFATFSTKFLKNGSLWDLMSSTTTSNVPMHVLGDLNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLOFGTEIVXXXXXX 420  
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V  
Sbjct: 389 QVHLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDSEKGGVLRGTEVVSDDQGT 448

Query: 421 XXXXXXXXXXXXXVPLMIRLMHQCFPER--TFSWEGRLKELVPGYGIKLNNPERADEI 478

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +  
 Sbjct: 449 IAALLGASPGASTAAPINLNLEKVFGRVSSPQWQATLKAIVPSYGRKLNQDVAATERE 508

Query: 479 IAYTAKVLDI 488

+ YT++VL +

Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq  
 1 atggcgccgg cggaataaaa acgccccctc gctgtcgatt tccagcacat  
 51 agcgtccggt ctgcacggcg gcatagccgc ttttgccctgc ctgatagggg  
 101 tgcaggcgcg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc  
 151 ggcgatattg cccaccagtt tggcaaacaa ggtatggcac acgccgtttt  
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg  
 251 acgacggctt ccaagtctgt gggatgcttt ccggtcagcc ggacggcggt  
 301 ttgttcggcg aagcctttaa tcggataact gatttgtttt ttgccgtcgt  
 351 tggttttgcc ttcgtacttt tgtcccaaag ccaaaccggc aatcgccgta  
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcg cttgtgccgc  
 451 attttgcggc tgttcgcgcg tattttcgga tttgccgcag gcggcaagca  
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc  
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtcgaaacg tggcaggcg  
 601 aggttcggac ggcatgggt ttatttcaac gggcgatgc cgaccgcac  
 651 gcgtacttta tccaacaatt cgcgcgctt tttgcgcgc tttgcgcgc  
 701 ctgctgcaa aatctcttcg atttgcgga gattagaggt caatgcggtg  
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep  
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF  
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQV GMLSGQPDGV  
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDF ENRFRRALCR  
 151 ILRLFRIRFG FAAGKQQA AOHGKRYFOH SALLMVSKCR LKRLKRGRR  
 201 RFRHVVYFN GRMPTASRTL SNNRSASLRA FCAPACKISS ICEGLEVNAL  
 251 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq  
 1 ATGGCGCGG CGGAAATAAA ACGCCCCTTC GCTGTCGATT TCCAGCACAT  
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCCTGC CTGATAGGGT  
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC  
 151 GGCGATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT  
 201 CTGCCCAACC TGCCGGAAGT TCCTTATCAT CGGTTTCCAT ACATTGCGCG  
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT  
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT  
 351 TGGTTTGCC TTCGCTGCTT TGTCCCAAT CCAAACCGGC AATCGCCGTA  
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC  
 451 GTTTTGCGGC TGTACCGCGG TATTTwCGGA TTTGCCGCaC GGCaArgCAG  
 501 CAGGCAGCCG CCAATACCG CAAAFawGT WTTcAGCATT CCACaYTCCT  
 551 GATGGTTTCA AAATGCCGTC TGAAACCGCG CAGCGGAGG TTCGGACGGC  
 601 ATCGGTTTCA TTTCAACGGG CGGATGcCGA CCGCATcGT ACTTGTTCCA  
 651 ATAATTGCGG TGCTTCTTTA CGCGCTTTCG CCGCGCTGC CTGCAAAATC  
 701 TCTTCGATTT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep  
 1 MAAABIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN \*VIRQFAAVF  
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI  
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR  
 151 VLRLYRRIXG FAATAXQQA AQYKXXXQH STXLMVSKCR LKRRRRFRGR  
 201 HRVFNGRMP TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL\*

Computer analysis of this amino acid sequence gave the following results:

m204/q204

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

```

a204.pep
1  MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVIRQFAAVF
51  GDIAHQFGKQ GMAHAVCRPA RRRALSVGFH TFADDGFQVV GMLAQGPDDV
101 LFRQAF... ..
151 ... ..KRFGR
201 HWVYENGRIP TASRTLPNNS RASLRAFCAP ACKISSCEG SAVSSL*

```

**m204/a204 54.5% identity in 246 aa overlap**

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSFGFHTFADDFQVVGMLAGQPDQVLFQAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNRRIVDIYDFENRFRRLYRVLRLYRRXGFAATAQQAAAQYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKRRRFRGRHVFNGRMPASGTLNNSRASLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNSRASLRAFCAPACKISSICEG					
		110	120	130	140	150
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgectgc tgettgcgcg
51  ctgcggcaaa tccgaaaata cggcgaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggttttg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggagg aaaaaggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgacg aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCELLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGDAPS GWAENGVCHT LFAKLVGNIA EDGGLTDYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS BGAIFYRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAawa CwTyTTTtGC CGTATTGGGC GGCTGCCTGC TGcYtTGCCG
51  tGCGGCAAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CCGTACAAAG
101 CGCGCCGAAA CCGGTTTtCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAAAATGTA
301 TGGAAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGATGCG CCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

m205.pep

```

1  MLXTXFAVLG GCLLXCRCCK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLTDL VSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

m205/g205

	10	20	30	40	50	60
m205.pep	MLXTXFAVLGGCLLXCRCCKSXNTAVQPQNAVQSAPKPVFKVIYIDNTAAGLDLGQSSE					
g205	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTAAGLALGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m205.pep	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSFAGWAENGVCHT					
g205	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m205.pep	LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH					
g205	LFAKLVGNIAEDGGKLTDLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH					
	130	140	150	160	170	180
m205.pep	YX					
g205	Y					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

a205.seq (partial)

```

1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
51  CAAGCATCCC AACGACTTGG AAGCGTCGT CGGCAAATGT ATGGAAACCG
101 ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGCGGT GTGCCATACC
151 TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACTGAC
201 GGATTACCTG ATTTGCGATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251 GCGGCTATGC CGCGGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301 GAGGGGGCGT TTTATTTCCG CCGCGCCAT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

a205.pep (partial)

```

1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
51  LFAKLVGNIA EDGGKLTDLV ISHSALQPYQ AGKSGYAAVQ NGRYVLEIDS
101 EGAFYFRRRH Y*

```

m205/a205 88.3% identity in 111 aa overlap

	50	60	70	80	90	100
m205.pep	KVIYIDNTAAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC					
a205	SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC					
	10	20	30			
	110	120	130	140	150	160
m205.pep	METDDKDSFAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ					



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

1	ATGCTGAAAA	TACCTTTTGC	CGTGTGGGCG	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAAAT	CGCGCAAACAT	GCCGCAAAAT	GCGGCACAAA
101	GCGCGCCGAA	ACCTGGTTTC	AAAGTCAAAAT	ACATCGACAA	TACGGCGATT
151	GCGGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GCGAAACCAC	ACAGCGGCAC
201	AAAACAAATC	AGTTATCCGA	TTAAGGCTT	GCCGGAACAA	AACGCCGTCC
251	GGCTGACCGG	AAAGCATCCC	AACGACTATCG	AAGCCGTGCT	CGGCAAAATG
301	ATGGAACCCG	ACGGAAGAGA	CGCGCTTCG	GGCTGGCGGT	AAAACGGCGT
351	GTGCCATACC	TGTTTGGCCA	AACGTGTTGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	TGATTACCTG	ATTTCGCATT	CCGCCTGCA	ACCTATACAG
451	GACGGCAAAA	GCGGCTATGC	CGCCGTGACG	AACGGACGCT	ATGTGCTGGA
501	AATCGACAGC	GAGGGGCGCT	TTTA		

1 MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI  
51 AGIALGQSSE GKTNDGKKQI SYPTKGLPEQ NAVRLTGKPH NDLEAVVGKC  
101 METDGGKDAF GAEWGVCHT LFAKLVGNIA EDGGKLTDPY ISHSALQPYQ  
151 AKSGGYAAVO NGRYVLEIDS RFAF

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTCGCGCAAA	TCCGAAAAAT	CGCGGAAAC	GCCGCAAAAC	GCGGTACAAA
101	GC GC GCGCGAA	ACC GG TTTTC	AAGTCAAA	ATATCGACAA	TACGGCGATT
151	GCGGGTTTGG	ATTTGGGACA	AAGCATCGAA	GCGCAAAACA	ACGCGGCGAA
201	AAAACAAATC	AGTTATCCGA	TTAAGGCTT	GCCGGAACAA	AATGTTATCC
251	GACTGATCGC	CAAGCATCCC	GCGCATTTGG	AAGCCGTCAG	CGGCAAAATG
301	ATGGAACCCG	ATGATAAAGA	CAGTCCGCGA	GGTTGGGCGA	AAACCGCGGT
351	GTGCCATACC	TGTGTTGGCA	AAGTGGTGGG	CAATATCGCC	GAAAGCGGGC
401	GCAAACTGAC	GGATTACCTA	GTTGTCGCAT	CCGCCCTGCA	ACCTGTACAG
451	GCAGGCAAAA	GCGGCTATGC	GCCTGTCGAG	AACGGACGCT	ATGTGCTGGA
501	ATACGCACAG	GAGGGGGCGT	TTTATTTCGC	CCGCGCCAT	TATTGA

1 MLKTSFAVLG GCLLLAACGK SENTAEQPQN AVQSAPKPVF KVKYIDNTAI  
51 AGLDLGQSSE GKTNDGKKQI SYPTKGLPEQ NVIRLIGKHP GDLEAVSGKC  
101 METDDKDSPA GWAENGVEHT LFLAKLVGNIA EDGGKLTDPH VSHAALQPYQ  
151 AGSKGYAAOV NGRVYVLEDS BGAFYFRRRH Y\*

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSA	PKVPVKYIDNTA	IAGLALGQSS			
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPQNAVQSA	PKVPVKYIDNTA	IAGLDLGQSS			
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTN	DGKKQISYPIKGLPEQNAVRLTGKHPNDLEAV	VGKCMETDGD	KADPSGWAENG	VCHT	
m205-1	GKTN	DGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVS	GKCMETDDKDS	PAGWAENG	VCHT	

481

```

              70      80      90      100     110     120
          130      140      150      160      170
g205-1.pep  LFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNGRYVLEIDSEGA F
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m205-1      LFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNGRYVLEIDSEGA FYFRRRH
          130      140      150      160      170      180
m205-1      YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TCGGGCTGG GCGGCAACG GCCTGTGCCA TACCTTGTTF
151 GCCAACTGG TGGCAATAT CGCCGAAGAC GCGGCAAC TGACGGATTA
201 CCTGATTCG CATTCCGCC TGCAACCCTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCCGCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTATT TCCGCCGCC CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKME TDGKGAPSGW AANGVCHTLF
51  AKLVGNI AED GGKLT DYLI SHSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRH*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep  KYIDNTA IAGLD LGQSSE GKTNDG KQISYP IKG LPEQNVIR LIGKHPG DLEAVSGK ME
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a205-1      PLKGLPEQNVVRLTGKHPNDLEAVVGKME
          10      20      30
          110      120      130      140      150      160
m205-1.pep  TDDKDS PAGWAENG VCHTLF AKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a205-1      TDGKGAPSGWAANGVCHTLF AKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNG
          40      50      60      70      80      90
          170      180
m205-1.pep  RYVLEIDSEGA FYFRRRH YX
          |||:|||||:|||||:|||||:|||||:|||||:|||||
a205-1      RYVLEIDSEGA FYFRRRH YX
          100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc cggacaaaac ccttttcctc tgtctcggcg cactgctcct
51  cgctcatgc ggcacgacct ccggcaaaac ccgccaaccg aaaccctaac
101 agacagtcgc gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctccgactca tcggcacgac
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgatttct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgcaat tcattcatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttggg gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

m206.seq

1	ATGTTTCCCC	CCGACAAAAC	CCTTTTCCTC	TGTCTCAGCG	CAC TGCTCCT
51	CGCCTCATGC	GGCAGGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAAATCCAA	GCCGTCCGCA	TCAGCCACAT	CGACCCGACA
151	CAAGGCTCGC	AGGAAGTCAT	GCTCCACAGC	CTCGGACTCA	TCGGCAGCGC
201	CTACAAATGG	GGCCACTGCA	GACCCGCAAC	CGGCTTCGAT	TGCAGCGGCA
251	TGATTCAATT	CGTTTACAAR	AACGCCCTCA	ACGTAAAGCT	GCCGCGCACC
301	GCCCGCGACA	TGGCGGCGGC	AAGCCGsAAA	ATCCCCGAcA	GCCGcYTCAA
351	GGCCGGCGAC	CTCGTATTCT	TCAACACCGG	GGGCGCACAC	CGTACTACAC
401	ACGTCGGACT	CTACATCGGC	AACGGCGAAT	TCATCCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAAAACGA	AAAGCTCTCC	ACACCCGTTT	ACGCCAAAAA
501	CTACCTCGGC	GCACATACTT	TTTTTACAGA	ATGA	

m206 . pep . .

1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT  
51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT  
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS  
151 GKTIKTEKLS TPFYAKNVLG AHTEPTE\*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPDPKTLFLCLSA	LLASCGTTSGKH	RQPKPKQTVRQI	QAVRISHIDRTQGS	QEMLMHS	
	:					
g206	MFSPDKTLFLCLG	AllLASCGTTSGKH	RQPKPKQTVRQI	QAVRISHIGRTQGS	QEMLMHS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSS	TATGFDCSGMIQFV	YKNALNVKLPR	TARDMAAASRKIP	DSDRXKAGD	
	:					
g206	LGLIGTPYKWGGSS	TATGFDCSGMIQLV	YKNALNVKLPR	TARDMAAASRKIP	DSDRLKAGD	
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSH	VGLYIGNGEFIHAP	SSGKTIKTEKLSTP	FYAKNYLGAHTFF	TFTEX	
	:	:				
g206	IVFFNTGGAHRYSH	VGLYIGNGEFIHAP	SSGKTIKTEKLSTP	FYAKNYLGAHTFF	TFTE	
	130	140	150	160	170	

a206.seq

1	ATGTTTCCCC	CCGACAAAAC	CCTTTTCCTC	TGTCTCAGCG	CACTGCTCCT
51	CGCCTCATGC	GGCAGGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAAATCCAA	GCCGTCCGCA	TCAGCCACAT	CGACCCGACA
151	CAAGGCTCGC	AGGAATCAT	GCTCCACAGC	CTCGGACTCA	TCGGCAGCGC
201	CTACAAATGG	GGCGCGAGCA	GACCCGACAT	CGGCTTCGAT	TCGAGCGGCA
251	TGATTCAATT	CGTTTACAAA	AACGCCCTCA	ACGTCAAGCT	CGCCGCGACC
301	GCCCGCGACA	TGGCGGCGGC	AAGCCGCAAA	ATCCCCGACA	GCCGCCTTAA
351	GGCCGGCGAC	CTCGTATTCT	TCAACACCGG	CGGCGCACAC	CGTACTACAC
401	ACGTCGGACT	CTATATCGGC	AAGGCGCAAT	TCATCCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAACACGA	AAACTCTCC	ACACCGTTTT	ACGCCAAAAA
501	CTACCTCGGC	GCACATACTT	TCTTTACAGA	ATGA	

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRTQGSQELMLHS
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFYK NALNVKLPRP
101 ARDMAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS				
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS				
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFYKNALNVKLPR	TARDMAAASRKIPDSRXKAGD			
a206	LGLIGTPYKWGGSSTATGFD	CSGMIQFYKNALNVKLPR	TARDMAAASRKIPDSRLKAGD			
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIG	NGEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
a206	LVFFNTGGAHRYSHVGLYIG	NGEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
51  tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggtttg gccaacatcg ttgccgccat aatgatggcg
251 aggatgtagt aggggtcggc gcggctgagg tcgtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccagc tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 tcgctgcggc tatttttctt tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaaagg taggaggcgt tggccaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttgtgc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctcgg gatgtttgcg
701 ataacggatg tggtttcggg accggcatac aggttgaccg ccattttcgg
751 ttttgccccc cgggttgagg tagcgggtaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
m209.pep
1  MLRHLGNDFA LGALFFDAAV DVPLLDGQVE VVDHPVENQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDQDQVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRQTAA QRVDLVEFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQPEE ERRCEPVYFT VVFCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGCT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTGTTG CGCCATACGG
451 TCGTCGCGGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGCGTGT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTGCGGG TTTTGCEGAT GTATTGCGCC
951 TCGGATTGTC CGGATTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDL DLQOHRQAAA QRVDVLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDCDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTLVLYSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSKSE KLTFWKLPSG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

```

m209/g209
      10      20      30      40      50      60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHVPENQTGREEEEHDGENQRHDFHHFR
          10      20      30      40      50      60

      70      80      90      100     110     120
m209.pep LHRVGRRRVQISLGEHRCRHNDGDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      LHRVGRRRVQIGLGEHRCRHNDGDVVGVGAAEVGNPAQPRCLAQFYGGEQCPVQADEG
          70      80      90      100     110     120

      130     140     150     160     170     180
m209.pep DLQOHRQAAAQRVDVLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      DLQOHRQTAAQRVDLVFEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGVGQW
          130     140     150     160     170     180

      190     200     210     220     230     240
m209.pep IQYGFDDDGXNDNRPAVADDVVQLVQEP EERGEPVYFAVVFGQLQVVG DVCDDGCGLR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVG DCDNGCGLR
          190     200     210     220     230     240

      250     260     270     280     290     299
m209.pep AGVEVDGGFGF-APFWMAAKGTLTLVLYSLRLMSMLHSPAAQTLCLPLGWRIQVDMK
          :||:| | | | |
g209      TGIQVDRHFRFWPPGWDSG
          250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

485

```
51 TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATC3GG TCGGTCGGCG
201 GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451 GTCGTCGCGG TATTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAA GAGGGGGGAG GCGAACCAGT
651 GTACGTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTCTGCG CATGTTTGGC
701 ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801 CAGCTTGTCG TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGCGCG
851 AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCSSA TGTATTCGGC
951 CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

a209.pep

```
1 MLRHLGNDEA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEHHDGE
51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVQGW IQYGFDDDG* NDNRPAFVAD
201 DVVQLVQPK EGGGEPVYFA VVFGQLQVVG DVCNCGGLW AGVEVDGGFG
251 FAPFWIAAKG TLTLVLYSL LRRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*
```

m209/a209 95.6% identity in 341 aa overlap

	10	20	30	40	50	60
m209.pep	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR					
a209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
a209	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
	70	80	90	100	110	120
m209.pep	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
a209	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
	70	80	90	100	110	120
m209.pep	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
a209	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
	130	140	150	160	170	180
m209.pep	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
a209	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
	130	140	150	160	170	180
m209.pep	IQYGFDDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
a209	IQYGFDDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
	190	200	210	220	230	240
m209.pep	IQYGFDDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
a209	IQYGFDDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
	190	200	210	220	230	240
m209.pep	AGVEVDGGFGFAPFWMAAKGTLTLVLYSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGFGFAPFWIAAKGTLTLVLYSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
m209.pep	AGVEVDGGFGFAPFWMAAKGTLTLVLYSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGFGFAPFWIAAKGTLTLVLYSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
m209.pep	CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX					

a209                    |||||  
                      CSIMPSQFVGVLRMYSASDLPLDASSSKSEKLTFWKLPSGVX  
                      310            320            330            340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

g211.seq  
 1    atgttgcgga   ttgctgctgc   caatcagttg   ggcggtcgaa   atggtgcggc  
 51    ggtgggaaac   ggggtcgata   agtttgggcg   tgggtctgat   aatcaggttg  
 101   agtttttggg   aggaaacctg   attgtagtcg   gcgcgtccgg   gcgtgccgct  
 151   gtaacggtag   ccgtaggcga   attcgagcgt   gcgtttgttg   tccttcagcg  
 201   agaagttacc   ttctttggcg   aagatgatgt   tgcgcgcgcc   gtttttgtcc  
 251   tgttcgcgca   ggaacaggtt   ttcatgatg   ccggattcgg   tgtcaaaggt  
 301   ttcgacgaaa   taaaccctgc   cgttgcgctt   gcccaagtta   ttgaactcgc  
 351   cggcttcac   caaagacaat   tcctgcttct   gttcaaaat   ttcggcatat  
 401   tcgcggctgc   gcagctctgc   ccacgggtatc   acccaaagct   gcattgacggc  
 451   aatcaggatg   gcaaacggca   cggcaaacgt   catgacgggg   cgtatccact  
 501   gtttcaacgc   caatccgcag   gatag

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

g211.pep  
 1    MLRIAAANQL   GGRNGAAVGN   GVDKFRGAD   NQVEFLEGNL   IVVGASGRAA  
 51    VTVAVAQFER   AFVVVQREV   FFGEDDVAA   VFVLFQEQV   FHDAGFGVKG  
 101   FDEINPAVAL   AQVIELAGFH   QRQFLLLQN   FGIFAAALC   PRYHPKLHDG  
 151   NQDGKRHGKL   HDGAYPLFQ   QSAG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

m211.seq  
 1    ATGTTGCGGG   TTGCTGCTGC   CAATCAGTTG   GCGGTCGGA   ATGGTACGGC  
 51    GGTGGGAAAC   GGGGTGATG   AGTTTGGGCG   TGGTGCTGAT   AATCAGGTTG  
 101   AGTTTTTGGG   AGGAAACCTG   ATTGTAGTCG   GCGCGTCCGG   GCGTGCCGCT  
 151   GTAACGGTAG   CCGTGCGCGA   ATTCGAGCGT   GCGTTTGTG   TCGTTCAGCG  
 201   AGAAGTTACC   TTCTTTGGCG   AAGATGATGT   TGTGCGCGCC   GTTTTGTGCC  
 251   TGTTCGCGCA   GGAACAGGTT   TTTTCATGATG   CCGGATTCGG   TATCGAAGGT  
 301   TTCGACAAA   TAAACCCTGC   CGTTGCGCTT   GCCCAAAGT   TTGAACCTGC  
 351   CTGCCTCCAC   CAAAGACAAT   TCCTGCTTCT   GCTTCAGGAT   TTCAGCGTAT  
 401   TCGCGGCTGC   GTAGCTCTGC   CCACGGGTATC   ACCCAAAGCT   GCATGACGGC  
 451   AACCAAAACG   GCAAACGGCA   CGGCAAAGT   CATCACCGG   CGTATCCATT  
 501   GTTTCAATGC   CAATCGCAG   GATAG

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

m211.pep  
 1    MLRVAAANQL   GGRNGTAVGN   GVDEFGRGAD   NQVEFLEGNL   IVVGASGRAA  
 51    VTVAVAQFER   AFVVVQREV   FFGEDDVAA   VFVLFQEQV   FHDAGFGIEG  
 101   FDKINPAVAL   AQTVELACLH   QRQFLLLQD   FSVFAAAXLC   PRYHPKLHDG  
 151   NQNGKRHGKL   HHRAYPLFQ   QSAG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

m211/g211

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
g211	MLRIAAANQLGGRNGAAVGNVVDKFRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVAAVFVLFQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH					

```
a211.seq
1  ATGTTGCGGG  TTGCTGCTGC  CAATCAGTTG  GGCGGTGCGA  ATGGTACGGC
51  GGTGGGAAAC  GGGGTGCGAT  AGTTTGCGCG  TGGTGCTGAT  AATCAGGTG
101 AGTTTTTGGG  AGGAAACCTG  ATTTGATGCG  GCGCGTCCGG  GCGTGCCGCT
151 GTAACGGTAG  CCGTGCGCGA  ATTCGAGCGT  GCGTTTGTG  TCGTTCAGCG
201 AGAAGTTACT  TTCTTTGGCG  AAGATGATGT  TGTGCGCCGC  GTTTTGTGCC
251 TGTTCGCGCA  GGAACAGGTT  TTTTCATGAT  CCGGATTCGG  TATCGAAGGT
301 TCGACAAAA  TAAACCTGCG  CTTTGCGCTT  GCCAAACTG  TGTAAACGCG
351 CTGCCTCCAC  CAAAGACAAT  TCCTGCTTCT  GCTTCAGGAT  TTCAGCGTAT
401 TCGCGGCTGC  GTAGCTCTGC  CCACGGTATC  ACCCAAAGCT  GCATGACGGC
451 AATCAAAACG  GCAAACGGCA  CGGCAAACCT  CATCACCGGG  CGTATCCATT
501 GTTTCATATG  CAATCCGCGA  GATAG
```

a211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDFEFGRGAD	NQVEFLEGNL	IVVGASGRAA
51	VTVAQAQFER	AFVVVQREVT	FFGEDDVVAA	VFVLFAQEQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACLH	QRQFLLLQD	FSVFAAA*LC	PRYHPKLHDG
151	NONGKRHGKLL	HHRAYPLFOC	OSAG*		

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGN	GVDEFGRGADNQVEFLEGNLI	VVGASGRAAVTVAVAQFER			
a211	MLRVAAANQLGGRNGTAVGN	GVDEFGRGADNQVEFLEGNLI	VVGASGRAAVTVAVAQFER			
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVA	AVFVLF	FAQEQVFHDAGFGIEGFDKIN	PAVALAQTVELAC	HLH	
a211	AFVVVQREVTFFGEDDVVA	AVFVLF	FAQEQVFHDAGFGIEGFDKIN	PAVALAQTVEPAC	HLH	
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLC	PRYHPK	LHDGNGN	KRRHGK	LHHRAYPL	QCQSAGX
a211	QRQFLLLLQDFSVFAAAXLC	PRYHPK	LHDGNGN	KRRHGK	LHHRAYPL	QCQSAGX
	130	140	150	160	170	

g212.seq (partial)						
1	atggacaatc	tcgatgagg	cggcattccc	gacatccgca	cactcgacca	
51	aaccatccgc	aaacacgcac	acccgctcaa	cctgatgttc	tgccctccccg	
101	ataatcagat	tcccgatatt	caaacgcgca	aagatgtctc	ggactcgga	
151	tgccgtctga	agcacgcttt	ggatcaggca	accagtgcc	tcaggttcga	
201	cagcatcaac	ctcatogaac	acatcctgcc	cgatgtccgc	ttctggctgg	
251	ttcccccttc	acgcacccgc	cgctctgcag	aacacttcca	ccacatttcc	
301	tggcagaccg	agaccatccc	gcaaacccga	agcaagtcg	acaaacctcg	
351	gtttgcactt	ccacaacatc	ccgaacggaa	aaaaaccgaa	cacqctctcc	



```

401 tcatcggtgc aggcattgcc ggccatcgca ccgcccacgc cttagcatca
451 caccgcatctt cgtttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggtc acggctacac caaacgcctg
601 ctccggacaca tccctgcccga ctccgacact tggggcgcca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccc aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcaccctcct cagccatccg ctgatcgaa tatatgaaaa cacaacgtta
901 acccgcatctt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagccctt
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacccggcc tcacaccgct caccctgttt tccgaacaac tgcgttgccg
1101 cgtttcaggc gaaagctaca tcagcccgct gtggcacgga ctgcaactgct
1151 accggcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacccgca agcattggca cacttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQTIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFFHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAFALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSABE
251 EKIAIGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCVAVG ESYISPSWHG LHCYGASFIP NSSNTGWNBA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCCTCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GCGCGGGCAA CCGCCACGCG CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CACGCGCAAC CGCAAGGGC TGCTCTACGC CAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTGCGCGCT ACGGCTACAC CAAACGCCCTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTGCTCC
851 GCACCCCTCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCGAACAAC TGCCTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCGA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGACACACC TTCCCTTAGT CCGCGCACTC
1351 GCGGACATTG CCGCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AACTACCGC ATCGACACCC CATGCCATA CCGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CCGCACCCGC GGAATCGCCA CCGCCCCAT CTGCGCCGCC

```

1501 GmCAwTGCAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT  
 1551 gCGCCACGCC cTACACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA  
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep

1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE  
 51 CRLKHRLDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHPHHIS  
 101 WQTEAIPQTE SKPDKPWFAL PQTSEKQKPE HILVIGAGIS GAATAHALAS  
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL  
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA  
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTFL  
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG  
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA  
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDS PDHPLVLGAL  
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA  
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng)

from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII	CLPDNQIPDFQTAQDASDAECRLKHRLDQA				
g212	MDNLVWDGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRKHRLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSEKQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	PQTSEKQKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTFL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEASNRQALAHLPALSESSE					

490

```

      |||||
g212  SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSNTGWNEAEEASNRQALAHLPALAESL
      370      380      390      400      410      420

      430      440      450      460      470      480
m212 . pep  FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
      |
g212        F

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

```

a212 . seq
1  ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51  AACCATCCGC AAACACGCAC ACCCGCTCAA CCTGATTGTC TGCCTCCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAC AAGATGCTTC GGACCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ACCCAGTGCC TCCAGTTTCA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCCTGCACG AACACTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCG ACAAACCTTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGGCATATCC GCGCGGGCAA CCGCCACGCG CTTAGCATCA
451 TACGGCATT T CCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCCG
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAAAC CGAACTGCTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACATA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAAAC ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCAGGCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACACG CCCTACGCCG AACCATTATG
801 CGGACTGTTT TGGCAGTACG CGGTATGGCT CAATCCTCCC ACATTGCTCC
851 GCGCCCTCCT CAGCCATCCG CTCATTGGAC TACACGAAGA CACACCGTTA
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCGGA AACCAACCTC GCCACCTGCG CCCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACGCTC CACCCCGTTT TCCGAACAAC TGCGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCAGGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGGACCAAC TTCCCTAGT CGGGCGACTC
1351 GGCGACATTG CCGCTATGCA ACAAACCTAC GCCAACTCG CGCTGGACAA
1401 AAATATCGC ATCGATGCCC CCTGCCGTA CCTGCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCAT CTGCGCCGCC
1501 CGCGTTGAG CCGAAATCCT AGGCTTGCCC CATCCCTCT CAAAACGCCT
1551 GCGCCACGCC CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

```

a212 . pep
1  MDNLAWNGIP DIRTLDQFIR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51  CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKPDKPWFAI POTSERQKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITQAEA
251 EKIAGIPLNT PYAEPLCGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTPL
301 TDISHDGEKW IASTPNGTFT ATHIITYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
401 EAASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDSPDHLPLVGAL
451 GDIAAMQQTY AKLALDKNYR IDAPCPYLPN AYANTAHGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIRA IVRRKDLTP*

```

m212/a212 93.7% identity in 539 aa overlap

```

      10      20      30      40      50      60
m212 . pep  MDNLVWDGIPDIRTLDQAIRKHAPPLNLIICLPDNQIPDFQTAQDASDAECRLKHLRLDQA
      |||||:|||||: ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||
a212        MDNLAWNGIPDIRTLDQTIRKHAEPPLNLIVCLPDNQIPNFQTAQDASDAECRLKHLRLDQA

```

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	MQCLQFDSINLIEHILPDVRFWLVPSPSRTHHLHEHFHHISWQTEAIPQTESKPKPWFFAL					
	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	PQTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGCVWLNPPAFVRTLLNHPGLGLHEDTPL					
	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	TDISHDGEKWIASTPNGTFTATHIYCTGANSPLYLPETNLAALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	SEQLRCAVSGESYISPSWHGLHCYASFI PNSSHTGWNEAEASNRQALAHLPALSES					
	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN					
	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	AYVNTAHGTRGLATAPICAAAXAAQIXGLPHFPXQRLRHALHPNRTIIRAIIVRRKDLTPX					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

g214.seq

```

1  atgatacaaa agatatgtaa gctatattgtt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtaacgctc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaagcgggcg aatccgtgag ggcggaaggt
251 tcgcccgctc gcttcagcca aacgttggac gggggcacaag ggacggtgag
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaaggtgag
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

```

1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQRTTFS
51  GNVIIROGTL NISASCVNVT RGRQRRRIRE GGRFARPLQP NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQHQH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTACGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGTAAT GCCAAAGTAC AGCGGCGCG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGRQRRRIRE GGRFASPLQP DIGRRQRHGA
101 RTGKQRCLEI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQHQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

m214/g214

	10	20	30	40	50	60
m214.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS L	DQANQSTTFS	GNVVIRQGT L
g214	MIQKICKLFV	LIVIFATSPA	FALQSDSRRP	IQIEADQGS L	DQANQRTTFS	GNVIRQGT L
	10	20	30	40	50	60
m214.pep	NISAARVNVT	RGRQRRRIE	REGGRFASPL	QPDIGRRQRH	GARTGKORCL	FI CRQHRSLNRX
g214	NISASCVNVT	RGRQRRRIE	REGGRFARPL	QPNVGRGQR	CGARSGKQRY	LFLRRKHCRSDRQ
	70	80	90	100	110	120
m214.pep	CQSTARRRCR	RRCGDYIQH	QNRSLYHQHQ	HKI		
g214	CQSAARRRRC	RRCGHYLQHQ	NRSLYHQHQ	HEIGCEIRFQN	RQGQRRHPAF	KHTKNRITPM
	130	140	150	160	170	180
m214.pep	PSETETQFRR	HLPTEMPRRD				
g214	PSETETQFRR	HLPTEMPRRD				
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGC AAAGCGGCG AATCCGTGAG GCGGGAAGGT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GCGGCAAAG GCACGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

493

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTGCG CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLV LIAFFSASPA FALQSDSRQP IQIEADQGS LQANQSTTF S
 51 GNVVIRQGT L NISAARVNV T RGXQRRRIE GGRFASPLQ F DIGRRQRHG A
101 RTGQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDIYQH Q NRSLYHQRH
151 KIRRKIRFQI RQGQRRYPAF EYAKIRIIFM PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLV	LIAFFSASP	FALQSDSRQ	PIQIEADQS	LQANQSTTF	SGNVVIRQGT
a214	MIQKICKLV	LIAFFSASP	FALQSDSRQ	PIQIEADQS	LQANQSTTF	SGNVVIRQGT
	10	20	30	40	50	60
m214.pep	NISAARVNV	TRGRRRIE	REGGRFAS	PLQPDIGRR	QRHGARTG	KQRCLEFICRQHRSLNRX
a214	NISAARVNV	TRGRRRIE	REGGRFAS	PLQPDIGRR	QRHGARTG	KQRCLEFICRQHRSLNRX
	70	80	90	100	110	120
m214.pep	CQSTARRRC	RRRCGDIY	QHQNRSLY	HQRQHKI		
a214	CQSTARRRC	RRRCGDIY	QHQNRSLY	HQRQHKI		
	130	140	150			
m214.pep	PSETXTWFG	RHLPTEIL	KRYLX			
a214	PSETXTWFG	RHLPTEIL	KRYLX			
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTGTG TTAATTGTAA TTTTGCAC
 51 TTCTCCCGCT TTGCCCTTC AAAGCGACAG CAGACGGCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTCCG CCTCGCGCT
201 CAACGTCACA CGCGCGGCA AAGCGGCGA ATCCGTAGG GCGGAAGGT
251 CGCCCGTCCG CTTAGCCAA ACGTTGGACG GGGGCAAAGG GACGGTCCG
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CGGCAGCAG
451 AAATCGGGTG CGAAATCCG TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLV LIVIFATSPA FALQSDSRP IQIEADQGS LQANQSTTF S
 51 GNVVIRQGT L NISASRVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGT V R
101 GQANNVTYSS AGSTVLTGN AKVQRGSDVA EGAVITYNK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTGTG TTAATAGCAT TTTTTCGGC
 51 GTCCCCCGCT TTGCCCTTC AAAGCGACAG CAGGCAGCT ATTCAGATG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAGCAC CACATTAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCT

```

494

```

201 CAATGTTACA CGCGGCGGCA AAGCGGCGCA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACC GGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQEADQGS L DQANQSTTF
51 GNVVIRQCTL NISAARVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 QQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
151 KSGAKSASKS GRVSVVIQPS STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQEADQGS L DQANQSTTF GNVVIRQCTL					
g214-1	MIQKICKLFV LIVIFATSPAFALQSDSRRP IQEADQGS L DQANQSTTF GNVVIRQCTL					
	10	20	30	40	50	60
m214-1.pep	NISAARVNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGTVR GQANNVAYSS AGSTVVLTGN					
g214-1	NISASRVNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGTVR GQANNVYSS AGSTVVLTGN					
	70	80	90	100	110	120
m214-1.pep	AKVQRGGDVA EGAVITYNTK TEVYTISGST KSGAKSASKS GRVSVVIQPS STQKSEX					
g214-1	AKVQRGGDVA EGAVITYNTK TEVYTINGST KSGAKSASKT GRVSVVIQPS STQKTEX					
	130	140	150	160	170	

g214-1/p38685

sp|P38685|YHBN ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)  
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF\_0185 [Escherichia coli]  
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185  
Score = 97.1 bits (238), Expect = 6e-20  
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQP IQEADQGS L DQANQSTTF GNVVIRQCTL NISAARVNVT R--GGKGG 76

PAFA+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G

Sbjct: 24 PAFAVTGDTPQPIHIESDQQLDMQGNVVTFTGNVIVTQGTIKINADKVVTTRPGGEQK 83

Query: 77 ESVRAEGSPVRF SQ TLDGGKGTVR GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVIT 136

E + G P F Q D GK V G A + + Y A VVLTGNA +Q+ +G IT

Sbjct: 84 EVIDGYGPATFYQMDNGK-PVEGHASQMHYELAKDFVLTGNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142

Y K +

Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1 ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGGC
51 GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGCCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCT
201 CAATGTTACA CGCGGCGGCA AAGCGGCGCA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACC GGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQEADQGS L DQANQSTTF

```

495

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR  
 101 GOANNVAYSS AGSTVVLTGN AKVORGGDVA EGAVITYNTR TEVYTISGST  
 151 KSGAKSASKS GRVSVVIQPS STQKSE\*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLI	AFFSASP	AFALQSDSRQFIQIEADQGS	LDQANQSTTFSGNVVIRQGTI		
m214-1	MIQKICKLFVLI	AFFSASP	AFALQSDSRQFIQIEADQGS	LDQANQSTTFSGNVVIRQGTI		
	10	20	30	40	50	60
a214-1.pep	NISAARVNVT	RGGKGGESV	RAEGSPVRFSSQ	TLDGGKGTVR	GOANNVAYSS	AGSTVVLTGN
m214-1	NISAARVNVT	RGGKGGESV	RAEGSPVRFSSQ	TLDGGKGTVR	GOANNVAYSS	AGSTVVLTGN
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGESV	RAEGSPVRFSSQ	TLDGGKGTVR	GOANNVAYSS	AGSTVVLTGN
m214-1	NISAARVNVT	RGGKGGESV	RAEGSPVRFSSQ	TLDGGKGTVR	GOANNVAYSS	AGSTVVLTGN
	70	80	90	100	110	120
a214-1.pep	AKVORGGDVA	EGAVITYNTR	KTEVYTISGST	KSGAKSASKS	GRVSVVIQPS	STQKSEX
m214-1	AKVORGGDVA	EGAVITYNTR	KTEVYTISGST	KSGAKSASKS	GRVSVVIQPS	STQKSEX
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq

```

1  atgaaagtaa gatggcggta cggaattgcg ttccattga tattggcggg
51  tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
151 ttggacggaa ggcggtttga cgaacaggga tacttgaaag aacatttgag
201 cgcgaaaggt gcgaaacagt ttccgaaaaa cagcgacatc cattttgatt
251 cgccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc tttttaaaaa
351 caacgttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaaag
401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaac
451 gatacgcttg tcagtttcca atatggcgcg tcgcaaggtc aggcgggcgg
501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
551 aagccgcgat ttatgataca aaagatatgt aa
```

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep

```

1  MKVRWRYGIA FPLILAVLGL SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS
51  LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPHLVFF QEGRLLYEVG
101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETEKLH VDTESQYAQT
151 DTPVVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAIYDT KDM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)

```

1  ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
51  CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG CGCGAAGGGC
151 GCGAAACAGT TTCCGGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
201 CGTGTTCCTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG
301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAAAC GATACGCCTG
401 CAGTTTCCA ATATGGTGCA TCGCAGGTC AGGCGGGCGG CATGACTTAC
451 GACCACAwWA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
501 TTATGATACA AAAGATATGT AA
```

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)

```

1  ..SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
51  AKQFPENSDI HFDSPHLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNVV
101 LTKTADGKRQ AGKVEAEKLH VDTESQYAQT DTPVVSFQYGA SHGQAGGMTY
```



496

151 DHXTGMLNFS SKVKATIIYDT KDM\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
g215	MKVRWRYGIAFPLILAVALGSL	SAWLGRISEVEIEEVRLNPDEPQYTM	MDGLD	GRRFDEQG		
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQ	EGRLLYEVGS	DEAVYHTENKQVLFKNNVV	
g215	YLKEHLSAKGAKQFP	ENS	DIHFDS	PHLVFFQ	EGRLLYEVGS	
	70	80	90	100	110	
	110	120	130	140	150	
m215.pep	LTKTADGKRQAGKVEAE	KLHVD	TESQYAQ	TDT	PVSFQYGASHGQAGG	
g215	LTKTADGRRQAGKVET	EKLHVD	TESQYAQ	TDT	PVSFQYGASHGQAGG	
	130	140	150	160	170	
	170					
m215.pep	SKVKATIIYDTKDMX					
g215	SKVKAIIYDTKDM					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTTGA	TATTGGCGGT
51	TGCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GGCGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTTGAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTCTGACT
251	CACCGCATCT	CGTGTCTTTC	CAAGAAGGCA	GGTTGTTGTA	CGAAGTCGGC
301	ASCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTT	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCAAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAAA	CAGGCATGTT	GAACCTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence &lt;SEQ ID 756; ORF 215.a&gt;:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTM
51	LDGRRFDEQG	YLKEHLSSKG	AKQFPESDI	HFDSPHLVFF	QEGRLLYEVG
101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLH	VDTESQYAQT
151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIIYDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
a215	MKVRWRYGIAFPLILAVALGSL	SAWLGRISEVEIEEVRLNPDEPQYTM	MDGLD	GRRFDEQG		
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQ	EGRLLYEVGS	DEAVYHTENKQVLFKNNVV	

q216.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

q216.pep (partial)

The following partial  $\overline{\text{DNA}}$  sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

1	ATGGCAATGG	CAGAAAACGG	AAAATATCTC	GACTGGGCAC	GCGAAGTGTT
51	GCACGCCGAA	GCGGAAGGCT	TGCGCGAAAT	TGCAGCGGAA	TTG <sub>6</sub> ACAAAA
101	ACTTCGTCCT	TGCGGCAGAC	GC <sub>6</sub> TTGTTGC	AGTGCAAGGG	CAGGGTCGTT
151	ATACACGGGA	TGGTCAAGTC	GGGACATATC	GCGGCCAAAA	TGGCGCGCAAC
201	TATGGCGCTCG	ACCGGCACGC	TCGCGTTTTT	CGTCCACCCCT	GCGGAAGCGGG
251	CACACG <sub>9</sub> CGA	TTTGGGTATG	ATTGTGGACA	rCGACGTGGT	CGTCGCGATT
301	TCCAATTCCG	GCGAAAGCGA	CGAAATCGCC	GCCATCATCC	CCGCACTCAA
351	ACGCAAAAGC	ATCACGCTTG	TCTGCATCAC	CGCCCGCCCC	GATTCAACCA
401	TGGCGCGCCA	TGCCGACATC	CACATCACCG	CGTCGGTTTC	CAAGAAGGCC
451	TGCCCGCTGG	GGCTTGCCCC	GACCAACAGC	ACCACCGCCG	TATCGGCTTT
501	GGGCGATGCG	TTGGCGGTCG	TCCT <sub>6</sub> GCTGCG	C <sub>9</sub> cACGCGCG	TTCACGCCCG
551	ACGATTTCGC	CTTGAGCCAT	CCTGCCGGCA	GCCTCGGCAA	ACGCTACTTT
601	TTGCGCGTTG	CCGACATTAT	GCACA <sub>6</sub> AAAGC	GGCGGCCTGC	CTGCGCTCCG
651	ACTCGGCACG	CCCTTTAAAG	AAGCCATCGT	CAGCATAGTG	GA <sub>6</sub> AAAGGGC
701	TGGGCTATGTT	GGCGGTAAAG	GACGGGCAAG	GCGCTCTGAA	AGCGGTATTC
751	ACCGACGGCG	ATTTGCGCCG	CCTGTTTCAA	GAATGCGACA	ATTTTACCGG
801	TCTTTGATA	GACGAAGTCA	TGCATACGCA	TCCTAA <sub>6</sub> AACC	ATCTCCGCCG
851	AACGCTCTCG	CACCAAGCC	CTGAAAGTCA	TGCAGGCAAA	CCATGTGAAC
901	GGGCTTCTGG	TTACCGATGC	AGATGGCGTG	CTGATCGGCG	CGCTGAATAT
951	GACGACCTG	CTGGCGGCAC	GGATTGTATA	G	

This corresponds to the amino acid sequence <SEO ID 760: ORF 216>:

m216.pcp

1 MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAD ALJHCKGRVV

Homology with a predicted ORF from *N. gonorrhoeae*

m216/q216

```

              70          80          90          100          110          120
m216.pep    TMASTGTPAFFVHPAEAAHGDLGMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVCI
              ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g216                MISISSVPSDEITAIIPALKRKDITLVCI
                      10          20          30

              130          140          150          160          170          180
m216.pep    TARPDSMTARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g216    TARPDSMTARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              40          50          60          70          80          90

              190          200          210          220          230          240
m216.pep    ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g216    ALIHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRL
              100          110          120          130          140          150

```

a216.seq

1	ATGGCGATGG	CAGGAAACGA	AAAATATCTT	GATTGGGCAC	GCGAAGTGT
51	GCACACGCAG	GCGGAAGGCT	TGCGCGAAAT	TGCGGCGGAT	TTGGACGAAA
101	ACTTCGCCCT	TGGCGCGGAC	GCGTGTGTTC	GATGCAAAAG	CAGGGTCTTT
151	ATTCACGGCA	TGGCGCAAGTC	GGGACATATC	GGGCGCAAAA	TGGCGCGCAA
201	CATGGCCTCG	ACCGGCACGC	CCGCGTTTTT	CGTCCACCCT	GCGGAAGCGG
251	CACACGCGCA	TTTGGGCGAT	ATTGTGGACA	ACGACGTGTT	CGTCCGATTT
301	TCCAATTCCG	GTGAAACGCA	CGAAATCGCC	GCCATCATCC	CCGCGCTCAA
351	ACGCAAAAGT	ATCACGCTTG	TCTGCATCAC	CGCCCGCCCC	GATTCAACCA
401	TGGCGCGCCA	TGCCGACATC	CACATCACGG	CGTCGGTTTC	CAAAGAAGCC
451	TGCCCCGTCG	GGCTTGCCCC	GACCAACGAC	ACCACCGCGG	TTATGGCTTT
501	GGCGGATGGT	TGGCGGCTTG	TCCTGCTGCG	CGCCCCGCGG	TTACAGCCCG
551	ACGACTTCGC	CTTAGGCCAC	CCTGCGGGCA	GCCTCGGCAA	ACCGCTACTT
601	TTGCGCGTTG	CCGACATTAT	GCACAAAGGC	GGCGGCCTGC	CTGCCGTCGG
651	ACTCGGACAG	CCCTTGAAAG	AAGCCATCGT	CAGCATGATG	GAAAAAGGGC
701	TGGCGCATGT	GGCGGTAACG	GACGGGCAAG	GCCGTCTGAA	AGGCGTATTC
751	ACCGACGGCG	ATTTGCGCGG	CCTGTTTCAA	GAAATGCGACA	ATTTACACGG
801	TCTTTTCGATA	GACGAAGTCA	TGCATACGCA	TCCTAAAACC	ATCTCCGCCG
851	AACGTCTCGC	CACCGAAGCC	CTGAAAGTCA	TGACGGCAAA	CCATGTGAAC
901	GGGCTTCTGG	TTACCGATGC	AGATGGCGTG	CTGATCGGCG	CGCTGAATAT
951	GACACGACCT	TGGCGGCGCG	GATTTGTATA	G	

a216.pep

1	MAMAGNEKYL	DWAREVLHTE	AEGLREIAAD	LDENFALAAD	ALLHCKGRVV
51	ITSGMSGSGHI	GRKMAATMAS	TGTPACFFVHP	AEAAHGDGLGM	IVDNDVSVVAAI
101	SNMGSEDEIA	AIIPALKRKMD	ITLVCCITAPR	DSTMARHADI	HTIFASVSSVKE
151	CPLGLAPTTS	TTAVMALGDT	LAVVLLRARA	FTPDFFALSH	PAGSLGKRLLL
201	LRVADIMHKG	GGLPAVRGLT	PLKEAIVSMS	EKGLGMLAVT	DQGRKLNKGVFF
251	TDGDLRRRLFQ	ECDNFTGLSI	DEVMTHTPKT	ISAERLATEA	LKMOVANHVVH

301 GLLVTDADGV LIGALNMHDL LAARIV\*

m216/a216 97.2% identity in 326 aa overlap

m216.pep	MAMAENGKYLDWAREVLHAEAEGLREIAAELXKNFVLAADALLHCKGRVVITGMVKS	10	20	30	40	50	60
a216	MAMAGNEKYLDWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVVITGMKSGHI	10	20	30	40	50	60
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD	70	80	90	100	110	120
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD	70	80	90	100	110	120
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA	130	140	150	160	170	180
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA	130	140	150	160	170	180
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT	190	200	210	220	230	240
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT	190	200	210	220	230	240
m216.pep	DGQGRLLKGVFTDGDRLRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN	250	260	270	280	290	300
a216	DGQGRLLKGVFTDGDRLRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN	250	260	270	280	290	300
m216.pep	GLLVTDADGVLIGALNMHDLAARIVX	310	320				
a216	GLLVTDADGVLIGALNMHDLAARIVX	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcgcatg acgggttgggt gcggcaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctgagggt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccgga
151 acgcgccacc cattcgccga ccgtcgagg ttgcccgc atccgggcaa
201 tatccgacag gggttcgagg aaggcggaac aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgtgaca tccgtccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatcccca
401 tggacgttca aatcggaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgg aaacggcgca acacggcgcc gggttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcactccaac
551 gcataaaaaa acggttgccg gcggctgatt ttcaagtcgg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgtata gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence &lt;SEQ ID 764; ORF 217.ng&gt;:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKRBHFAD FKTAQQQVGH ALQRIKKRLP AADFHVRNGI

```

1	ATGGCGGATG	ACGGTGTGCG	GCGGCAACTG	TCCGGAAAAAT	TGCGCCAATT
51	CGGTTTCCCG	CTrCCATTAG	ACCAATTCTGT	TTTCAAGGTT	TTGGACTGAC
101	TTTTTGGTCAT	CGGCTTTTCG	TTGGAACAAT	GTTTCAAGCA	AATCCCGGCA
151	ACGCGGCCACC	CATTCCGCCGA	CCGTTTCGGG	CTGCGCCCAT	ATCCGTACAA
201	TATCCGTCAG	GGTTTCGAGG	AAGGCGGCAA	AACGTCGGA	CATGCGCGTT
251	TGATTACAGT	CGGCATACCA	CGCGCTGACA	TCCTGCCACA	TCGGATTGCC
301	GCCTTTTGGG	AGCATCCAGC	CCAATATCAT	CGGTTCTACC	GCTCGCTTCC
351	AGGTGAACAG	CTGATCCGTG	CCGCGCCGCA	TTTCTCCGTG	CAAAACCCAG
401	TGAGCGTTCA	AATCGGCAAC	CATGTCTGTG	AAAGCGGTA	AATGCTCTCT
451	AGTCAGTCCG	AAACGGCGCA	ACACGGGCGC	GGTTTCTAAA	AGCACAAAGCA
501	CTTTATCGAC	TTCAAATCGG	CTTTCCAACA	AGTCGAACAG	GCATGACAAA
551	GCATGAAACA	GCGGTTTGGG	GCGGCTGATT	TTCACGTCTG	ACACGGAATA
601	CGGCAATGCC	TGGGTCACCg	GcgtGCGCCT	TCCGAACACG	GCTTCGATAA
651	AAGGCGTATA	GGATTGATA	TTCCGGGGTA	A	

1	MADDGVRRQL	SGKLRQFGFR	<u>LPFDPFVFKV</u>	<u>LDXLLVIGFS</u>	LEQCCKQIPA
51	TRHPFADRCG	LPPYPYNIRQ	GFEEGGKTSE	HGGLIHVGIP	RADILPHRIA
101	AFGQHPAQYH	AFYRLLPGEQ	LIRAAAHFSV	QTPVDVQIGN	HVVQKRXIVL
151	SQSEATQHGK	GFXKKHKHFD	KFSAFQOQVE	AQXSMKQRLA	AADFHVXHGI
201	ROCLRTLGLRL	SEHGFDKRR1	GFDRG*		

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m217.pep	MADDGVRRLQSLGKLRQFGFRLPFDPFVFKVLDDXLLVIGFSLEQCCKQIPATRHHPFADRCG					
	:           :             :         :					
g217	MADDGLLRLQLSEKPSQSALFLPFDPPVFVEVLDCLLVIGPGLKQCCKQIPATRHHPFADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIROGFEEGGKTSEHGGLIHVGIPRADILPHRIAAFGQHHPAQYHAFYRLLPGEQ					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVAAFGQHHPAQYHTVCRLLPKGKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFVSQTPVDVQIGNHVVKRXIVLSQSETAQHGRGFXXKHIFIDFKSAFQQVEQ					
	:           :             :					
g217	LIRAAAHFVSQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKAFAQQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAADFHVXHGIHQCLRTGLRLSEHGFDKRRIGFDIRGX					
	:					
g217	ALQRIKKRLPAADFHVNRNIGIRQCLRLAGLRLSEHGFMKRRIGFDIRG					
	190	200	210	220		

1	GTGGCGGATG	ACGGTGTGCA	GCGGCAACTG	TCCGGA A AAT	TGCGCAATT
51	CGGTTTCCGC	CTGCCATTG	ACCAATTCTG	TTTCGAGGCT	TTGGACTGCC
101	TTTGTGTCAT	CTTCTCTCGAC	TTGGAACAAT	GTTTCAAGCA	AATCCCGGCA
151	ACGCGCCACC	CAGTCGTCAA	CCGTGCGCAG	TGCGCGCCAT	ATCCGTACAA

501

```

201 TATCCGTCAG GGT'TTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTCTTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGT'TCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC GCGCCGG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

a217.pep

```

1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCFKQIPA
51 TRHPFVNRRL LPPYPYNIHQ GFEEGKTSQ QGGLVHVGIQ RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

	10	20	30	40	50	60
m217.pep	MADDGVRRQLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCFKQIPATRHPPFADRCG					
a217	VADDGVQRQLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCFKQIPATRHPPFVNRRL					
	10	20	30	40	50	60
m217.pep	LPPYPYNIHQGFEEGKTSQGGGLIHVGIQPRADILPHRIAFAFGQHPAQYHAFYRLLPGEQ					
a217	LPPYPYNIHQGFEEGKTSQGGGLVHVGIQPRADPLPHRIAFAFGQHPAQYHAFYRLLPGEQ					
	70	80	90	100	110	120
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFQKHKHFIDFKSAFQQVEQ					
a217	LIRAAAHFSVQTPADVQIGNHVQKRXIVLSQSEMAQHGRGFQKHKHFIDFKSAFQQVEQ					
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFQKHKHFIDFKSAFQQVEQ					
a217	LIRAAAHFSVQTPADVQIGNHVQKRXIVLSQSEMAQHGRGFQKHKHFIDFKSAFQQVEQ					
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIRIGFDIRGX					
a217	AXQSMKQRLSAADFHIRNGIRQCLRAGLRLSEHGFDKRRIRIGFDIRGX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

g218.seq

```

1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgccgcg
51 caatcagggt tggatcaca ctatggatga aatccacggc gatatgatgc
101 tcggtgcggc aggcgattat cttttggaaa cggcagcttc actgaccatt
151 attatggttg tcagcggcgt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tggtgccgga
251 atctgcacgg cgcgtttgga acttgggtgt cgttgatttt actgtcgttc
301 tgccctgtcg gtattgcttg ggcaggtatt tggggcgcca aattcgtgca
351 ggcttggaat cagttcccgg ccggcaaatg ggggtgtcgaa ccgaaccccg
401 tttcaatcgt gccgaccac ggcgaggtat tgaatgacgg caaggttaag
451 gaagtgcggt ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccaataac attggaaacc
551 gtcgaccgtt tcgcgcgga aatcggtttc aaaggcggtt atcagttgaa
601 tttgcccaaa ggcgaggacg gggatggac tttgtcgag gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

g218.pep

```

1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAG NRRFORALSVE  
 201 FAQRRGRGMD FVAGFYEL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq  
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCA3TA CCATGCCCGG  
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC  
 101 TCGGTGCGGC AGGCGATTAT CTTTGGAAA CGGCAGCTTC ACTGACCATT  
 151 ATTATGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGC GCGGCAT  
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAr GGC GCGTCTCT TGGTGGCGGA  
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTC  
 301 TGCCTGTCGG GTATTGCTTG GCGGGTATT TGGGGCGGCA AGTTCGTACA  
 351 GGCTTGGAGT CAGTTCCTG CCGGTAAATG GGGTGTGCAA CCGAACCCCG  
 401 TTTCAGTCGT GCCGACCCAC GCGAGGTAT TGAATGACGG CAAGGTTAAG  
 451 GAAGTGCCGT GGGTTTTTGA GCTTACGCCT ATGCTGT'TT CAGGGACGac  
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAACCG  
 551 TCGACCGCTT TCGCGCGnGA AATCGTTTC AAAGGGCGTT ATCAGTTGAA  
 601 TTTGCCCAA GCGGAGGACG GCGTATGGAC TTTGTGCGAG GATTCTATGA  
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep  
 1 MVAVDPYTAK VVSTMPRNQG WYYTMDEIHS DMMLGAAGDY LETAASLTI  
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRRFORALSVE  
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQG WYYTMDEIHS DMMLGAAGDY <u>LETAASLTI</u> IMVVSGLYLW					
g218	MVAVDPYTAKVVNTMPRNQG WYHTMDEIHG DMMLGAAGDY <u>LETAASLTI</u> IMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKGXARS WWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQRGIKAMLLPKSRARS WWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVLELTPMPVSGTTVGKDGINPDEPMT					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVLELMPMPVSGTTVGENGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRRFORALSVEFAQRRGRMD FVAGFYEL					
g218	IGNRRPFRAGNRRFORALSVEFAQRRGRMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

## a218.seq

```

1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51 CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAAAT GGGTGTGCAA CCGAACCCTG
401 TTTCACTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTGGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTCGAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

## a218.pep

```

1 MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51 IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLF
101 CLSGIAWAGI WGGKFVQAWS OFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQALSAE
201 FAQRRGRMD FVAGFYEL

```

## m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMD	EHSDMMLGAAGDYLLETAASLTIIMVVSGLYLW				
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS	DMMLGSTGDYLLLETAASLTIIMIISGLYLW				
	10	20	30	40	50	60
	70	80	90	100	110	120
m218.pep	WVKRRGIKAMLLPSKXARSWWRNLHGT	FGTWVSLILLFCLSGIAWAGIWGGKFVQAWS				
a218	WVKRRGIKAMLLPPKGRARSWWRNLHGAF	GTWVSLILLFCLSGIAWAGIWGGKFVQAWS				
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVVPTIHGEVLNDG	KVKEVPWVLELTPMPVSGTTVGKGINPDEPMT				
a218	QFPAGKWGVEPNPVSVVPTIHGEVLNDG	KVKEVPWVLELTPMPVSGTTVGKGINPDEPMT				
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQALSAEFAQRRGRMD	FVAGFYEL				
a218	LETVDRFARXNRFQALSAEFAQRRGRMD	FVAGFYEL				
	190	200	210			



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1  atgacggcaa ggtaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt ggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaccgctc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcggttatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtccgaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatattatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggt ggagcgtggt gggaacgct gtgttctgcc
401 ttgccgtgat tttatcggc atcagcggct gcgtgatgtg gtggaaacgc
451 cgtccgtccg gcgtggcggg cattgttctt ccggcgcaaa aaatcaaaact
501 gcccgtcttg tggcgatgg cattgccgct gctgttgatt gcaactgctt
551 tcccgaccgc gctgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgtgtgctc ggattccctg gttgaggaaa tggtttaaata ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1  MTARLRKCRG FWSLCLCLSQ GRLWVKTALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV VFCLAVIFIG ISGCVMWWR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLEPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1  ATGACGGCAA GGTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGaCyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTTC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCCGACCGCA
251 CGGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTG GCGGAACGTC TTGTCTGCC
401 TTGCCGTGAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTGCG GGATTCCTGT TTTGAGGAGA TGGTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1  MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTSRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWWR
151 RPTGAVGIVP PAQKVLPVW WMMALPLLAI ALLEPTSLA IAVIWLLDTL
201 LLSRIPVLRR WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPSALRGEIGFKGRYQLNLPKG					
g219	MTARLRKCRGFWSLCLCLSQGRLWVKTALTPPSPITLETVDREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
g219	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG					

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219 . pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	:     :     :     :     :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMMWKRRPSGAVGIVPPAQKIKLPVWAMALPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219 . pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	:     :     :     :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219 . seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTGC GCGG .GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CCGTGACATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTG GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCGG GCGCGGTGGG CATGGTTCCG CCGGCGCAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTGTGCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219 . pep
1  MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*

```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219 . pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSALRGEIGFKGRYQLNLPKG					
	:     :     :     :     :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219 . pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	:     :     :     :     :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219 . pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	:     :     :     :     :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPSGAVGMVPPAQKIKLPVWAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219 . pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	:     :     :     :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

```

g221.seq
1  atgcacgacc  acggcgcccat  ggatcgccgc  ctccccgctt  tcggaagttc
51  gatcgggcga  gccgtaaatc  adatcgacgc  tgacggattc  gaacctcgcc
101  tcacggcgcg  catcgatgac  ttctttggtt  tcttcgtatg  ttctgatgcg
151  gttgactgcc  gcctgcactt  tggggtcgaa  atcctgaatg  ccgacgctca
201  tgcggttgaa  gccgagtcgt  ccgagcatga  ggacgggtgc  gcggctgact
251  ttgcgcgggt  cgatttcgat  ggaatattcg  ccggacggbt  tcagttcgaa
301  atgttttcgg  atcatgcgga  agacacgttc  gatctgtctc  tcgctcaaaa
351  aggtcggcgt  gccgcgcgcg  aagtcgagtt  gggcaagctg  gtgccgtccg
401  ttcagatgtg  gagcgcgcgc  ttccatttct  ttttcaagat  attcgatgta
451  ggtatcgcg  cggcttttgt  ctttgggtgat  gattttgttg  cagccgcagt
501  agtagcagat  ggtgttgcaa  aacggaatgt  gaatgtaaa  gaaagcggt
551  ttqtttaa

```

g221.pep

1	MHDHGAMDRR	LPAFGLSMRR	AVNXIDADGF	EPCLTGGIDD	FFGFFVALDA
51	VDCRLHFGVE	ILNADAHAVE	AESAHEHDGV	AADPARVDFD	GIFAGRQFPE
101	MFADHAEDTF	DLFVAQKGRR	AAAEVOLGKL	VPSQVMWSEQ	FHFFFKIFDV
151	GIGAAAFVFGD	DFVAAAVVAD	GVAKNRNVVK	GKREF*	

```
m221.seq
1  ATGGYGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGGTG ACCGCCCGCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCCGGG CTGACTTTGC GCGGGTCGAT TTCGATGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATC TGTTCTGTCG TCAAAAAGGt GCGTGCCcCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCCGT CCGTTCAGAT GTGAGCGAG CAGTTCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGCTTTGGT
451 GATGATTTTG TTTCAGCCGC AGTAGTAGCA GATGGTGTGT CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTTA A
```

```
m221.pep
1  MXVLMXRSLV  RQAVNQIDAD  GFEPFRFARRI  DDFGFFVFTL  DAVDRRLHFG
51  VEILNADAHA  VEAESAEHED  LVAADFARVD  FDGVFAGGDX  LEMFAYHAED
101 TFDLFLVAQG  ACPAEVLQGLK  LVPVSQMWSE  QFHFFFKIFD  VIGAAAFVFG
151 DDFVAAAVVA  DGVAAERNVNV  KGGKRFV*
```

**Homology with a predicted ORF from *N. gonorrhoeae***

m221/q221

```
mz21.pep      MXVIMXKRSLVQRQAVNQIDAGDFEPRFARRIDDFFGFFVTLDVDRLHFGVE  
                ||::||| |||||| | :: ||||| :||| |||||  
g221          MHDHGAMDRLRPAFGSLMRRVNXIDAGGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE  
               10    20        30         40           50       60
```

```
mz21.pep      ILNADAHAVEAESAEHEDGVAA DFARVDFDGV F AGDXLEMFAYHAETFDLFVA Q KGA -  
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
g221          ILNADAHAVEAESAEHEDGVAA DFARVDFDG I FAGRYQFEMFDAHE TFDL F VA Q KG RR  
               70     80        90         100            110      120
```

```
               120      130        140         150           160      170
```

507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
             |||||
g221        AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
             130      140      150      160      170      180

m221.pep    GKRFBVX
             |||||
g221        GKRFBVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51 CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACCTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGCGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTCTTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1  MVVLMRLSLV RQAVNQIDAD GFEPFRARRI DDFGFFVTL DAVDRRLHFG
51 VEILNADABA VEAESAHEHED GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFKKF DVGIGAAAFV
151 GDDFVAAAVV ADGVAERNVN VKGRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

m221.pep    10      20      30      40      50      60
             MXVLMXRLSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDAVDRRLHFGVEILNADABA
             | | | | |
a221        10      20      30      40      50      60
             MVVLMRLSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDAVDRRLHFGVEILNADABA

m221.pep    70      80      90      100     110     119
             VEAESAHEHEDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
             | | | | |
a221        70      80      90      100     110     120
             VEAESAHEHEDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVAQKGRRAAAEVQLG

m221.pep    120     130     140     150     160     170
             KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFVX
             | | | | |
a221        130     140     150     160     170
             KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1  atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51 tttcgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggtc atcgaagccg aaacggcgcg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtaa ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgct gagcagctct tgttactga tctctttgcg
301 ccagtatatt tcttggcgca atttcaattc acggaaggcg cgcacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..



70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttacc
151 gtcaaccgag cccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccgcg ggccggcaat gccgacaaac tcacggcgag cgcgatgcgg
301 cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgcgcgc cactcggcg gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgccgcg cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcggccgc cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNPSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTTCAAACC CGGCAGTTTG GCGGTTTGT TGGCTGAWGT TTGCCGTCGG
51  CCCCGCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTGTCCGAA GACGAACAGC CCGTTTTACC CATCAACCGA
151 GCCCCGCCCC GCGGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCG TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCATGGG GCTTAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCC GCGCGGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTGGGTATT GCCTACCGCT
401 ACGCGGCAC ATCGGTTTCT ACCGGTTTGT ACTGCAGCGG CTTCATGCAG
451 CACATCTTCA AACCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551 ATATGGTGTT TTTCCGCACG CTCGGCGGCA GCCGCATTTC CCATGTCGGA
601 CTTTATATCG GCAACAACCG CTTATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCCGCCG GGTCAGAAA AACGACCGT CCCGCTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQPVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QPVLVNRAP ARRAGNADEL IGNAMGLLGI AYRYGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTFFVARSEL QPGDMVFFRT LGGSRISHVG
201 LYIGNNRFIH APRTGKNIET TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

```
m225/g225
10 20 30 40 50
m225.pep FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRRAPARRAG
| : ||||| ||||| ||||| ||||| ||||| : |||||
g225 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
```

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	10	20	30	40	50	60
m225 . pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA					
g225	NADELIG-----GAMGLNEQPVVVRVNRAXARRAGNA					
				70	80	90
m225 . pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR					
g225	DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225 . pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAHPTGKNIETSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAHPTGKNIETSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225 . pep	240	249				
	VKKNDPSRFLNX					
g225	VKKNDPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225 . seq
1  ATGGATTCTT TTFTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCTG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTACCC
151 ATCAACCGAN CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTACC CGTCAACCGA GCCCCGCGCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACCGCAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CCGCACATCG ATTTCTACCG GTTTGACTG CAGCGGCTT ATGCAGACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGCAA CAACGCTTC ATCCACGCGC CGCGCACGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225 . pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQVLPV
51  INRXPARRAG NADELIGSAM GLNEQPVLVP NRXPARRAGN ADXLIGNAMG
101 LNEQPVLVPV RVPARRAGNA DELIGNAMGL NEQPVLVPNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAHPTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225 . pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225 . pep	NADELIGSAMGLNEQPVLVPNR-----VPARRAGNA				

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```

      |||
a225  NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
      70      80      90      100     110     120

      90      100     110     120     130     140
m225.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      |||
a225  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
      130     140     150     160     170     180

      150     160     170     180     190     200
m225.pep MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      |||
a225  MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
      190     200     210     220     230     240

      210     220     230     240     249
m225.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
      |||
a225  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt tttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcgcgtccg cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttacc
151  gtcaaccagag ccccccggcg gcggcgccgc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgcacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcacggcgag cgcgatgcgg
301  cttttgggta ttgctaccg ctacggcggc acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgcgcgc cagtcggcgc gaacagggcg ggtggggcgc acccgttgcc
451  cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcaccc
551  acgcccgcgc caggggaaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAV AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RPIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDSRPF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCCCG CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTGCCGAAG ACGAACAGCC CGTTTACCC
151  ATCAACCAGAG CCCCCGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGCCCCCG CCCGCGGGC
351  GGGCAATGCC GACGAATCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGT TTCCGACGCG TCGGCGGCAG CGCATTTCC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCGCGCGG GTCAAGAAAA ACGACCCGTC CCGCTTCTTG
751  AACTGA

```



This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep  
 1 MDSFFKPAVW AVWLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP  
 51 INRAPARRAG NADELIGSAM GLNEQPVLPV NRVFARRAGN ADELIGNAMG  
 101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG  
 151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS  
 201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL  
 251 N\*

m225-1/g225-1 84.9% identity in 251 aa overlap

	10	20	30	40	50	60
m225-1.pep	MDSFFKPAVWAVWLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG					
g225-1	MDSFFKPAVWAVWLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPVNRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m225-1.pep	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
g225-1	NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA					
		70	80	90		
	130	140	150	160	170	180
m225-1.pep	DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225-1	DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
	190	200	210	220	230	240
m225-1.pep	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR					
g225-1	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
	250					
m225-1.pep	VKKNDPSRFLNX					
g225-1	VKKNDPSRFLNX					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq  
 1 ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT  
 51 TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC  
 101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTACCC  
 151 ATCAACCGAN CCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG  
 201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC  
 251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG  
 301 CTTACGAAC AGCCCGTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC  
 351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC  
 401 CCGTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGG CAATGCCGAC  
 451 GAACTCATCG GCAACCGGAT GGGACTTTG GGTATTGCCT ACCGCTACGG  
 501 CCGCACATCG ATTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGCACA  
 551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG  
 601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT  
 651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT  
 701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC  
 751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAA ACCTGTCGC  
 801 CCGCGGGTC AAGAAAACG ACCCGTCCCG CTTTCTGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep  
 1 MDSFFKPAVW AVWLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP  
 51 INRXFARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG  
 101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD  
 151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ  
 201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI  
 251 EITSLSHKYW SGKYAFARRV KKNDDPSRFLN \*

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a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep  MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
|||||
m225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
      10      20      30      40      50      60

      70      80      90     100     110     120
a225-1.pep  NADELIGSAMGLNEQPVLPVNRXPARRAGNADKLIGNAMGLNEQPVLPVNRVPARRAGNA
|||||
m225-1      NADELIGSAMGLNEQP-----VLPVNRVPARRAGNA
      70      80      90

      130     140     150     160     170     180
a225-1.pep  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSISTGFDCSGF
|||||
m225-1      DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSVSTGFDCSGF
      100     110     120     130     140     150

      190     200     210     220     230     240
a225-1.pep  MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
|||||
m225-1      MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
      160     170     180     190     200     210

      250     260     270     280
a225-1.pep  IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLNX
|||||
m225-1      IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLNX
      220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451 tttctgttgc ctccgcctct cctgcccgcg ctcggcccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Ccgggcctcg cccctccctt cttataa

```

This corresponds to the amino acid sequence &lt;SEQ ID 806; ORF 226.ng&gt;:

g226.pep

```

1  MSEILROPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
101 GSVTGIVTGM YFAAWLGPDT QFSFPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKKLRPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCGGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTCG CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

514

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep  
 1 MNEILRQPSV LLFLTAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKLIGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKLIGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
	:					
g226	QFSFPPRLQYLLFTPSGIPHTLYARVLPFPPLPPLPRLGPHTLRRFTILPKLRPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq  
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC  
 51 CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT  
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC  
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT  
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC  
 251 GCCGTAAAT CTTCAACCAA TGGCTGCCCC TCATCGTTTC GCAGCTTGCG  
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG  
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC  
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC  
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA  
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGCATGCGCG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep  
 1 MNEILRQPSI LLFLTAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep  MNEILRQPSVLEFLTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
          |||||||:|||||
a226      MNEILRQPSILLEFLTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
          10      20      30      40      50      60

          70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAE
          |||||||:|||||
a226      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAE
          70      80      90      100     110     120

          130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSV
          |||||||:|||||
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSV
          130     140     150     160     170     180

          190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
          |||||||:|||||
a226      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgcccgcgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccgcc agcatcgctc
101 gcatggcgct gctgtttgcg cttttgcagg cgggttgct caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgtgttcct
201 cgtgccgcc tgcgtggcgg tcatcagcta tttggattg attgccgacg
251 attggtttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLF LQAGWLKTS
51  WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTtKGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCGCC.TGCG TGGCGGTCAT CAGCTATTG GATTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTLFLV PCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

          10      20      30
m227.pep  TSXLQQLTDALMSNLTLFLVPPCVAVISYL
          || |||||:|||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
          20      30      40      50      60      70

          40      50      60

```

516

```

m227.pep    DLIADDWFSILVSASASTLCVLLVTGKVRWIRGIIRX
            |||||||||||||||||||||||||||||:|
g227        DLIADDWFSILVSASASTLCVLLVTGKVRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAACCAGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTGCG CTTTTCAGG CGGGTTGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TCGTGCGCG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGGTTTTC GATACTGGT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGTTTACAG GCAAGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLF LLQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVRHWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep                                10      20      30
                                TSXLQQLTDALMSNLTLFLVPPCVAVISYL
                                || |||||:|||||||
a227      TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
            20      30      40      50      60      70

m227.pep      40      50      60
            DLIADDWFSILVSASASTLCVLLVTGKVRWIRGIIRX
            |||||||||||||||||||||||||:|
a227          DLJADDWFSILVSASASTLCVLLVTGKVRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE BAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

a228.pep  
 1 MKKLLIAAM AAALACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA  
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD  
 101 KMKDAAK\*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq  
 1 atggctgccg tategggcgg cgggtgcggtc ttcctgataa tgcttcaca  
 51 tattgcccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag  
 101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtcgc cgccaagag  
 151 gttttgcccg acaaacggca cgggtccgaa cgagcgcgtt accgaacggt  
 201 tttgatggcc gaacgacagg cgcaggttct gttcgctgaa atctttgtta  
 251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgcc  
 301 gcccgcatcg atttcgcgcg acacgcccaa gccgtagcgc aaaccgtgtg  
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat  
 401 tcaatcgttt ttctggacga agcgttggtt atagcggatt aacaaaaatc  
 451 aggacaaggc ggcggggcgc aggcagtagc gatggtagcg aaccggttcg  
 501 cccggtgctt ggacgcctta gggaaccgtt ccttttgagc cggggcgggg  
 551 caaccgtac cggttttgtg tcatccgcca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep  
 1 MAAVSGGAV FLIMLPHIAR VQROPFAFAQ ASGEIGIEAA GEIVSAAAE  
 51 VLPDKRHGAE RARYRTVLMA ERQAQVLF AE IFVIPIMHAA ADAVEEMMP  
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKE  
 151 RTRRRAAGST DGETPVRPVL GRLREPFPLS RGGATRTGFC SSAILC\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)  
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC  
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG  
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC  
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC  
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCCGCA CACGCCTAAG  
 251 CCCTAGCGCA AACCGTGTGC CTTTTCGGGC AGGCTGTCCG CGGTTTTCGT  
 301 CCAGCTTCTG CCCGCAAAAT CAATCGTTT TCGGACGAA GCGTTGTTTA  
 351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA  
 401 AATAGTACGG AACCGATTCA CTGGTGCTT CAGCACCTTA GAGAATCGTT  
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)  
 1 ..AQLGEIGIE AADEIVSAA XEVLLDKRHD AERARYRTVF IAEROAQLF  
 51 AEIFVIPIMH AAAADA VEE MMPARIDFAR HAXALACTVC LLRQAVGGFR  
 101 PASARKFNRF FGRSVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR  
 151 SLFCSSAILC \*

Computer analysis of this amino acid sequence gave the following results:

m229/g209

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

**m229/a229** 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      A QALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                               ||| ||||| ||||| ||||| ||||| |||||
a229    MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                               10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep    RARYRTVFIAERQAQALFAEIFVPIPMHAAAADAAVEEMMPARIDFARHAXALAQTVCLL
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a229    XARYXTVFIAERQAQALFAEIFVLIVHAAAADVSVEEMMPARIDFARHAQAVAQTVCLL
              70      80      90      100     110     120

```

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```

          100      110      120      130      140      149
m229.pep  RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---
          |||||
a229      RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX
          130      140      150      160      170      180

          150      160
m229.pep  -----RSLFCSSAILCX
          |: ||||:|
a229      AKARQRRRTGFCSSII
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttcatt ccatcgaaaa atacagaaca cccgccaag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttccatc
101 cgggcgccga ctacatcgtc caagtggcg acgaaaaat cagcgagcac
151 tcaatcaaca acgcatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtgtg
401 tcgaagaaat ccgcgatcag ttgacctgac agaatttggg aagcctcgtc
451 caaacaggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgccca agtcaaagcg tctgaagccg atttgagaa atttataat
601 gcgaacaaaa aagactatct gctgcgcgag gcggtcaaat tggatatgt
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaaa gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgatgcgtt caatcatccc tctcgccttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaac acctaataca tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tgcgtcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEQIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHME DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ ABQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELMKMK AVADPNKAKE KLGDDAFNHP SSLABAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EKNNLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCAC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAaT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCc.GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGTTT AAACCTCGTC

```



520

```

451 CAAACGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGCA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCAG GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACCG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATGGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
  1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
 51 SINNAIQNEQ ADGGGSPDA VFQSLQRAY LKQGAKLMGI SVSSEIQIKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFPN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDVAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLITINSET
351 AWVVRakeVR EEKTLPPFAE KDAVRQAYIR TEAAKL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

m230.pep	10	20	30	40	50	60
	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	70	80	90	100	110	120
	ADGGGSPSDAVFQSLQRAYLKQGAKLMGISVSSEIQIKIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAKLMGISVSSEIQIKMIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	130	140	150	160	170	180
	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRITIRSHTFN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRITIRSHTFN					
	130	140	150	160	170	180
m230.pep	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFPYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFPYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGSGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTCCTTGC AGAATTGGT AAACCTCGTC
451 CAAACGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GTTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCCT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGA KLMI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWWVVRKEVR EEKTLPF AEAKDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPDAVFQSLQRAYLKQGA KLMI SVSSEQIKQII VDDPNFHDANGKFDHALLN					
a230	ADGGGSPDAVFQSLQRAYLKQGA KLMI SVSSEQIKQII VDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

522

m230.pep	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRLTQ	VNRTIR	SHTFN
a230	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRLTQ	VNRTIR	SHTFN
	130	140	150	160	170	180		
m230.pep	PDE	FIAQVKV	SEADLQ	KFYNA	NKKDYLL	POAVKLE	YVALNL	KDFADKQTV
a230	PDE	FIAQVKV	SEADLQ	KFYNA	NKKDYLL	POAVKLE	YVALNL	KDFADKQTV
	190	200	210	220	230	240		
m230.pep	ERVARL	PANEAK	PSFEQ	EKA	AVENEL	KMKKAV	ADFNKA	KEKLGDDAV
a230	ERVARL	PANEAK	PSFEQ	EKA	AVENEL	KMKKAV	ADFNKA	KEKLGDDAV
	250	260	270	280	290	300		
m230.pep	GLKVET	QETWLS	RQDAQ	MSGMP	ENLIN	AVFSDD	VLKKKH	NSEVLTIN
a230	GLKVET	QETWLS	RQDAQ	MSGMP	ENLIN	AVFSDD	VLKKKH	NSEVLTIN
	310	320	330	340	350	360		
m230.pep	E	EKTLP	F	AEAKD	AVRQ	AYIR	TEAA	KL
a230	E	EKTLP	F	AEAKD	AVRQ	AYIR	TEAA	KL
	370	380						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCGGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACTTTTC TCGGCTTCGG CGTCAGCACG GTTTCCTATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCTTTCGC AGAATTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCAGACCA TCCGTTGCGA CACTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATG
651 CCGCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCCTTTGAA GAGCGCGTGG CGCGTTTGGC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAGAGGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTI CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGCTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAACAAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCGGCTATG TCAGACTGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCTGCGA AACAGGCTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGCGAT GGTACGTA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV OVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQAKLMGI SVSSEQIKQM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHME DQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQOAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TFPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIRQT
501 KGAQSVDNQD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAAAT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCGA TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCGCA CACTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAT TGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTGAA GAGCGCGTGG CGCGTTTGCC GCGAATGAA
751 GCGAACCTT CTTTCGAGCA GGA AAAAGCC GCGCTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTGCGG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 AGCATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GCTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCC TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCGCTT
1101 TGCCGAAGCC AAAGACGCGG TACGTACGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGCG AAACGGCAAA CCCGCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTGCAAGT ACAGGCTGTA ACCCGCGCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGCGAACAG CAGTCTGCCA
1451 ATACITTCGA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTACGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAKLMI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKTLFFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQOAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TFPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIRQT
501 KGAQSVDNQD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAIQNEQ					
	10	20	30	40	50	60
m230-1.pep	ADGGGPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	ADGGGPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	RYLSQRHSEDDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180

a230-1.seq

1	ATGTTCCCA	CCATCGAAAA	ATACAGAACG	CCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACTTCGT	TCGGCTTCGG	GGTCAGCAGC	GTATCCCATC
101	CGGGTCGCCA	CTACATCGTC	CAAGTGGGCG	ACGAAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	GCGGACGGCG	GCGGGCCCTC
201	CGCGGACGCG	GTGTTCCAAT	CCCTGCTCA	ACGCGCCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGCGAAT	TCGGTTCTCT	CCGACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	AACGGCAAT	TGACCACCG
351	GCTTTTAAAC	CGCTACCTTT	CCCAAGTCA	TATGCTGAA	GACCAAGTTG
401	TCGAAAGAA	CCGCGATCAG	TTTGCCTTGC	AGAATTGGT	AAACCTCGTC
451	CAAAACGCGG	TATTGGTCGG	GACGCGCGAG	GCGGAACAG	TGATCAGGCT
501	GACGCAAGCT	AACCGGACCA	TCGTTTCGCA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCTGAAGCCG	ATTTCGAGAT	GTTTATATAAC
601	GCAACAAAAA	AAGACTTACT	GCTTCCCAA	CGGTCAGAA	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTGCAAGCAA	ACAGACCGTC	AGCGAAACAC
701	AAGTGA AAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAATTGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	CCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCGC	ACTTCAATA	GGCAAAAGAA	AAGCTSGGCG
851	ATGACCGCGT	CAACCATCTT	TCCTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAG	TCGAAACCCA	AGAAACTTGG	CTGAGCAGGC	AGAGTSCGCA
951	AATGTCGGAT	ATGCCCGAAA	ACCTGATCAA	TGCCGTATTG	AGCGACGAGC
1001	TATTGAAGAA	AAAAACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	CGTGGGTCG	TCGCGCCAA	AGAAGTCCG	GAAGAGAAA	CCCTGCGGTT
1101	TGCCGAAGCC	AAAGACCGGG	TACGTACGCG	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTTGC	CGAAAACAG	GCAAAAGACG	TGCTTACCCA	ACTGAACCGG
1201	GGCAAGGCTG	TTGACGTGAA	ATGGTCGAAA	GTGTCGGTT	TGGGCGCACA
1251	GCAAGCAAGG	CAAGTCCATG	CGCCCGAGGC	TTATGCGGAA	CTGCTGAAAG
1301	CAAAACCGCG	AAAGCGCAAA	CCCGCCTACG	TCAGGCTATG	CGGCTGCGCG
1351	GCACCGGTGA	TTGTGCGAAG	ACAGGCTTGA	ACCCCGCGGG	ATGATATGCG
1401	CGCACAGCTT	CGCCTTGCAA	AACAGGCTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTTCA	CTGTTTGATA	CGTTATTATCA	ACGGCAAGAT	CAACAGAGCC
1501	AAAGGACCGC	AATCGGTCGA	CAACGCGGCA	GGTCAGTA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

## a230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFGVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAklmgi SVSSEIQIKOI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakevr EEKTLPFaEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVkWE VSVLGAQQAR QSMPPeAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPDIDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVdNGD GQ*

```

## a230-1/m230-1 99.8% identity in 512 aa overlap

	10	20	30	40	50	60
a230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
m230-1	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKOIIVDDPNFHDA					
m230-1	ADGGGSPSRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKOIIVDDPNFHDA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a230-1.pep	RYLSQRHMEHQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNR					
m230-1	RYLSQRHMEHQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a230-1.pep	PDEFIAQVKVSEADLQKFYNANKDYLLPKAVKLEYVALNLKDFADKQTVSE					
m230-1	PDEFIAQVKVSEADLQKFYNANKDYLLPKAVKLEYVALNLKDFADKQTVSE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a230-1.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHP					
m230-1	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHP					
	250	260	270	280	290	300
	310	320	330	340	350	360
a230-1.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAW					
m230-1	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAW					
	310	320	330	340	350	360
	370	380	390	400	410	420
a230-1.pep	EEKTLPFaEA KDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVkWE					
m230-1	EEKTLPFaEA KDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVkWE					
	370	380	390	400	410	420
	430	440	450	460	470	480
a230-1.pep	QSMPPeAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPPDIDIAAQL					
m230-1	QSMPPeAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPPDIDIAAQL					
	430	440	450	460	470	480
	490	500	510			
a230-1.pep	QSANTFDLLIRYFNGKIKQTKGAQSVdNGDGQX					
m230-1	QSANTFDLLIRYFNGKIKQTKGAQSVdNGDGQX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```
g231.seq
1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgcccgtt gaaaataatc cgccatttta ccgtaaaaac cgccgcctga
101 acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151 ggcgcgcggt ttcagacggc atttgccgtt caaggccgtg cgggtgcttt
201 accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251 ccgcccgtcc tgccctgccg gcggtacgcc cagggcgctt gcggattttt
301 agctttccac aatcctttgc gttccctttc cgcctgaatt tgagcgtcgg
351 catagtcggc aaaatccgac ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgccccgtc ctgcacctgc atcaggttca aatcggtttt
451 gccggcggat acctgcgcca cttcgcgctg atagcggctg gtttcaaaca
501 caggtacact gactttccta cctccgccc cgcgcgcgag gttgtcgcgc
551 gaacgtgtac cgtaagcctg tttcatctcc ggtgcgtcga tatacgccat
601 ccgaatttta tgtttcgcgc cgtcgcgcgc gatgacgtga agggatcgcg
651 cgtcatagac tttggacacc gtgctgtgtg agctgtggcc ggatttcgcc
701 gatgcccgtc ggcgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa cgcgcgtccg caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgac gtctgaacat
901 ctctga
```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```
g231.pep
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFVAV QGRAVSLPNA OPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLSVGIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMPMPSEH
301 L*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```
m231.seq (partial)
1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCAGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACATTTCG GC....
```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```
m231.pep (partial)
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFVAV QGRAVSLPNA QPFG.....
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng)

from *N. gonorrhoeae*:

m231/g231

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFVAV					
g231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFVAV					
	10	20	30	40	50	60
	70					
m231.pep	QGRAVSLPNAQPFG					
	:					
g231	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLSVGIVG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGCGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGAACA
501 CGCGGACGCT GACTTTCCTG CCTCCGCGCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGCTGTCCG
651 CGTCATAGAC TTTGGACACC GTGCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGCGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTT
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQTGF
151 ADRNLRHFAL VAVGVEHADA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFEDFFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFPG					
a231	QSRVSLPNAQPFHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGCGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG cgegcgcCAG GTTGtcgcGC
551 GAACgTGtAC CGTAagcgtg Ttcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGTTtcgcgc cgtcgcCgtc gATGACGTGA AGGgtatcGC
651 CgtcATAGAC TTTGGACACC Gtgccgtcgt AGctGTGGCC GGAtttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```



528

101 SFQSFAPFF RLNLVGVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF  
 151 AGGYLRHFAL IAVGFKHTYN EFTRLRRRAQ VVARTCTVSV FHLRCVDIRH  
 201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

## m231-1.seq

1 ATGTCAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGCGGAACT  
 51 GCCGCGGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCGCGCTGA  
 101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG  
 151 GCGCGCGGTT TTCAGACGCG ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT  
 201 ACCAATGCCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC  
 251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTTT  
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG  
 351 CATAATCGGC AAAATCCGCC TTATCTGCT GTTCTTTAGC ATAACTTTAA  
 401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT  
 451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTG GTATCGAACA  
 501 CGCGCAGCT GACTTTCCTG CCTTCCGCGC CCGCGCGCAG GTTGTCGCGC  
 551 GAACGCTGCG CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT  
 601 CCGGATTTTG TGTTCGCGC CGTCGCCGTC GATAACGTGA AGGTTGTGCG  
 651 CGTCATAGAC TTTGGACACC GTGCCCTGTG AGCGGTGGCC GGATTTCGCC  
 701 GATGCTCGGC GGCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC  
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCGG CACCGCTCG CTGCCGTACC  
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC  
 851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT  
 901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

## m231-1.pep

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR  
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF  
 101 SFQSFAPFF RLNLVGVIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF  
 151 ADRNLRFHFA VAVGIEHAHA DFFAFRRRAQ VVARTRAVSL FHLRRVDIRH  
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTEVPCRA  
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRGDGG KPFHDFNLIH IFQMMPMPSEH  
 301 IGIGFQTAS\*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	OGRAVSLPNAQPFAGHIHPILIAAPACPAVRPRRLRIFSFQSFAPFRLNLVGVIG					
m231-1	QSRVSLPNAQPFAGHIHPILIAAPACSAVRPRRLRIFSFQSFAPFRLNLVGVIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILLFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFTRLRRRAQ					
m231-1	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRNLRFHFAVAVGIEHAHADFFAFRRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIIVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITORTQKRGDGGKPFHDFNLIHIFQMMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

## a231-1.seq

1 ATGTCAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGCGGAACT  
 51 GCCGCGGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCGCGCTGA  
 101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTGC CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCCTGCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTCAACA
501 CGCGGACGCT GACTTTCCCT CCTTCCGCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTTATCTCC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT ACCGCTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGCGGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGGTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

**a231-1.pep**

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVD FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNHLH IFQMPMPSEH
301 IGIGFQTAS*

```

**a231-1/m231-1** 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
	70	80	90	100	110	120
a231-1.pep	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGVEHADADFPFRRRAQ					
m231-1	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHAHADFPFRRRAQ					
	130	140	150	160	170	180
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAVIDFGHRACVAVAGFRRCSAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNHLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNHLHIFQMPMPSEH					
	250	260	270	280	290	300
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

**g232.seq**

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccattcctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgctt tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctgttt

```

530

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtggaaat
201 tgtccgtggg acaaaatccc tgctgcgtga aacggtgcgg cacaaatccc
251 tttttaccgc cattatcggc atctcgtggg tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgccgccc
401 gttcgggtact gtgtgccaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacggtt tgccgcctgg ttttgggttg
501 gctgacgcac ggacaccggt ttgaagggtt gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggatgatgac gctgatcggc
601 tttttcggcg gattttttctc cgttccgctc tatacctggc tgcaaacgc
651 cagcagcgag actttccgcg cccgcgcgct tgccgccaac aatatcgtaa
701 acggcatctt tatggtttcc gccgccgttt tgagcgcggt attgctgttt
751 ttggttgaca gcattttccct gctgtatctg attgtcgcct tgggcaatat
801 tccgttggcg gtatttttga ttaagcgca aaggcggttt ttaggcgcgg
851 cggaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWVGVAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGNLGI FWFLSQGWAY PVMAVMTLIG
201 PFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLE
251 LFDISISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51 CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC ACAAATCCC TGCTGCGTGA AACGGTGGCG CACAAGCCCG
251 TTTTACCAGC CATTATCGGT ATTTCTGGT TTTGGTTTGT CCGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TGCGGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CCGTATGATG GCTGATCGGC
601 TTTTTCGGCG GATTTTCTC CGTTCCGCTC TATACCT (g) TG CAAACCGCCA
651 TAGCGAGATT TCCGCGCCCg GCCGTGCGC CCAACAATAT CGTTAACGGT
701 ATTTTATGCG TTTCCGCTGC CGTTTGTAGC GCGGTGTTGC TGTTTTGTG
751 TGACAGCATT TCCTTGTGTT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGCGCGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWVGVAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FXFLSQGWAY PVMAVMTLIG
201 PFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

               10      20      30      40      50      60
m232.pep      MMGNSLIESGTFVAILFGQILGTAAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
               |||||
g232           MMGNSLIESGTFVAILFGQILGTAAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
m232.pep	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	70	80	90	100	110	120
m232.pep	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	130	140	150	160	170	180
m232.pep	190	200	210	220	230	
	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAANAANNIVNGIFMVS					
	190	200	210	220	230	240
m232.pep	240	250	260	270	280	289
	AAVLSAVLLFLFDSISLLYLI VALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLI VALGNIPLAVFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTC
101 AAACCGCGCT GTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAACCTG GCGCGTTGC TGTATTATTT
201 GCCGTATTTC CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTGC
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCGCG TGCTTTTGGC
351 GTGTCTGTTT TGCAATGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTGTGCGCC ATCCTGTTGC GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATGTCGGG ATACTGGTTT
551 TGCTGGTCGC CGTAGGAGGC ACGTCCGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGAATATATG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTG GCGCGGTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CGGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCGGCGGA
1051 TTTTCTCTCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTAA
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGTG TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTGAT AAGCGCGAAA GCGGTTTTT AGCGCGGCG GCAATCAGGA
1301 AAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232.pep
1  MYAKKGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAQOMLNL GALLFILPYF LFSLSGLQG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLACL FCMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPSV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WFWGAVYTTQ
251 LPTFTQIHLG GNDNVFNLM ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

532

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG  
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAVL SAVLLFLFDS  
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP\*

m232/a232 95.9% identity in 290 aa overlap

m232.pep				10	20	30
				MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTILFGPLKYAILPDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP					
	120	130	140	150	160	170
m232.pep		40	50	60	70	80
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG				
a232	YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
	180	190	200	210	220	230
m232.pep		100	110	120	130	140
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSXERLMLAW				
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSRERLRLAW					
	240	250	260	270	280	290
m232.pep		160	170	180	190	200
		VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFXFLSQGWAYPVMAMVTLIGFFGGFFSVPL				
a232	VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFWFLSQGWAYPVMAMVTLIGFFGGFFSVPL					
	300	310	320	330	340	350
m232.pep		220	230	240	250	260
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS				
a232	YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
	360	370	380	390	400	410
m232.pep		270	280	289		
		VFLIKRERRFLGAAAIRKKPX				
a232	VFLIKRERRFLGAAAIRKKPX					
	420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq  
 1 atgaacgca aaaatatcgc gctgattccc gccgccggca tcggggtgcg  
 51 tttcgggtgcg gacaaaccca agcaatatgt cgaaatcgga agcaaaacccg  
 101 ttttagaaca tgtacttggg atttttgaaac ggcatgaggc cgtcgatttg  
 151 accgctcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac  
 201 ggcatttcca caggttcggg tgtggaaaaa cgggtggacag acccgcgccg  
 251 aaactgtccg caacggtgtg gcaaaactgt tggaaaccgg tttggcggcg  
 301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgcccgc  
 351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg  
 401 ggatttttgc agttcccggt gccgatacgc tcaagcgcg agaaagcgga  
 451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgcaaacgcc  
 501 gcagcttttt caagcgggtt tgctgcaccg cgcattggct gcggaaaact  
 551 tgggcggcat taccgatgaa cgctcccgcc tggaaaaact ggggtgtgct  
 601 ccgctactga tacagggcga cgcgcgcaat ttgaaactga cgcagccgca  
 651 ggacgcatac atcgtcagcc tgctgctcaa tgccgtctga

This corresponds to the amino acid sequence &lt;SEQ ID 858; ORF 233.ng&gt;:

g233.pep  
 1 MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLBHVLG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR  
 201 PLLIOGDARN LKLTOPDAY IVRLLLNAV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTAGAC  
 201 GGCATTTCCA CAGGTTCTGGG TGTGGAAAAA CGCGCGACAG ACCCGCGCCG  
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGCGC  
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GC  
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)  
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNVLVHDA ARCLPSEAL TRLEQAGNA AEGGILAIPI ADTLKCADGG  
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIG IFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLG IFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
m233.pep	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
	:					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTAGAC  
 201 GGCATTTCCA CAGGTTCTGGG TGTGGAAAAA CGCGCGACAG ACCCGCGCCG  
 251 AAACGTGTCG CAACGGTGTG GCAAAATGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG  
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GC  
 451 AACATTAGTG CAACCGTCCA GCGGACGAGC CTTTGGCAGG CGCAAACGCC  
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTTGCT GCGGAAACT  
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC  
 601 CCTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA  
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGCTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFF QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDV*
```

m233/a233 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
a233	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
a233	AENLDGITDEASAVEKLGIRPLLVQGDARNLKLTQPQDAYIVRLLLDVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgctcga
151 acattcgaca accgctccag cttccaaaaa gccattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca caccgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttcccg caaagcgag aacctgaaag gcgcagatta
351 tgcgttacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctatc
501 cacacagggc gcggcgcaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRPNV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGTSGY DATLNGKVL D
201 LAIREAVDNL VQAVDNGANQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .GTCAACAGC CTGTTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)  
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW  
 51 QPNR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

				10	20	30
m234.pep				GAGEYALSNREI	IGFGGTSGYDATLNGKVL	
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREI	IGFGGTSGYDATLNGKVL			
	140	150	160	170	180	190

	40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX	
g234	DLAIREAVDNLVQAVDNGAWQSNRX	
	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)  
 1 AACCGCACCT ATTTGAACGC ATTAAACAG GAATCCGGCA TTTCCGGCAA  
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG  
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGEGT  
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA  
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG  
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT  
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA  
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)  
 1 NRTYLNALKQ ESGISGKAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG  
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD  
 101 ATLNGKVLDL AIREAVNSLV QAVDNGAWQP NR\*

m234/a234 100.0% identity in 54 aa overlap

				10	20
30					
m234.pep				GAGEYALSNREI	IGFGGTSGYDATLNGKVL
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQGA	GEYALSNREI	IGFGGTSGYDATLNGKVL		
	50	60	70	80	90

	40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX	
a234	DLAIREAVNSLVQAVDNGAWQPNRX	
	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq



g235.pep

1	<u>MKPLIILGLAA</u>	<u>VLALSACQVR</u>	<u>KAPDLDYTSF</u>	<u>KESKPASILV</u>	<u>VPPLNESPDV</u>
51	<u>NGTWGMLAST</u>	<u>AAPISEAGYY</u>	<u>VFPAAVVEET</u>	<u>FKENGLTNAA</u>	<u>DIHAVRPEKL</u>
101	<u>HQIFGNDAVL</u>	<u>YITVTYEGTS</u>	<u>YQILDSVTVT</u>	<u>SAKARLVDSR</u>	<u>NGKELWSSGA</u>
151	<u>SIREGSNNNS</u>	<u>SGLLGALVRA</u>	<u>VVNQIANSLT</u>	<u>DRGYQVSKTA</u>	<u>AYNLLSPYSR</u>
201	<u>NGILKPRFV</u>	<u>EEOPK*</u>			

m235.seq

1	ATGAAACCTT	TGATTTTAGG	GCTTGCGGCC	GTGTGGCGCG	TGCTGCGCTG
51	CCAAGTTCAA	AAAGCGCCCG	ATTTTCGACTA	CAGGTCATTG	AAGGAAAGCA
101	AACCGGCTCT	AATTTTGGTG	GTTCCGCGCG	TGAACGAATC	GCCCGATGTC
151	ACGGGAACAT	GGGGTGTACT	GGCTTCGACC	CGCGCGCGCG	TTTCCGAAGC
201	CGGCTATTAC	GTCTTCCCGG	CCGCAGTCGT	GGAGGAAACC	TTCAAACAAA
251	ACGGCTTGAC	CAATGCCGCC	GATATTACAG	CCGTCCGGCC	GGAAAACTG
301	CATCAGATTT	TCGGCAATGA	TGCGGTTTGT	TACATTACGG	TTACCGAATA
351	CGGCACCTTCA	TATCAAAATT	TAGACAGCTG	GACGACCGTA	TCGGCCAAAAG
401	CACGGCTGGT	CGATTCCCGC	AACGGAAAAG	AGTTGTGTGT	GGGTTCCGCC
451	AGCATCCGCG	AAGGCAGCAA	CAACAGCAAC	AGCGGCCTGT	TGGGGGCTTT
501	GGTCAGCGCA	GTTGTCATCT	AGATTGCCAA	CAGCGCTGACC	GACCGCGGTT
551	ATCAGGTTTC	CAAAACGCGC	GCATACAACC	TGCTGTGACC	CTATTCTCAC
601	AACCGCATCT	TGAAGAGTCC	GAGATTCTGT	GAAGAGCAGC	CAGAAATAA

m235 . pep

1	MKPLILGLAA	VLALSACQVQ	KAPDFDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGVLAST	AAPLSEAGYY	VFPAAVVEET	FKQNGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITVTVEYGS	YQILDVTVTV	SAKARLVDSR	NGKELWSGSA
151	SIREGSNNNS	SGLLGALVSA	VVNQIANSLT	DRGYQVSKTA	AYNLLSPYSH
201	NGILKGPRFV	EEOPK*			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/q235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPD	FDYTSFKESK	PASILVVPPLNES	FDVNGTGW	GLAST	
g235	MKPLILGLAAVLALSACQVRKAPDL	DYTSFKESK	PASILVVPPLNES	FDVNGTGW	GLAST	
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYVVFPA	AVVEETFKQ	NGLTNAADIH	AVRPEKLHQ	IFGND	AVLYITVTEY
g235	AAPISEAGYVVFPA	AVVEETFK	ENGLTNAADIH	AVRPEKLHQ	IFGND	AVLYITVTEY
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          ||||||||||||||||:||||||||||||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTCAA AAAGCGCCCG ATTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTGGTG GTTCGCGCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TGCGGTTTGT TACATTACGG TTACCGAATA
351 CGGCATTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGCT CGATTCCCGC AACGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGT S YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST
          10      20      30      40      50      60

          70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT S
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT S
          70      80      90      100     110     120

          130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130     140     150     160     170     180

          190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          ||||||||||||||||:||||||||||||||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g235.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTGACAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTGCGATT TTTCGCGGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCCT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCCGGCGC GGTAAATTCG
251 GCTTCCGCTT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGATTGCC GTCCATTTT
351 TCACCAAGTTC GGCTTCGGCT TTTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGGCGGGC GCGGCTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTTTGCAG CCGCGCGGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacagG AAGCTCAAGG
801 TATTGCGGAT GCGCGCGTAG CTTTCGGTAA CGGTTTGAG GATTTCCTTG
851 GAAatcgCCA ATtcgcgct gTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATT CGACATTTTG CGGCGTTTT GTTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TGC CGCTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGGNGKFI
51 TDFHFCFRHQ QGKAQFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV FHGVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQBAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRFQAO
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTGGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCAACAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCKTCTTCGC CGCCGCGGwT GayGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAAC GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACaTG TCTTTTACGG CAAAGTGGAa kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG ACACTCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCTTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGGFFV DGRELVPSME
51 EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQSSLC AAACMAVCFH
101 GVEAVFQDVE VERTQVFRAE RNXYFYGKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LPIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng)

from *N. gonorrhoeae*:

m236/g236

539

		10	20	30			
m236.pep		LHGRTDGFVGAQRLDGGGYRFAGFADCRPF					
g236	FRHQQKKAQFFAQSIQIAGHFFRRGNFGFRLQGRITDSFVGAQRLDSGGYCFARFADCRPF						
	60 70 80 90 100 110						
		40	50	60	70	80	90
m236.pep	FHQFGFGFFVDGRELVPMSMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQGS						
g236	FHQFGFGFFVDGRELVPMSMEEDAVFAAADDVPRFFAGEAQNRCNQENQAARDVVQGLR						
	120 130 140 150 160 170						
		100	110	120	130	140	150
m236.pep	AAACMAVCFGGVEAVFQDVEVERTQVFRAERNXVFGKVEITRIVIACTLLQLTQCYH						
g236	AAAGAAVFGGVEAVFQDVEVERAQVFRAERNNVFHGEVEGIARIVTACQTLLQPPRQYQ						
	180 190 200 210 220 230						
		160	170	180	190	200	210
m236.pep	GVAVDFHHIRLLHGI FNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGR						
g236	GVAVDFHHIRLLHGI FNRIKVAQIGKQEAQGIADAAVAFGNAFEDFFGNRQFAAVIGGR						
	240 250 260 270 280 290						
		220	230	240	250	259	
m236.pep	PQAQDVCAEFVINLLRCNDVADGFRHFFAFAVDNETMGQQLFIRRATHX						
g236	PQAQDVRAEFVIDFLRRDDVADGFRHFAVLNVHETVGGQQLFIRCASHG						
	300 310 320 330 340						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGACAG
51  CGGTTTCATG GCCTGCAACC GCGCCACAT CGCGSGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTCACCATC ACTGGCTTTA GCGGCAACCG CAAGTTCGCT
151 GCCTACTTTC ACTTCTGCTT TAGACACCAG CAAAGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCCGGCGC GGTAATTTTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCCGGCG GCAAAGGCTC
301 GATGGCGCGG GTTACCGCTT CGCGGGCTTC GCGGATGCG GTCCATTTT
351 TCACCAAGTC GGCTTCGGCT TTTTCGTTGA TGGTCCGGAA CTCGTGCCAA
401 GTATGGAATA GCACGCTGTC TTCTGCGCCG CCGCCGATGA TGTCCACGCG
451 TTCTTCGCGG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGCGG GTTTCGCGCG TCGCGCGGCG GCGGCTGTCTG
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTT TTTACGGCA AAGTGAAGG
651 CATAACGCGG ATAAAAATCA CCGGCAACGC GTTCTTCGAG CCGCCTTGCC
701 AACACCAAGG CATAGCGGTC GATTTCACAC ATATCCGCCT GTTGACGCGC
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTGAG GATTTCCTTG
851 GAAATCGCCA ATTCGCCGCT GTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCGCGC CCGAATCGT TATACACTTC TTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTT CGCCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTACCG CGCGCGACCC ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```

a236.pep
1  MARFAFSADI LCTAFADGFM ACNRAHLAGV VPAAFAFFT I TGFSNGKFWA
51  AYFHFCFRHQ QSKAQFFAQSI QIAGHFFRR GNFGFGLQGR TDGFVGAQRL
101 DGGGYRFAGF ADCRPFFHQF GFGFFVDGRE LVPSMEKHAV FCAAADDVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAAG AAVGFGGIEA VFQDIEVERA
201 QVFRAERNHF FHGKVEGITR IKITGNAFLQ PPCQHQGIIV DFHHIRLLHG
251 IFNRIEVAQV GKQKAQGIAD TAVAFGYALE DFFGNRQFAA VIGGCRPQQA
301 DVRAELVIHF LRRDDVADGF RHFAVPLIHH ETMGQQLFVR RATH*

```

540

m236/a236 81.0% identity in 258 aa overlap

m236.pep					10	20	30
					LHGR	TDGFVGAQRLDGGGYRFAGFADCRPF	
a236	FRHQ	QSKAQFFAQSIQIAGHFFRRGNF	GFGLQGR	TDGFVGAQRLDGGGYRFAGFADCRPF			
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
		FHQFGFGFFVDGRELVP	SMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQGS	LC			
a236		FHQFGFGFFVDGRELVP	SMEKHAVFCAAADDVPRFFAGEAQNRCNQENQAARDVVQGLR				
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
		AAACMAVCFGGVEAVFQDVEVERTQV	FRAERNXVFYGVK	VEXITRIVIA	CQTLLQLTCQYH		
a236		AAAGA	AVGFGGIEAVFQDIEVERAQV	FRAERNHFFHGKVEGITRIKITGNAFLQPPCQHQ			
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
		GVAVDFHHIRLLHGIFNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGRCR					
a236		GIAVDFHHIRLLHGIFNRIEVAQVGKQKAQGIADTAVAFGYALEDDFFGNRQFAAVIGGCR					
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
		PQAQDVCAEFVINLLRCNDVADGFRHFFAFVDNETMGQQLFIRRATHX					
a236		PQAQDVRAELVIHFLRRDDVADGFRHFAPVLIHHETMGQQLFVRRATHX					
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq

```

1  atgctgggaca aggttgccg taatatcgca ctccccgccc cactgaatatt
51  cgattctaac atcggaagc tgcggaaaaa ctttaagcat atcttgccg
101 acaagctcgg tcatacgccg aggattgtcg ataaattcgt tatccttacc
151 gccgaaaagc agcctgccgt ccgcgctgag gcggaataa tccaaaatat
201 gccggttgct gcatactgcc atattgttg gcgataagcc tttgtgccc
251 gcgccaagg gttcgggtgc aataataaag gtgctgacgg caatcgctt
301 gcgttccaaa ggccggaata tcgggttcaa accgacataa gtattgacgg
351 catagaccac atttttacac tcgacgctgc ctcgggctg gtaaaccagc
401 caaccgtttt gatacgggtc gatgcgcgtc atcggggatt gtcgaaaaat
451 ctgcgcgcgc gcttcggcag cgcgcgtggc aacaccaaac gtgtaattga
501 gcggatgaag atgcccggac aagggatcga actgtgcgcc ttggtacata
551 tcgctgtcaa gctgctgtt caactcggct ttatcccaa gttgataatg
601 actcgcaccg taatgccgtt ggcggtgttc atgccactgc tgcaactctt
651 cccaatgctg cggacggacg gcaaccgtgg cataaccgcg ctgccaatcg
701 caatcgatgg catgtttgcg gacgcgttcg tccaccagtt cgaccgcctg
751 caaagactgt tgccaaaacc attgcgcctg ctccaagccg acctgtttt
801 caatttcccc cataccgcag gcgtagtcgc tgataacctg cccgccactc
851 ctgccggacg cgcgaagcc gatacgtgcg gcttccaaa cgacggcttc
901 atgtccgtgt tccgccagcg gcaatgcggt acacaaaccg ctcaaaccgc
951 cgccgataat gcaggtttcg gctttcagac ggcattggag tttcggataa
1001 acagtatgcg gattaaccga actaaaataa taagaaggca gatattcttg
1051 aaaatcagg cgaatcattg tgtttgctt atcgggtata ttttcggacg
1101 gaatgataca gactgtcggg ccatatcgtc caaacagaaa atcggttga

```

This corresponds to the amino acid sequence &lt;SEQ ID 882; ORF 237.ng&gt;:

g237.pep

```

1  MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51  AEKQFAVRAE AVIQNMAVV AYCHIVADKP FCARAQFGG NNGGADGNRL

```

541

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN  
 151 LRAGFGSGAG NTQRVIERMK MPQGIELCA LVHIAVKLLF QLGFIPKLIM  
 201 TRTVMLGVF MPLQLQFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTGCFQNDGF  
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL  
 351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq  
 1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT  
 51 CGATTTTGAC ATCGGCAAGC TCGGGAAGAA CTTTAAGCAT ATCTTGGCGG  
 101 ACAAGCTCGG TCATACGCTC AGGATTGTGC ATAAACTCGT TATCCTTACC  
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT  
 201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGGC  
 251 GCCCCCAAGG GTTCGGTCCG AATAATAAAG GTGCTGACAG CAATCGCCTT  
 301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG  
 351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTGCGGCGT GTAAACACAGC  
 401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT  
 451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCCAA GTGTAAGTGA  
 501 GCGGATGCAG GTGTCCGGAT AAGGGGTCCA ATTGTGCCCC TTGGTACATA  
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG  
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT  
 651 CCCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA  
 701 CAATCGACGG CATGTTTTCG GACGCGTTCG TCCACCAGTT CGACCGCCTG  
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT  
 801 CAATTTCCTC CATACCGCAG nCGTAATCGC TGATAACCTG CCCGCCACTC  
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC  
 901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCAATCCGC  
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA  
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG  
 1051 AAAATCAGGG CGAATCATTTG TGTTCGCTTT ATCAGGTGTA TTTTCGGACG  
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep  
 1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT  
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL  
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN  
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPKLIM  
 201 TRTVMLGVF MPLQLQFPML RTDGNRGITA LPTIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRAET DTRGFQHNRF  
 301 MSLLRQGQCS AQTQSAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL  
 351 KIRANHCVCF IRCIFGRNDT GCRAISSKQK IG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH	TLRIVDKLVILTAEKQSAVRAE				
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH	TRRIVDKFVILTAEKQPAVRAE				
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPF	FCARPQGFGRNNGGADSNRLAFQRPEYRVQ	TCISIDSIDH			
g237	AVIIQNMAVVAYCHIVADKPF	CARAQFGGNNKGADGNRLAFQRPEYRVQ	TDISIDGIDH			
	70	80	90	100	110	120
m237.pep	IFALDAAFGRVNQPTVLMRF	DARHRGLENLRTGFGSGT	SDAQSVSERMQVSGXGVELCP			
	130	140	150	160	170	180

[illegible]

```

a237.seq
1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCGCCGCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TCGCGAAAAA CTTTAAAGCAT ATCTTGGCGCG
101 ACAAGCTCGG TCATACGCGC GGGATTGTGC ATAAACTCGT TATPCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
201 GACGGTTGT C GCATATGCCC ATATTGTTGC GGATAAGCCC TTTTGACAGC
251 GCGCCCAAGG GTTCTGTGGC AATAATAAAG CTGCTGACAG CAATCGCCTT
301 GCGCTCAAA GGGTTGAATA TCGGATTCAA ACCGGCAATA GTATTGACGG
351 CGTACACCAG ATTTTTCGAT TCGACGCTGC CTTCGGGGGT GTAAACCAGC
401 CAACCGTTT GATAAGGTT C AATGCGTATC ATGGGAGAA T GCTCAAAAT
451 CTTCTGACCA GTCTCGGCAG CGCGCGCGGG GATGCCAAC GTGTAATTGA
501 GCGGATCGAG ATCCCGGAC AAGGATCGA ACTGTGCGCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTCAGTG TTATCCAGA GTTGATAATG
601 AGTTGCACCG TAATATTTT GGGCGTGCTC ATGCCATTGT TGCAAATCTT
651 CCCAATGCTG CGAACCGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701 CAATCAATGG CATCTTTGCG GACGCGTTTG TCACCAAGT GCAGCGCTCG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCAAACCG ACCTGTTTTT
801 CAATTTCTCT CATACCGCAG GCGTAATCGC TGATAACCTG CCCGCCACTG
851 CGTCCCAGCG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCTGCT TCCGCCAAGG GCAATGCAAT GCACAAACCA CTCATCCGCG
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTTCGATAA
1001 ACAGATATGAG GATTAACCGA ACTGAAATAA TAAGAAAGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCGGAG
1101 GAATGATACA GGCTGTGCGAG CCATATCGTC CAAACAGAAA ATCGGTTGA

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a237.pep

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMTVV	AYCHIVADKP	FCTRAQGGFC	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAAFGG	VNQPTVLIRF	NAYHGRMLKN
151	LRTSFGSGAG	DAQRVIERME	MPQGQIELCA	LVHIAVKLLL	QFSVIPELIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLLPKPLRL	LQTDLEFNFL	HTAGVIADNL	PATFSRRAET	DTRGFQHNRF
301	MSLLRQGQCS	AQTTQSAADD	TGIGFQTALK	FRNSMRINR	TEIIRRQIFL
351	KIRANHCVCVF	IGYIFGRNDT	GCRAISSKOK	IG*	

## m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRI	FDIDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE				
a237	MRDKVGGNVALPAPRI	FDIDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE				
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMMAVVAYCHIVTDKPF	CARPQGFGRNNKGADSNRLAFORPEYRVQTCISIDSIDH				
a237	AVIIQNMMAVVAYCHIVADKPF	CTRAQGFGRNNKGADSNRLALQRLLEYRIQTGISIDGVHQ				
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFD	DARHRLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP				
a237	IFAFDAAFGRVNQPTVLI	RFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFI	PKLIMTRTVMLGVFMPLQLF	PMLRTDGNRGITALPITIDGMEA			
a237	LVHIAVKLLQFSVIP	ELIMSCTVIFLGVLMPLQLF	PMLRTDGNRGITALPIAINGMEA			
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRL	LPKPLRLQLADLFFNF	PHTAXVIADNLPATPSRRAETDTRGFQHNRF			
a237	DAFVHQFDRLQRL	LPKPLRLQLADLFFN	LHTAGVIADNLPATPSRRAETDTRGFQHNRF			
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGC	SAQTQSAADDTGIGF	TALKFRINSMRINRTEI	IRRQIFLKIRANHCVC		
a237	MSLLRQGC	SAQTQSAADDTGIGF	TALKFRINSMRINRTEI	IRRQIFLKIRANHCVC		
	310	320	330	340	350	360
	370	380				
m237.pep	IRCI	FGRNDTGCR	AISSXQKIGX			
a237	IGYI	FGRNDTGCR	AISSXQKIGX			
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgcgtggcaa ataccatctg
151 tttggtaatg ctgcggcgag tgtaaaaaat cgcgtttgcg ccgtccaaac
201 atttgatgca actgcggtcg gcccatact gcctattaca cacgaacgga
251 caggatttga aggtgttata ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcactttctga
351 tttcagcggc gccgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcggg aatacatccc gcagacggat atgacggggc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaaaaa agataaacac tgttccgcaa gccctttttt
551 cagaccgctg gctaaaaaaa aatgccgggt ccgcttcggg ttttctcagc
601 cgtgcggatg aagcaggaaa actgatatgg gaaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cgcacatcgc caagggtcgg
701 ttaatccttt ttaaacgggt tttcaagggg tagggattgg ggcaattaca
751 gacagtgcgg taagcccggc cacagatata gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcacia cttgcgcgcg

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544

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851 cgagcctatt acaggacagt gccttttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtacgagagg ccgaggttac ggtttgagcg ggtaaaaaag
1001 tagaacttaa ccgacccaaa tgggattggg ttaaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctgcacaata tcggccacca acagaaaaaa aatcacatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1  MNLP IQKFMM LLAA AISMLH IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51  FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGS TTKKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTDI AAQOTLQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGIN
301 ARQWADAHFN ITATAOTALA VAEAAGTVWR GKVELNPTK WDWVKNTRYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNQNLNNI
401 AAQDPRLSLA IHEGKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYI IDSNEKRNKI KNHNLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1  ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51  GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCAGCGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAAGCGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTTCATCGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCCCCTTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACAA CTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGGCG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCGCCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAATCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAACC GGTAATTTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1  MNLP IQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51  FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

Homology with a predicted ORF from *N. gonorrhoeae*

m238/q238

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAI SMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	RVYAVQTFDATAVSPVLPI THERTGFEGVIGYETHFSGHGHEVHSPFDNHDHSDKSTSDFSG					
g238	RVCAVQTFDATAVGPILPI THERTGFEGVIGYETHFSGHGHEVHSPFDNHDHSDKSTSDFSG					
	70	80	90	100	110	120
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYVVKGTSTKTKTNI VPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYEPQGGARDIYSYHIKGTSTKTKTNI VPQ					
	130	140	150	160	170	180
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWVANRMD DVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMD D IRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238.pep	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQLAAASLLQDSAFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGNLSPEAQLAAASLLQDSAFAVKDGINS					
	250	260	270	280	290	300
m238.pep	AKQWADAHPNITATAQTALSAEEAAGTVVRGKKVELNPTKWDWVKNTGYKKPAARHMQTL					
g238	ARQWADAHPNITATAQTALAVAEAAGTVVRGKKVELNPTKWDWVKNTGYKKPAARHMQTV					
	310	320	330	340	350	360
m238.pep	DGEMAGGNKPIKSLPNSAAEKRKQNF EKFN SNWSSAS PDSVHKLTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPKPSI -TSE GKANAATYPKLVNQLNEQNLNIIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	420
m238.pep	RYTSLDGKITI IKDNENNYFRIHDNSRKOYLD SNGNAVKTGNLQKGQAKDY LQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTS GGGWLSRDGTRQYRPPTTEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
1 ATGAATTGCT CTATTCAAAA ATTCATGATG CTGTTTGAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGTTGGTAA ATACCATCTG
151 TTTGTAATG CTCGCGGCAG TGTAAAAAAT CGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GCGGTAGACG GTGGTTTTAC CGTTTACCAA CTTTCATCGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACTTCA ACAAACAA AGAGTAATAT TGTTCCTCCG GCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAPAAA
651 TTGGTGGGCT AACCCTATGG ATGATATTTC CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTGCGG TAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TTAATAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGACCAT GCATACTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
1 MNLPIQKFM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGKYHL
51 FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN HLGNSPEAQ LAAATALQDS AFAVKDGINS
301 ARQWADAHFN ITATAQTALA VAEAATTWVG GKVELNETK WDVKNTGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPPGKYHLFGNARGSVKN					
a238	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPPGKYHLFGNARGSVKN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
a238	RVYAVQTFDATAVGPILPITHERTGFEGIIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYVKGTS TKTKNIVPQ					
a238	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYVKGTS TKTKSNIVPR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m238.pep	APFSDRWLKENAGAASGFFSRADAGKLIWESDPNKNWWANRMDVIRGIVQGAVNPFLMG					
a238	APFSDRWLKENAGAASGFFSRADAGKLIWESDPNKNWWANRMDIRGIVQGAVNPFLMG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m238.pep	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQLAAASLLQDS AFAVKDGINS					

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```

|||||
a238      FQGVGIGAITDSAVSPVTDAAQQT LQGINHLGNLSPEAQLAAATALQDSAFVAVKDGINS
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHFNITATAQTALSAEEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL
          |||||
a238      ARQWADAHFNITATAQTALAVAEAAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNEFEKFNWNSSASFDSVHKTLTPNAPGILSPDKVK
          |||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttcacc ataaaggtat tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgata gcttcgtgat tcgccaacgc cgcctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcggaccg
301 gcagtcgcgt ccgccacacg caaaactgcg ctctcgcgcc tcgggttggc
351 ggcaatttcc gcttcacccg gctttaatgc cctgccacgc attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgccagctc cggcaggggc
451 tcgtgttgcg aatatTTTTT gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaaccgcc gccctctttc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttataaaag
601 atcgcgattg cctggaaggt gcgcgtcgca ggatcctgcc cccgctcgcg
651 agtacggacg tttgtgcca cgatctgcgc cagcttgccg gttgtatcga
701 ttggacttcc cggccgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLRII LLQGDFLFFR
51  LVQSCEVEPV LVLHHLNGKS GNAHRKQQKE IRFVHCRSDV FLCYYSGIGP
101 AVRSATRKTAL LLALGLAALS ASPGFNALPT IFRGSGSKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWRL
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTtry kGCCCgAAAC CGGCKGATGG AGGTTTGTGT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTCG TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCCTGCCC TCGGATTTGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCCAGCG CGGCAGGGGC
451 GCGTGTTCGC AATATTTTTT GACAACTGTC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTAATTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CTTGGAAGGT GCGCGTCGCA GGATCCTGCC CCGCTCGCG
651 AGTACGGACG TTTGTGCGCA CGATCTGCGC CAGCTTCCGG GTTGTATCGA
701 TTGGACTTTC CGCCGTTGC GCAACAATGG CGCGCGCAAT CCGGCGGCTA
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

Homology with a predicted ORF from *N. gonorrhoeae*

m239/q239

		10	20	30	40	50	60
m239.pep		MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRIILLQGDFLFFRLIQSCEIEPV					
		:					
g239		MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLRIILLQGDFLFFRLVQSCEVEPV					
		10	20	30	40	50	60
		70	80	90	100	110	120
m239.pep		LVLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
g239		LVLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYSGIGPAVRSATRKTALLALGLAAIS					
		70	80	90	100	110	120
		130	140	150	160	170	180
m239.pep		ASPGFNALPTTIFRGSSGKSASLTAAQGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239		ASPGFNALPTTIFRGSSGKSASLTAAQLGRGSCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
		130	140	150	160	170	180
		190	200	210	220	230	240
m239.pep		RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239		RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
		190	200	210	220	230	240
		250					
m239.pep		ATMARAIRRLNRSSPX					
g239		ATMARTIWRLNRSSPX					
		250					

```

a239.seq
1  ATGCTCCACC  ATAAAGGTAT  TGCCCCGAAAC  CGGCGGATGG  AGGTTTGTGT
51  TTTCTGCCCG  CGCCCTGTAT  GCTTCGTGGT  TCGCCAAACG  CGCCTGTGTT
101 AGCCTCATTG  GCGATAATC  CTGCTCCAA  CGGATTTCCT  GTTTTTCGCG
151 CTTATCCAAA  GCTGTGAAGT  TGAGCCTGTA  CTGGTTTTCG  TGCATCACAA
201 CGGAAAAGC  GGAAACGCAC  ACCGCAAGCA  GCAGAAGGAA  ATTCAATTG
251 TTCATTGCCA  TTCAGACGT  TTTCTCTGTG  ATTGTTCCGG  TATCGGACCG
301 GCGAGTCGGT  CCGCCACACG  CAAAACCGCA  CTTCGCGCC  TCGGATTGGC
351 GGCAATTTC  GCCTCACCCG  GCTTTAATGC  CCTCGCCCG  APTTTCAGGG
401 GCGGCTCGGG  CAAATCCGCT  TCCCTGACCG  CCGCCCAGCG  CGGCAGGGGC
451 GCGTGTTCGG  AATATTTTT  GCAAACTGC  TTCACAATGC  GGTCTTCCAA
501 CGAATGGAAA  GCAATGACCG  CAAAACGTCC  GCCCTCTTTC  AGACGACACA
551 TGACCTGCGG  CAATACTGCC  CCTACTTCT  CAAGCTCGCG  GTTAATAAAG
601 ATGCGGATTG  CCTGGAAGGT  GCGCGTCGCA  GGATCCTGCC  CCCGCTCGCG
651 AGTACGGACG  TTTTGTGCCA  CGATCTGCGC  CAGCTTGCGG  GTTGATTCGA
701 TTGACCTTTC  CGCCCGTTGC  GCAACAATGG  CGCGCGCAAT  CTGGCGGCTA
751 AACCGCCTCT  CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
1  MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
51  LIQSCEVEPV LVLLHHNGKS GNAHRKQKQE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPA IFRGSGSKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSF*
```

m239/a239 97.3% identity in 255 aa overlap

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILLQGDFLFFRLIQSCEIEPV					
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRRIILLQGDFLFFRLIQSCEVEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQKKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
a239	LVLLHHNGKSGNAHRKQKKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
a239	ASPGFNALPAIFRGSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
a239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIIRRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
1  atgatagaag tcatacattt cttcggcgcc gaaacgcgca gacagtttgc
51  ttgtgccgac gttggacgat tctgcataa tgccgcgcac atccaaagag
101 gggtaaacad gggatcatc gcgcacggga gacggtccga tttataagg
151 ctgcgtattc agccgttcgt tcaaatcggg ttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
251 acggcacggt tgcgccgctg ttcgctgtct gcccggccgg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttccg gcttttgct gatggtatc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcacaa caacttccgc gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttccg gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggttg cccatcgggt
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
1  MIEVIHFFGA ETRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
51  LRIQPFVQIG FARIQCLRNH ERFDCTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAQIONH HRSGFCLMVF DRLVOLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNFR AVFAIQAVFK RKFQTFLTFA
```

201 VNIGKSDDVC KQVAHRVMAF\*

m240.seq

m240 . pep

m240/g240

a240.seq

1	ATGATAGAAG	TCATACATTT	CTTCGGCACC	GAACGCGCA	GACAGTTTGC
51	TTGTGCGCAC	GTTGACGAT	TTCTGCATGA	TGCGCGCAC	ATCCAAAGAG
101	GGGTAAACAT	GGGTATCGCG	CACGGGAGAC	GGTCCGATT	TATAAAGCTG
151	CGTATTTCAG	CGTTCGTTCA	AATCGGTTTT	GCCCGCATCC	AATGCCTTTCG
201	CATTACAAAA	CGGTTTGATT	CCGGAACCGG	TTTCGATCAT	ATCGGTTACG

551

```

251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGCATCCA
351 AAACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1 MIEVIHFFGT ETRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFDCTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVERGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAERVMFA*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1 ATGATAGAAG TCATACATT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGCATCCA
351 AACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1 MPTRPTRAAN PPTPTTLWLT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS

```



```

51  ANRRENSHNA OPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

```

m241.seq (partial)
1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTTCCTC ATCGGATGCA TCGCGCACGC TTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCAC CAAAGGGAAT ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA TTGTTGGCAT CACATCATCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

```

m241.pep (partial)
1  ..RQSVVMTVR AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFDQDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

```

m241/g241

m241.pep                                10      20      30
                                RQSVVMTVR AVDMTVCDFL IGCIAHAFNC
                                |||:|||||:|||||:|||||:|||||:
g241      QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR TVDMTVCDFL IGCIAHAFNR
              70      80      90      100     110     120

m241.pep              40      50      60      70      80      90
SLKADFHACQ RMVAVHHRLA VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFDQDQ
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g241      SFKADFHACQ RMVAVHHRLA VGNIGYTIDD NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ
              130     140     150     160     170     180

m241.pep              100     110     120     130     140     150
LRILLAERIV GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g241      LRIMLTERIV GRKRHFDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL
              190     200     210     220     230     240

m241.pep              160     170
IMQRNHGIFH DSHICPFRNS RLITGAFX
|||:|||||:|||||:|||||:|||||:
g241      IMQRNHGIFC NSHICPFRNS RLITGAFX
              250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

```

a241.seq
1  ATGCCAACAC GTCCAACGCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

```

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```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCG GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
  1 MPTRPTRA AK HPTPTWLQT AYCPRPPYR PSVQTHPHE PASSTCAAKS
 51 ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFACQ RMVAVVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADDFDNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

m241.pep                                10      20      30
                                      RQSVVVMTVRAVDMTVCDFLIGCIAHAFNC
                                      |||||:|||||:|||||:|||||:
a241      QPTYLLHPSNKMPSMEQTLFRRHQIPPSQSVVVMTVRVTVDMTVCDFLIGCIAHTFNR
              70      80      90      100     110     120

              40      50      60      70      80      90
m241.pep    SLKADFACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVGFKHHADDFDNRHARIFDTDQ
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      SLKADFACQRMVAVVHRLTVGNIGYTIDDNIAGFRIVGFKHHADDFDNRHARIFNTDQ
              130     140     150     160     170     180

              100     110     120     130     140     150
m241.pep    LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              190     200     210     220     230     240

              160     170
m241.pep    IMQRNHGIFHDSHICPFRNSRLITGAFX
              |||||:|||||:|||||:|||||:|||||:
a241      IMQRNHGILHDSHICPFRNSRLITGAFX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
 51 TTGTGCCGAC GTTGGACCAT TTCTGCATGA TGCCGCGCAC ATCCAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTTGGGATC
301 GTAGCGGGGC GTATTGGCCA AGGCGAGGAT TTCCCGCGTG CGGGCATCCA
351 AACCACACAC CGTTCCGGCT TTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCCTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCCTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTCCGCTC
601 AATATCGGTA AATCCGATGA CGTGTGAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

554

## g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMVTR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDENR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

## m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCACG CCTCTCCAC CAAAGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACACCGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

## m241-1.pep

```

1  MPTRPTRAAN PPTPPTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMVTR
101 AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMVTRAVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMVTRVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVVHRLAVGNIGYTIDDNIAAGFRIVGFKHHADFDNREHARIFDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDDNIAAGFRIVRFKHHADFDNRRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

## a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCGCAAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCCGT CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRAAK HPTPPTWLQT AYCPRPYPYR PSVQTHPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KNPSEMEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFEGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRAANKHPTPPTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSQSVVMTVRVAVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSNKMPSEMEQLFRRHQIPPSQSVVMTVRTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQRMVAVHHRLAVGNIGYTIDNIAQFRIVGFKHHADFDNREHARIFDQ					
a241	SLKADFHACQRMVAVHHRLTVGNIGYTIDNIAQFRIVGFKHHADFDNREHARIFNTDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFEGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFEGFVQKLIVGIIHL					
	190	200	210	220	230	240
	250	260				
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aactgttgtt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgct gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgcggggc atagagccga tataggtagc gcggtgcccg cggatttcgc
201 tttcgtcgcg cacgccgccc aaggccatac ggacatatat ccgccccggt
251 gctttggcga tggattcgcc caaagagggt ttgcccacgc ccggaggggc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttggaacg
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtccggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgca gcagggtgct gatgtagttg cgtacgacgg

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501 tggattcggc agacatcggc ggcatacattt tgagtttttt cagttcggac
551 aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgctc ttcttcgccc aattccttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701 atttgcggtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcggtgcg ccagtttcaa ctgcaaatgc
851 gctgcgaccg tatecggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

```

g242 . pep
1  MIGELVVLFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51  LAGHRADIGT AVPADFAFVA HAAQGHDTDF PPRCFDGFQA QRGFAHARRA
101 DQTONRTFEL VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRHHHFEFF QFGQAFFFRF FGHTRLFDAC
201 LQGIQFAFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

```

m242 . seq
1  ATGATCGGCA AACTTGTGTG TTTGTTCCGG ATCGAGCACT TCGAGCAACG
51  CGCTGGCGGG ATCGCCTCGG AAGTCGTTAC CCAATTTGTC GATTTCGTCG
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTCCG
201 TTTCGTGCGC CACGCCGCCG AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTGCGC CAAAGAGGTT TTGCCACGCG CCGGAGGGCC
301 GACCAGGCAC AGAATCGGCG CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAATCCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCC
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCITTTGCTG CGCGGGATT
451 TTCTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATT TTAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCCTTGT
651 GTATCGCTTT AATCTGTTCG TTCAGATAAT ATTCGCGCTG GGAATTTTCC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGGAATTC CAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

```

m242 . pep
1  MIGKLVVLFV IEHFEQRAGG IASEVVTQFV DFVEQEQQVF HAGFCHILQN
51  LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGFQA QRGFAHARRA
101 DQAQNRAFEF VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFELE QFGQAFFFRF FGHTRLFDIC
201 FQGIQFAFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

```

m242/g24290.3% identity in 289 aa overlap
          10      20      30      40      50      60
m242 . pep  MIGKLVVLFVIEHFEQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA
          |||:||||| ||||:||||| :||:||||||| | :| |||||:|||||:
g242        MIGELVVLFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVSYACFCHILQNLGHRADIGT
          10      20      30      40      50      60

          70      80      90     100     110     120
m242 . pep  AVSPDFAFVAHAAQSHADIFPPRCFGDGFQAQRGFAHARRADQAQNRAFEFVHTFLDGEVF
          || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g242        AVPADFAFVAHAAQGHDTDFPPRCFGDGFQAQRGFAHARRADQTONRTFELVHTFLDGEVF
          70      80      90     100     110     120

```

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	130	140	150	160	170	180
m242.pep	QNPFDFDFFQAVVVG	IQHQSGFGDVFAD	AGFFLPRQLQESVD	VVAYDGGFRHRH	WHHFELF	
				:		
g242	QNPFDFDFFQAVVVG	IQHQSGFGDVFAD	AGFFLPRQSEQGV	DVVAYDGGFGHRH	RHHHFEFF	
	130	140	150	160	170	180
	190	200	210	220	230	240
m242.pep	QFGQAFFFRFFGH	TRLFDICFQGIQ	FAVFVFFAQFFV	YRFLNFVQII	FALGFFHLAF	DAS
			:			
g242	QFGQAFFFRFFGH	TRLFDACLQGIQ	FAVFVFFAQFFV	YRFLNFVQII	FALGFFHLAF	DAS
	190	200	210	220	230	240
	250	260	270	280	290	
m242.pep	AYAFFGLHNVFEG	FQLCQQEFHPF	ADFGNQLN	LALRQFQLQ	MRCDRIGX	
g242	AYAFFGLHNVFEG	FQLCQQEFHPF	ADFGNL	ONLALRQFQLQ	MRCDRIGX	
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID:921>:

```
a242.seq
1  ATGATCGCGGC  AACTTGTGTGT  TTTGCTCGGG  ATCAAGCACT  TCGAGCAACG
51  CGCTGGCGGG  ATCGCCCCGG  AAGTCGCTAN  CCAATTGTGC  GATTTCGTCG
101 AGCAGGAAAC  ATGGGTTTT  TACGCCGGCT  TTTGCCATAT  TCTGCAAAAT
151 CTTACCGGGC  ATGGAGCCGA  TATAGGTGCG  GCGGTGTCCC  CGGATTTGCG
201 TTTCTGTCGC  CACGCCGCC  AAAGCATTGC  GGACATATTT  CCGCCCCGTT
251 GCTTTGGCGA  TGGATTGCGC  CAAAGAGGTT  TTGCCACGCT  CTGGAGGGCC
301 GCCTAGCGAC  AGAATCGGSC  CTTTGAGTTT  GTCCATAGTT  TTTGGACGG
351 CGAGGTATTC  CAAAATCC3T  TCTTTGACTT  TTTCCAGGCC  GTAGTGGTTC
401 GTATCCAGCA  CCAATCCG3C  TTGGCGGATG  TCTTTGCTGA  CGCGGGATTT
451 TTTCTTCCAC  GGCAGTTCSA  GCAGGGTGTC  GATGATATTT  CTGACGACGG
501 TGGATTCCGC  AGACATCGSC  GGCATCATTT  TGAGCTTTTT  CAGTTCGGAC
551 AGGCATTTTT  CTTCCGCTTC  TTTGGTCATA  CCCGCCTTTT  TGATATCTCG
601 TTCCAAGGCA  TCCAGTTCGC  CGTTTTCGTC  TTCTTCGCCC  AGTTCTTTGT
651 GTATCGTGT  AATCTGTTGC  TTCAGATAAT  ATTTCGCGTG  GAGATTTTCC
701 ATTTGGCGTT  TGACGCGTCC  GCGTATGCGT  TTTTCGGCCT  GCATAAATGTC
751 GAGTTCGGAT  TCCAGCTGTG  CCAGCAGGAA  TTCCATCGT  TTGCCGATTT
801 CGGGAATTT  CAAAATCTGT  TGGCGTTGCG  CCAGTTTCAA  CTGCAAATGC
851 GCTGCGACCG  TATCGGTTAG
```

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242.pep

1	MIGELVVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
101	DQAQNRAFEF	VHTFLDGEVF	QNPFDFDFQA	VVVGIQHQSG	FGDVFADAGF
151	<u>FLPRQFEQGV</u>	DVVAYDGGGF	RHRRHHFELF	QFGQAFFFRF	FGHTRLFDIC
201	<u>FQGIQFAFV</u>	<u>FFAQFFVYRF</u>	<u>NLFVQIIFAL</u>	<u>GFHFLAFDAS</u>	<u>AYAFFGLHNV</u>
251	<u>EPGFQLCQVE</u>	<u>PHFPADGNGF</u>	<u>QNLLALRQFL</u>	<u>LMQRCDRIG+</u>	

**m242/a242 95.2% identity in 289 aa overlap**

	10	20	30	40	50	60
m242.pep	MIGKLVLVLF	GIHFEQRAGGI	ASEVVTQFVDF	VEQEQQGVF	HAGFCHILQ	NLTGHRADIGA
a242	MIGELVLLGI	KHFEQRAGGI	AEVAXQFVDF	VEQEQQWVF	YAGFCHILQ	NLTGHGADIGA
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGF	AQRGFAHARR	ADQAQNRAFE	FVHTFLDGEVF
a242	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGF	AQRGFAHARR	ADQAQNRAFE	FVHTFLDGEVF
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFFDFFQ	AVVVGIGIQ	HQSFGGDVF	ADAGFFLPR	QLQEQSDVV	AYDGGFRHR
	130	140	150	160	170	180
	QNPFFDFFQ	AVVVGIGIQ	HQSFGGDVF	ADAGFFLPR	QLQEQSDVV	AYDGGFRHR
	130	140	150	160	170	180

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```

a242      QNPFDFFOAVVVGIIQHSGSGFDVFADAGFFLPRQFEQGVDDVAYDGGGFRHRRHHFELF
           130      140      150      160      170      180

           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS
           190      200      210      220      230      240

           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHPEADFGNFQNLALRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHPEADFGNFQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGCC cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTC
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGyGGT TTTTCAACGA ATCCCACACG GGGGCGAaYA GGTCTTCCTC
201 TTCCTGCAAA CCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTC
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

m243/g243

```

           10      20      30      40      50      60
m243.pep  MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      MVIVWLPELPPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60

           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

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70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGGCA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRTSTISS TVTLPMSEFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRTSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRTSTISSVTLPMSFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccgccc gccgggttca gacggcattg ccgctttact
51  tccatcggtt taccgcaaaa accgcttcca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggag
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaaag catctgcaca cccattttca
351 ggcacatgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttcac ggcaaaactc tgccggcgga acttggtgct
451 atcggaatt tcctgctggt gccggcgagg caggttttgc tcgtttgcca
501 aagcgcgag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtcgcattt cctactgtct cgaagggttc caccgcctcc acattttcaa
651 ccgcttcttc actgctttgc tgcgtgtctc gttcgtcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTONALOEIN QIIPOTPSGF LPCHRNHSRA
51  QHTVGQGITL LHHTNHGIGF LLTGHLRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLAH IVSLKTNWKS KSGYPPSKIR
251 TFSRNFQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq



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```

1 ATGCCGTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51 TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCT CTTCATCACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTCCTTGA TTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTTCT GCACACCGTC
601 CGCATTTTCT ACTGTTTTCGA CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGTCTG TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAACAGAGA ATTCAAAAT CATTTTCAAA
801 TCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

```

m244.pep
1 MPSEARQAGS DGIAALLRSV YTONALQBIN QIIPQTPSGF LLRHRNHSRA
51 QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRS
101 IKCFQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNPLLVAQA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLCLFAHI VSLKTNWKS SKSYYPKIRT
251 FSRNFXQQR ISNSFSNPLP KKXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQBINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTONALQBINQIIPQTPSGFLPCHRNHSRAQHTVGQGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m244.pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVIRIRNPLLVAQAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVIRIGNFLLVAQAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244.pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVIRISYCLDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKXYRRX					
g244	KSGYYPSKIRTFSRNFKQROEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTATCACG CCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATGCGCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAA CTCTATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTC ACTGTTTTCG TGCTGTGTCT GTTGGCTCAT ATCGTATCCC
701 TTAACAACAA TTGGAAATCA AAATCCAGTT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEI	QIIPQTPSGFLLRHRNHSRAQHAVGQRITL				
a244	MPSEARQAGSDGIAALLRSVYTONALQEI	QIIPQTPSGFLLCHRNHSRAQHAVGQRITL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIAR	FRVDFDLRSIKCFLQLVQSHLHAHFQRIE				
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIAR	FRIDFLDLRSIKCFLQLVQSHLHAHFQRIE				
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQRHFQIILDRQHFHGKLLSGELVR	IRNFLVAAAQVLLVCQSA-LLVFQLRFQL				
a244	IAALIQRHFQIILDRQHFHGKLLSGELVR	IRNFLVAAAQVLLVCQSAQLLVFQLRFQL				
	130	140	150	160	170	180
	180	190	200	210	220	230
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGF	HRLHIFNRFFTVLLCLFAHIVSLKTNWKS				
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGF	HRLHIFNRFFTVLLCLFAHIVSLKTNWKS				
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQXORISNSFSNPL	PKKXYRRX				
a244	KSSYYPRKIRTFSRNFXQXORISNSFSNPL	PKKXYRRX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgcgcctg aagcccggcc ggcgggttca gacggcattg ccgctttact
```

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```

51  tcgatcggtt  tatacgcaaa  acgcgcttca  ggaaataaat  cagattattc
101  cccagacgcc  ttcaggcttc  cttccgtgcc  accgtaacca  tagccgggcg
151  caacacacgg  tcggacaggg  tataaccctt  cttcatcaca  ccaaccacgg
201  tattgggttc  ctgctcactg  gccaccgcct  gcacgcctg  atggatatte
251  ggatcgagct  tatcgcccg  tttaggattg  atttcttga  tttgcgtggc
301  atcaaacgcc  ttctgcaact  cattcaaagt  catctgcaca  cccattttca
351  gcgcatcgaa  attaccgctc  tgatccaaaa  ggcgcatttc  cagataatcc
401  ttgaccggca  acatttccac  ggcaaaactt  tgcgcggcga  acttgtgcgt
451  atcggcaatt  tcctgctggt  ggccggcgcg  caggttttgc  tcgtttgcca
501  aagcgcgcag  ttgttcgtct  ttcaactcgc  cttccagctc  ggcaatccgc
551  gccctgcaat  cctcataagc  cggctcggcg  gcagcctgtt  cctgtacacc
601  gtccgcattt  cctactgtct  cgaacggttc  caccgcctcc  acattttcaa
651  ccgctttctc  actgttttgc  tgctgtgtct  gttcgctcat  atcgatatcc
701  tcaaaacaaa  ttgaaatca  aaatccggtt  attaccggag  caagataagg
751  acattttcaa  gaaacttcaa  gcaaaggcag  gaaatttcac  atccgcccgc
801  gaatacccta  ccgcaaaaac  catataaacg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LPCRHNHSRA
51  QHTVGQGITL  LHHTNHGIGF  LLTGHRHLRL  MDIRIELIAR  FRIDFLDLRG
101  IKRLLQLIQS  HLHTHFQRIE  ITALIQKRHF  QIILDRQHFF  GKLLSGELVR
151  IGNFLLVAAA  QVLLVCQSAQ  LFVFLRFQL  GNPRLQILIS  RLGGSFLFLT
201  VRISYCLDGF  HRLHIFNRF  TVLLCLFAH  IVSLKTNWKS  KSGYYPKIR
251  TFSRNFQQRQ  EISHPPNTL  PQKPYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGCTCG  AAGCCCGACA  GCGGGGTTC  GACGGCATTG  CCGCTTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA  GGAAATAAAT  CAGATTATTC
101  CCCAGACGCC  TTCAGGCTTC  CTTCTGCGCC  ACCGTAACCA  TAGCCGGGCG
151  CAACACGCGG  TCGGACAGCG  TATAACCCCT  CTTATCACA  CCCACCACGG
201  TATTCGGCTC  CTGTTGCTT  GCCACCGCCT  GCATCGCCTG  ATGGATATTC
251  GGATCGAGCT  TATCGCCCGC  TTTAGGGTTG  ATTTCTTGA  TTTGCGTAGC
301  ATCAAATGCT  TTCTGCAACT  CGTTCAAAGT  CATCTGCACG  CCCATTTTCA
351  GCGCATCGAA  ATTGCCGCTC  TGATCCAAA  GCGCCATTTC  CAGATAATCC
401  TTGACCGGCA  GCATTTCCAC  GGCAAACCTT  TGTCGGCGCA  ACTTGTGCGT
451  ATCCGCAATT  TyCTGCTGGT  GCGCGCGCG  CAGGTTTTGC  TCGTTTGCCA
501  AAGCGCGCTG  CTCGTCTTTC  AACTGCGTTT  CCAGCTCGGC  AATCCGCGCC
551  TGCAATCCT  CATAAGCCGG  CTCGTGCGCA  GCCTGTTCCT  GCACACCGTC
601  CGCATTTTCT  ACTGTTTCT  CGGTTTCCAC  CGCTCCACA  TTTCAACCG
651  CTTCTTCACT  GTTTGCTGC  TGTGCTGTT  CGCTCATATC  GTATCCCTTA
701  AAACAAATTG  GAAATCAAAA  TCCAGTTATT  ACCGCGCGCA  GATAAGGACA
751  TTTTCAAGAA  ACTTCAAKCA  AAACAGAGA  ATTTCAAATT  CATTTTCAAA
801  TCCCTACCG  AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101  IKCFLLVQVS  HLHAHFQRIE  IAALIQKRHF  QIILDRQHFF  GKLLSGELVR
151  IRNFLLVAAA  QVLLVCQSAL  LVFQLRFQL  NPRLQILIS  LCGSLFLHTV
201  RISYCFDGFH  RLHIFNREFT  VLLCLFAHI  VSLKTNWKS  SSYPYRKIRT
251  FSRNFXQQR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCRHNHSRAQHTVGQGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFLQ					
g244-1	ITALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSAQLFVFQLRFLQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTF SRNFXQXQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTF SRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTC GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTATCAGC GCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCGCG TTTAGGATTG ATTCCTTGA TTGCGTAGC
301 ATCAAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCAGC CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAATTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCGC CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TCAACTGCG CTTCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCAATT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCCTTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAACACAAA TTGGAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGCGAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTCA CCGAAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLOLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAQ LLVFQLRFLQ GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLOLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLOLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSA-LLVFQLRFLQ					
a244-1	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSAQLLVFQLRFLQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
	180	190	200	210	220	230
	190	200	210	220	230	240

```

g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgccct tcgttttcga
51  ccagacacag cgtgcccggt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgtctga aatatcgcgc agggctttgc gggcgaatcc
151 agtcagtgtg tccacgtcgt ctgtaagcgg tgtgcgcagg ttttgcgtga
201 ccagtcctgt gactcgtttc ttggttttat ggatgcgggg catcacgata
251 tgggtcggta ttctgcctgc catttggaag ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 ctctgcctga catggatttg ccttgacca tcagcttgcc gtttttggtc
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtactttc acgcccaact tagtcagggt ttcttccaa tgctccagca
501 qcqcqqgtaa

```

g246.pep

1	MYGRNGSTQA	AVAFVFDQTQ	RARFGNGEVY	AAQADIGSAV	NIAQGFGAES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFPAD	HGFAPDHQLA	VFGCDDVDVN	LAGFGRGFRP
151	VYFHAQLSQV	FFQLLQRG*			

```
m246.seq (partial)
1 ATGCACGGGC GGTACGGTGG TACTCAAGCG ACGTTgCTT CGTTTTCCAC
51 CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCATCCAAAC
101 GCACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTCAGCGGC GTACCCAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACGATAT
251 GGGTCGGTTT TTGCGCTGCC ATTTGGACGA TGAACTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGCTTT TGCTTCAAGA TAATGrTTCA GCTCGATTC
351 CTCGCTGACC ATCGATTTC CTTTGACCAT CAGCTTGCCG TTTTGGCTG
401 TGATGATGTC GTGGATATG TGGCAGGCTT CGGTGGGGT TTTCTGCCG.
```

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQIQ	RTCFSGNGKVY	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFGFVDSR	HHDMGRFFAC	HLDDLEAQVA
101	FYRFNAFCFK	IMXQDLFLAD	HREAFDHOLA	VFGCDDVVDN	LAGEGRGFCP...

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVHQ	TQRTCF	SNKGVI	YATQTD	IGSAV	NIACQCFTEAGQLVYIVCQR
	: :	: :	: :	: :	: :	: :
g246	MYGRNGSTQA	AAVAFV	PDQTOR	ARFNGE	VYAAQAD	IGSAVNIACQGFAGESGQLVHVVKCR
	: :	: :	: :	: :	: :	: :
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANLFF	GFVDSR	HRHDMGR	FFACHL	DDLEAQ	VAFYRFNAPCFKIMXQLDFLAD
	: :	: :	: :	: :	: :	: :
g246	CAEVLVEQFADLFF	GFMDCG	HRHDMGR	FFACHL	DDKLAQ	VAFHRLNAPCFKIMVOLDFFAD
	: :	: :	: :	: :	: :	: :

565

	70	80	90	100	110	120
m246 . pep	130	140	150			
	HRFAFDHQLAVFGCDDVDNLAGFGRGFCP					
g246	130	140	150	160		
	HGFAFDHQLAVFGCDDVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

```

1   ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTTCCT
51  CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCACTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGG
201 ACAGTTCGCT AACCTGTTCT TTGGTTTTAT GGATTGCGGG CATCACGATA
251 TGGGTCGGTT TTTACCTGTC CATTGGGACG ATGAAGTCGC CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTG CCTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGAGGCT TCGGCCGGTG TTTCCGCCCA
451 GTGTACTTTT ACGCCCACT TGGTCAGGT TTCTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

```

1   MHGRNGGTQA TVAFVFHQQTQ RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51  GQLVYVVR*R CAEVLVEQFA NLFFGEMDCG HHDMGRFFTC HLDDELAQVA
101 FHRFNAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVDVD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQQTQRTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
m246 . pep	70	80	90	100	110	120
	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCHLDELAQVAFHFRNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
m246 . pep	130	140	150			
	HRFAFDHQLAVFGCDDVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDVDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

```

1   atgaaacgta aaatgctaaa cgtaccaaag ggcggttatg atggtatgaa
51  ggggttttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccggaa attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaatgttc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaactcaa
301 tctaaccttg caaaacccgg tgccaaacaa gaaaatcccc tttttcctt
351 aaaaaggagc ggcattgata acaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggtatcg atgatcttga tgcgagtgcg gagactgttg tagtcagcag
501 ctgttccaaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatic

```

566

```

601 acccgctcaga aacatgtggt caatgcctat gcggtcggca ggtttggcaa
651 taatgaggaa agtttgttcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaagggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttgtcc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tgcacaaatc caaaaatgct gttacgcctg
851 ccggggtgga ggttttattg gatagcggcc ttaatgcca gattgcccgt
901 tcttcagaca atagtattta tgcttaccgt atcaatgcga caatacgcgg
951 gggaaatgta tgcgcaaaaca gaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pep

```

1 MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIIVVS SYFTSRKLND
51 VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQTO
101 SNLAKPGAQK ENPLFSLKRS GMDKQLIPVA ESIDIKYPGF IQRLNALVFQ
151 YGIDDLASA ETVVSSCSK IAKPGKKIST LQEAKSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLFRFQLDDK GKWGNPQLLV KKVKRMDVRY
251 IYVSGCPEDE DAGKEEFKY TNKFDKSKNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

```

1 ATsAGACGTA AAATGCTAAA CGTwsyArAA GGCAGTTATG ATGGTATGAA
51 AGGTTTACC ATTATGAAT TTTTGGTTGC GGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTC AATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AAGTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

```

1 XRRKMLNVXX GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPTDQQN
101 SPFSLKRNGI DKLPIAESS NINYQNFFQV GSALIFOYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKGKW GNPQL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGS SYFTSRKLND AANERLAAQQ					
	:      :      :      :      :      :					
g247	MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIIVVSSYFTSRKLNDVANERLAIQQ					
	10	20	30	40	50	60
	70	80	90	100		
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONSPFSLKRN					
	:      :      :      :      :					
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAAPGAQENPLFSLKRS					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LPIAESSNINYQNFFQVGSALIFOYGIDVNASTATTVVSSCAAISKPGKQIPT					
	:    :    :    :    :    :					





568

	170	180	190	200	210	220
m247 . pep	PGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIADEESLFRFQI.DDKGKW					
a247	PGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNAYAVGRIAGEEGLFRFQLDDKGKW					
	190	200	210	220	230	
m247 . pep	GNPQL					
a247	GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEKFKYTGTFSSTNAVTPAGVEVLLSXG					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1 CCCGGTGCCA AACAAAGAAA TCCCCTTTT TCCTTAAAA GGAGCGGCAT
51 GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG AAGGGCAA GTGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGT ATGGATGTGC GGTATATTTA TGTTCGGGT
451 TGTCTGAAG ATGAAGATGC CGGCAAGAG GAAAATTCA GATATACGAA
501 TAAATTCGAC AAATCCAAA ATGCTGTAC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGGGACAATA CGCGGGGAA ATGTATGCGC
651 AACAGAACA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1 PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYGIID
51 LDASAETVVV SSCSKIAPG KKISTLQEAK SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIASSDNS
201 IYAYRINATI RGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1 ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51 AGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAACG AGCGTCTTGC CGCGCAACAG GATTTCGGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCGAATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCAGGTT GGTAGCGCAT
401 TGATTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGGACTACC
451 GTCGTACGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAGAGT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCCGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAATGC
801 TGTTACGCCG GCCGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1 MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPTTQQN
101 VPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 SVSSCAAIK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEGLF RFOLDKKGW GNPOLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TOTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```

569

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

      70      80      90     100     110     120
m247-1.pep  NAATLIVRDARMAGGFGCFNMSEHPATDVI PTTQONSPFSLKRNIGDK-LIPIAESSNI
      | : | : | | | | : | | | | : | | | | : |
g247-1      PGAKQENPFLSLKRSMDKQLIPVAESIDI
              10      20      30

      130     140     150     160     170     180
m247-1.pep  NYONFFQVGSALIFQYIGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDODK
      : | : | : | | | | | | | | : | | | | : | | | | : | : |
g247-1      KYPGFIORLNALVFQYIGIDDLASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK
              40      50      60      70      80      90

      190     200     210     220     230     240
m247-1.pep  EONGNIAQRHVVVNAYAVGRIAD-EEGLFRFQDDKKGWGNPQLLVKKVRHMKVRYIYVS
      | | | | : | | | | | | | : | | | | | | | | | | | | | |
g247-1      -QNCNITRQKHVVVNAYAVGRFGNNEESLFRFQDDKKGWGNPQLLVKKVRMDVRYIYVS
              100     110     120     130     140

      250     260     270     280     290     300
m247-1.pep  GCPEDDDAGKEETFKYTDKFDQAQNAVTPAGVEVLLSSGDTKIAASSDNHIYAYRIDAT
      | | | | : | | | | : | : | | | | | | | | : | | | | | | | |
g247-1      GCPEDDAGKEEKFRYTNKFDKSKNAVTPAGVEVLLDGLNAKIAASSDNSIYAYRINAT
      150     160     170     180     190     200

      310
m247-1.pep  IRGGNVCANRTLX
      | | | | | | | |
g247-1      IRGGNVCANRTLX
      210     220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

```

a247-1.seq (partial)
1  AATAATACAG CTAAATTGAT TCCTATGCT GAATCCACAG ATATTAAATA
51  TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TCGGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCTCAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGCG AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCTCGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCC ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTSGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTATATG TTACCGTATC GATGCGACAA TACCGGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 958; ORF 247-1.a&gt;:

```

a247-1.pep (partial)..
1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAQSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

              10      20      30
a247-1.pep  NNTAKLIPIAESTDIKYPGFAQARPALIFQ
              | : | | | | | | : | : | : |
m247-1      GFGCFNMSEHPATDVIPTTQONSPFSLKRNIGDKLIPIAESSNINYNQFFQVGSALIFQ
              80      90     100     110     120     130

              40      50      60      70      80      89
a247-1.pep  YGIDDLASAETVVVSSCSKIAKPGKKISTLQEAQSALQITNDDK-QNGNITRQRHVVNA
      | | | | : | | | | : | | | | : | | | : | | | | | | | |
m247-1      YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIAQRHVVNA
              140     150     160     170     180     190

      90      100     110     120     130     140     149
a247-1.pep  YAVGRIAGEEGLFRFQDDKKGWGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY
      | | | | | | | | | | | | | | | | | | | | | | | |

```

g248.seq

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

g248 . pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

m248.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

m248.pep (partial)

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/q248

m248.pep

571

```

g248      MRKQNTLTGIPTSDGQSGSALFIVLMVMIVVAFVVTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :|||||: :||| |||||
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70      80      90      100     110     120

           110     120     130     140     150
m248.pep  TVEAVKRSCPA---NSTDLCDIKKGXEYKKGTRSVTKMPRYII EYLGXNGENVYRVTA
           :|||||||  |||||:| ||:|: :|:||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLGXNGQNVYRVTA
           130     140     150     160     170     180

           160     170     180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           ||||| ||||| ||||| :|||
g248      KAWGKNANTVVVLQSYVGNINDEX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCTA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLGXNGENV YRVTAWGWK NANTVVVLQS YVSNINDEX*

```

m248/a248 89.4% identity in 180 aa overlap

```

           10      20      30      40
m248.pep  GFALLIVLMVXIVVAFXXVTAQSYNTEQRI SXNESDRKLAXS
           |||:||||| ||||| ||||| ||||| ||||| |||||
a248      MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNNDNEEAFDNIVVQKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEAAALREGEFQVLDLEYDTSKVTFSENCGKGLCTAVNVRTNNDNEEAFDNIVVQKPT
           70      80      90      100     110     120

           110     120     130     140     150     160
m248.pep  VEAVKRSCPANSTDLCIDIKKGXEYKKGTRSVTKMPRYII EYLGXNGENVYRVTAWGWK
           ||||| ||:| |||:| |||||:|:||||||| ||||| |||||
a248      VEAVKRSCTAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLGXNGENVYRVTAWGWK
           130     140     150     160     170     180

           170     180
m248.pep  NANTVVVLQSYVSNINDEX

```

572

|||||  
a248 NANTVVVLQSYVSNNDX  
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq  
1 ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG  
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT  
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC  
151 AACGAATCAG ACAGGAATTT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG  
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG  
251 TTACATTTAG CGAAACTGT GGAAGGTC TGTGTGCCG AGTGAATGTG  
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG  
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG  
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC  
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTTGGGCG TGAAGAACGG  
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA  
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep  
1 MRKQNTLTGI PTSQGQGFALFIVLMVMIV VAEFLVTTAAQ SYNTEQRISA  
51 NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV  
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCPA NSTDLCKDK GMEYKGRTRS  
151 VSKMPRIIE YLGVKNGENV YRVTAANGK NANTVVVLQSYVSNND\*

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVTTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVTTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGELOVLDLEYDTDSKVTFSENCGRGLCAAVNVRTNND-NEEAFDNIVVQKPT					
g248	LAEALREGEFQVLDLEYAADSKEVTFSENCGRGLCTAVNVRTNNDNEEAFDNIVVQKPT					
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA----NSTDLCKDKGMEYKGRTRSVSKMPRIIEYLGVKNGENVYRVTA					
g248	AVEAVKRSCPAKSGKNSTDLCKDKGMEYKGAAGVSKMPRIIEYLGVKNGENVYRVTA					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNNDX					
g248	KAWGKNANTVVVLQSYVGNNDQX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVTTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVTTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGELOVLDLEYDTDSKVTFSENCGRGLCAAVNVRTNNDNEEAFDNIVVQKPT					
a248	LAEALREGELOVLDLEYDTDSKVTFSENCGRGLCTAVNVRTNNDNEEAFDNIVVQKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCKDKGMEYKGRTRSVSKMPRIIEYLGVKNGENVYRVTAANGK					
a248	VEAVKRSCPAKSTGLCKDKGMEYKGRTRSVSKMPRIIEYLGVKNGENVYRVTAANGK					
	130	140	150	160	170	180

```
g249.seq
1  atgaagaata atgattgctt ggcctgaaa aatccccagt cgggataggc
51  gttgatagaa gtccttggtc ctatgctctg tctgcacatc ggtattctgg
101 cattgtgcga cgtacagctt ggcagctcgt cttccgcaag ggaaggcgaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaattgt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgctgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgcggatgct ggtagctatt cattacgcgc
401 tctgcaagga ttcgtcgggt ggcgcgccga cattgtccga cagcgggtct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcgga
601 ggtcgtgaat ga
```

```
g249.ppep
1  MKNNDCLRRLK  NPQSGMALIE  VLVAMLVLTI  GILALLSVQL  RTVASVREAE
51  TOTIVSOITQ  NLMEGNLMNP  TIDLDSNKKK  YSLYMGKQTL  SAVDGEFMIL
101 AEKSKAQLAE  EQLKRFSHBL  KNALPDVAIV  HYAVCKDSSG  DAPTLSDSGA
151 FSSNCDNKAN  GDTLIKVLWV  NDSAGDSDIS  RTNLEVSGDN  IVYTYQARVG
201 FSS*
```

```
m249.seq
  1  ATGAAGAATA  ATGATTGCCT  CCGCTGAAA  GATTCCCAGT  CCGGTATGGC
51  GCTGATAGAA  GTCTTGGGT  CTATGCTCGT  TCTGACCATC  GGTATTTTGG
101 CACTATTGTC  TGTACAGTTG  CGGACAGTCG  NNNNNNNNNN  NNNNNNNNNN
151 NNNNNNNNNN  NNNNNNNNNN  NNNNNNNNNN  NNNTTGATGG  AGGGAATGTT
201 GATGAATCCG  ACCATTGATT  CGGACAGCAA  CAAGAAAAAC  TATAATCTTT
251 ACATGGGAAA  CCATACACTA  TCAGCTGTGG  ATGGCGATT  T  TGCAGTTATG
301 GCCATGAAAA  CTAAGGGGCA  ATTGGCAGAG  GCACAATTGA  AGAGATTTTAG
351 TTATGAGCTG  AAAAAATGCCT  TGCCGGATGC  GGCAGCCATC  CATTACGCCG
401 TCTGCAAGGA  TTCGTCGGGT  AACGCGCCGA  CATTGTCCGG  CAATGCTTTT
451 TCTTCAAATT  GCGACAATAA  GGCAACGGG  GATACTTTAA  TTAAAGTATT
501 GTGGGTAAAT  GATTCCGCAG  GGGATTCCGA  TATTCCCGT  ACGAATCTTG
551 AGGTGAGCGG  CGACAATATC  GTATATACTT  ATCAGGCAAG  GGTCCGAGGT
601 CGGGAATGA
```

```
m249 .pep
  1  MKNNDCFRLK  DSQSGMALIE  VLVAMLVLTI  GILALLSVQL  RTVXXXXXXXX
 51  XXXXXXXXXX  XLMEGMLMNP  TIDSDSNKKN  YNLYMGNHITL  SAVDGDFAID
101  AMKTGKGLAE  AQLKRFSYEL  KNALPDAAAI  HYAVCKDSSG  NAPTLSGNAP
151  SSNCNDKANG  DTLIKVLWVN  DSAGSDSISR  TNLEVSGDNI  VYTYQARVGG
201  RE*
```

m249.pep MKNNDCFR LKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX  
| | | | : | : | | | | | | | | | | | | | | | : | : | :

574

g249	MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ	10	20	30	40	50	60
m249.pep	XLMEGMLMNPITIDSDSNKKYNLYMGNHTLSAVDGDFAIDAMKTKGQLAEAQLRFSYEL	70	80	90	100	110	120
g249	NLMEGMLMNPITIDLSNKKNYSLYMGKQTL SAVDGEFMLDAEKSQAQLAEEQLRFSHEL	70	80	90	100	110	120
m249.pep	KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVNSAGDSDIS	130	140	150	160	170	179
g249	KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVNSAGDSDIS	130	140	150	160	170	180
m249.pep	RTNLEVSGDNIVYTYQARVGGREX	180	190	200			
g249	RTNLEVSGDNIVYTYQARVGGREX	180	190	200			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```
a249.seq
1  ATGAAGAATA  ATGATTGCTT  CCGCCTGAAA  AACCCCCAST  CCGGTATGGC
51  GCTGATAGAA  GTCTTGGTCG  CTATGCTCGT  TCTGACCATC  GGTATTTTGG
101 CACTATTGTC  TGTTCCAGTTG  CGGCAGTCGT  CTTCCGTGAG  GGAGGCAGAG
151 ACGCAAACCA  TCGTCAGTCA  AATCACGCAA  AACCTGATGG  AAGGAATCTT
201 GATGAATCCG  ACCATTGATT  CGGCACAGCA  CAAGAAAAAC  TATAATCTTT
251 ACATGGGAAA  CCAATCATGCA  CTATCAGTTG  TGGATGGCGA  TTTTCAAGTT
301 GATGCCATAA  AAACCTAAGAC  GCAGTTGGCA  GAGGCACAAT  TGAAGAGATT
351 TAGTTATGAG  CTGAAAAATG  CCTTGCCGGA  TCGCGCAGCC  ATCCATTACG
401 CGCTCTGCAA  GGAATCGTCG  GGTGTTGCGC  CGACATTGTC  CGCCGGCAGT
451 ACTTTTCTT  CAAATTGCGA  TGGTAGTGCA  AATGGGGAIA  CTTTGATTAA
501 AGTATTGTGG  GTAATTGATT  CGGCAGGGGA  TTCCGATATC  GCCCGTAGCA
551 ATCTTGAGAC  GAACGGCAAC  AATATCGTAT  ATACCTATCA  GGCAAGGGTC
601 GGAGGTGCGG  AATGA
```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

a249.pep

1	MKNNDGFR	LK	NPQSGMALIE	VLVAMLVLT	I	GILALLSVQ	L	RTVASVREAE
51	TQTIVSQITQ		NLMEGMLMNP	TIDDSNKK	N	YNLYMGNHHA		LSVVDGDFQV
101	DAIKTKTQLA		EAQLKRFSYE	LKNALPDAAA		IHYAVCKDSS		GVAPTLSAGS
151	TFSSNCDGSA		NGDTLIKVLW	VNDSAGSDSI		ARTNLETNGN		NIVYTYQARV
201	GGRE*							

**m249/a249 81.9% identity in 204 aa overlap**

	10	20	30	40	50	60
m249.pap	MKNND	CFRLK	DSQSG	MALEI	VLVAM	LVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
a249	MKNND	CFRLK	NPQSG	MALEI	VLVAM	LVLTIGILALLSVQLRTVASVREAEQTQTIVSQITC
	10	20	30	40	50	60
	70	80	90	100	110	119
m249.pap	XLMEG	MLMNP	TDS	SNKK	NYNLY	MGNH-TLSAVDGDFAIDAMKTKGQLAEQ
a249	NLMEG	MLMNP	TDS	SNKK	NYNLY	MGNH-HALSVVDGDFQVDAIKTKTQLAEQ
	70	80	90	100	110	120
	120	130	140	150	160	170
m249.pap	LKNAL	PDAAA	IHYAV	CKDSS	GNAPT	LS-GNAFSSNCDNKANGETLIKVLWVND
a249	LKNAL	PDAAA	IHYAV	CKDSS	GVAPT	LSAGSTFSSNCDGSANGDTLIKVLWVND
	130	140	150	160	170	180

575

```
m249.pep      180       190       200  
               SRTNLEVSGDNIVYTYQARVGGRGX  
              :| ||||:::|| | || | || ||  
a249          ARTNLETNGNNIVYTYQARVGGRGX  
                190         200
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 973>:

m249-1.seq

1	ATGAAGAATA	ATGATTGCTT	CCGCCTGAAA	GATTCCCACT	CCGGTATGGC
1	GCTGATAGAA	GTCPTGGTTG	CTATGCTCTG	TCTGACCATT	GGTATTTTGG
501	CACATATTGTC	TGTACAGTGT	CGGACAGTCG	CTTCCGTCAG	GAGAGCGGGA
151	ACACAAACCA	TCGTAGCCCA	AATCAGCCAA	AACCTGATGG	AGGGAATGTT
201	GATGAATCCG	ACCATTGATT	CGGACAGCAA	CAAGAAAAAC	TATAATCTTT
251	ACATGGGAAA	CCATACACTA	TCAGCTGTGG	ATGGCGATT	TGGCATTTAT
301	GCCATGAAA	CTAAGGGGCA	ATTGGCAGAG	GCACAATTGA	AGAGATTTAG
351	TTATGAGCTG	AAAATGCGT	TGCCGGATGC	GGCAGGCATC	CATTACGCCG
401	TCTGCAAGGA	TTCTGCGGTT	AACGCCGCCA	CATTGTCGGG	CAATGCTTTT
451	TCTTCAAAAT	CGCACATAAA	GCGAAACGGG	GATACTTTAA	TAAACTATTT
501	GTGGGTAAT	GATTCCGCAG	GGGATTCGGA	TATTTCCCGT	ACGAATCTTG
551	AGGTGAGCGG	CGACAATATC	GTATATACTT	ATCAGGCAAG	GGTCGGAGGT
601	CGGGATGAGA				

This corresponds to the amino acid sequence <SEQ ID 974; ORF 249-1>:

m249-1. pep

1	MKNND CFR LK	DSQSGMALIE	VLVAMLVLT I	GILALLSVQL	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDSDSNKKN	YNLYMGNHTL	SAVDGDF AID
101	AMKTKGQLAE	AQLKRFSYEL	KNALPDAAAI	HYAVCKDSSG	NAP T LSGNAF
151	SSNC DNKANG	DTLIKVLWVN	DSAGDSDISR	TNLEVSGDNI	VYTYQARVGG
201	RE**				

m249-1/g249 90.1% identity in 203 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMAL	IEVLVAM	LVLTIGIL	ALLSVQLRT	VASVREAETQTIVS
g249	MKNND	CLRLKNPQSGMAL	IEVLVAM	LVLTIGIL	ALLSVQLRT	VASVREAETQTIVS
	10	20	30	40	50	60
	70	80	90	100	110	120
m249-1.pep	NLMEG	MLMNPTIDSDSN	KKNLYLMGN	HTLSAVD	GDFDAIDAM	KTGQLAEAQ
g249	NLMEG	MLMNPTIDLSN	KKNLYSLYMG	KQTLTSAVD	GDFMLDAE	KSQAQLAEQ
	70	80	90	100	110	120
	130	140	150	160	170	179
m249-1.pep	KNALP	DAAAIHYAVCK	DSSGNAPT	LSGN-AFSS	NCNDKANG	DTLIKVLVW
g249	KNALP	DAAAIHYAVCK	DSSGDAPT	LSDSGAFSS	NCNDKANG	DTLIKVLVW
	130	140	150	160	170	180

```

      180      190      200
m249-1.pep  RTNLEVSGDNIVYTYQARVGGREX
             |||||
g249        RTNLEVSGDNIVYTYQARVGGREX
             190      200

```

**a249/ L36117**

```

gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas
aeruginosa]
>gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader
sequence [Pseudomonas aeruginosa]
>gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185
Score = 50.4 bits (118), Expect = 9e-06
Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)

```

Query: 13 QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQNLMEGLMLNPTI 72  
QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M. +P  
Sbjct: 12 QSGFSMIEVLVALLISIGVLGMIANQGKTIQYTADSVERNKAAMLGSNLLESMSRASPKA 71

Query: 73 DSDSNKKNNLYLMGNHHALSVDGDFVDAIKTKTQLAEA---OLKRFSEYELKNALPDAA 129



576

D + M G A + T L +A +L ++ ++KN LP A  
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAPFTAPSSCTPLPDAIKDRLGCWAEQVKNELPGAG 126  
 Query: 130 AI---HYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTL-IKVLWVNDSSAGDSDIARTNL 185  
 + Y +C+ S +CDG G L I++ W + A ++  
 Sbjct: 127 DLLKSDYIICRSSK-----PGDCDG--KGSMLERLAWRGKQGACVNAADSSA 172  
 Query: 186 ETN 188  
 +T+  
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTI
a249	MKNND	CFRLK	NPQSG	MALIE	VLVAM	LVLTI
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLMEG	MLMNP	TIDSD	SNKKN	YNLYM	GNH-TL
a249	NLMEG	MLMNP	TIDSD	SNKKN	YNLYM	GNH-HA
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNAL	PDAAI	IHYAV	CKDSS	GNAPT	LS-GNA
a249	LKNAL	PDAAI	IHYAV	CKDSS	GVAPT	LSAGS
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTN	LEVSG	DNIVY	TYQAR	VGGRE	X
a249	ARTN	LETNG	NNIVY	TYQAR	VGGRE	X
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcctttgcc ttgggcattg atactcggta
101 tgcaggcgcg gcaaaaaggt atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcgccatat cctgatggg ggcggcgctt gccacgcaca tgaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTTASPRDE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHEN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCsGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACGTAA CCITTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAAATACCCG
301 TGAaaaaaAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/q250

```

              10      20      30      40      50      59
m250.pep      MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF
              ||::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
g250           MHTHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF
              10      20      30      40      50      60

60            70            80            90            100           110
m250.pep      ATVN LWAEPLILLIATVTFMINSRHI LMGGGACPA PERNTAEKS RARTVFYVX
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g250           ATVN LWAEPLILLIATITFMINSRHI LMGGGACHAHERNTAEKS RARAVFYV
              70            80            90            100           110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250.seq

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGCTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGCGG	CTCCGAGTTT	GCCACGGTA	ACCTGTGGGC
201	GGAACCTCTG	CCGATACTGC	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
251	CTCGGCATAT	CCTGATGGGG	G. CGGCACCT	GCCCCGACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACGTGT	TTTTATGTGT	GA

**This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:**

a250.pep

1 MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT  
51 GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCPAPER  
101 TAEKSARTV FYV\*

**m250/a250** 94.6% identity in 111 aa overlap

```

59          10          20          30          40          50
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMOGGQKGMSWLEMLLMTSMNFAGGSEF
          |
||:||||||||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMOGGQKGMSWLEMLLMTGMNFAGGSEF
          10          20          30          40          50
60

```

m250.pep

a250

```

60          70          80          90          100          110
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVFYVX
|||||:|||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCAPAPERNTAEKSRARTVFYVX
          70          80          90          100          110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

q251.seq

```

1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgcgcttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg qcqgaqqtcc qaaccaaaac qtcqtaacc

```

578

```

151 gaggttgacg ctgaggttgt ggcggatttt ggcggtatcg aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaa at caccgggtcg
251 gattttagt aggaagacgg cttgtcggca ctcggggcggc aatatttgtc
301 cgaaccgctg gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccc gtcgtaagag aggcgggcat aatccgcca agtgtcttta
401 tcggcattgg tatagacata tccaaaccg tagcggcttt tgggtgctg
451 ctgctgtaa aacacgccc taccgtattc cgcgcccacc tccgcaccgt
501 tttcaccgtt ggtaatcagc ccgtgtatt tgcggccgcc cgcgtatttg
551 ccgtagcctc tcatcgatcc gtatttttta tttcatcaa aaaccgcctt
601 ggtcaggaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcg
651 tgcgttcgag tatgcgcgc atgtagtgc gtttgtttc aaacgaaaa
701 cccggcgga acagccacga cggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1 MPDPGILFA AVGVDFFAV LRGRFORIGA VGMLIIIIIL AEVGTKT VVT
51 EVDAQVADF GGIEGFECR LQEPVAFPVN HAVGFVVGRR LVGTRAAIFV
101 RTVGGTVRL KMIQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFVVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYRS VFFIFIKNRL
201 GQECRNRIIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1 ATGCGTGC TG CGGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCACC
51 TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTTT CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTCACTGCC GTTGGGGCTG ATTTTTCGCGT CGTTGTTTTC AGGGGGCTG
251 TTCGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCCGAG ATTACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTCGAT ATGCCGCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTGTCCGA ACCGTCCGCA GAACAGTCCG
501 CTGCTGAAA ATGATTATCC AAACCGATGC CCTGCCGTC GTAAGAGAGG
551 CGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAAC AACCCGTAC
651 CGTATTCGCG GCCCACCAGC GCACCGTTT CGCCGTTGGT AACAGTCCG
701 CCGTATTTGT GGTGCCCCGC GTATTGCGG TTACCGGGCA AAGAACC CGC
751 CTGTTTTTTA TTGTCATCAA AAACCGCCTT GGTGAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGAAA GTTTGTTGCG TGTGTTGAG TATGCCGCG
851 ATGTAGTGCC GCTTATTCTC AAAACGAAAA CCGGGCGGGA ACAGCCACGA
901 CCGGCTTTCG TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1 MRAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDARRAV RISIVAQAAD
51 LPRNDISPA GDPIGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIIIILMA
101 EIRAKAVKPE IHAQVADFG GIEGFECRL QEPVAFPVNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFVRL VVKHARTVFR AHQRTVFAVG KQSAVFVVAR VFAVTGQRT
251 LFFIIKNRL GQECRNRIIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40          50          60          70          80          90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAVGDPGAGFTAVGADFFAVVLGRVRRIGAVG
          ||||| :|||:||||||| :|||||
g251      MPDPGILFAAVGVDFFAVLRGRFORIGAVG
          10          20          30

```



```
a251      ADPIGLVLAAVGVGGF----RGRFRRIAGVGMLIIIIILMAEIRVKAVKTEIHAQVVDVDFG
              70          80          90          100         110

m251.pep      130          140          150          160          170          180
GIEGFFECLRLQEPVAFPVNHAIGFVIGKRLVGTRAAIFVRTVGRTVRLCLKMIIQTDLALPV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a251      GIEGFFECLRLQEPVAFPVNHAVGFVVGKRLVGTRAAIFVRTVGRTVRLCLKMIVQTDALPV
              120          130          140          150          160          170

m251.pep      190          200          210          220          230          240
VREAGIIRPSVFFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHCRTVFVAVGKQSASFVVAR
|||::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a251      VREAGLIHPSVFFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHCRTVFVAVGKQTAFFVVAR
              180          190          200          210          220          230

m251.pep      250          260          270          280          290          300
VFAVTGQRTRLFFICIKNRLGQECCNRNHIARVESLLRVFEYAADVPLILKTCTRAEQPR
|||::|:|:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a251      VFVAVSYRS-VFSIFIKNRLGQECCNRNHIARVESLLRVFEYAADVVPFVKTKTRAEQPR
              240          250          260          270          280          290

m251.pep      PAFVX
               ||||

a251      SAFVX
               300
```

g253 . seq

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253 . pep

1	MIDRDRMLRD	TLERVVRSF	WLWVVASMM	FTAGFSGTYL	LMDNQGLNFF
51	<u>LVL</u> AGVLGMN	TLM <del>L</del> AVLAT	LFLRVKVGRF	FSSPATWFRG	KGPVNQAVLR
101	LYADQWRQPS	VRWKIGATAH	SLWLCTLLGM	LVSULLLLLV	ROYTFNWEST
151	LGSNAASVRA	PMLAWLPSP	LGFPVPDARA	VIEGRNLNGI	ADARAWSGLL
201	VLSIVCYGIL	VELLA <del>W</del> VCK	ILKLTSENGL	DLEKTYQNAV	IRRWNQKITD
251	ADTRRETUSA	VSPKIVLND	PKLWLMLETE	WODGOWFEGR	LAOE <del>W</del> LDKGV

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301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGA  
 351 VVQLLAEQGL SEDLSEKLEH WRNALTECGA AWLEPDRVAQ EGRLKQD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

m253.seq  
 1 ATGATTGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC  
 51 GGGGTCGTTT TGGTTGTGGG TGGTGGCGGC GACGTTTGCA TTTTTTACCG  
 101 GTTTTTCAGT CACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT  
 151 TTGGTTTGG CGGGCGTGTT GGGCATGAAT ACGCTGATGC TGGCAGTATG  
 201 GTTGGCAATG TTGTTCTGTC GTGTGAAAGT GGGGCGTTTT TTCAGCAGTC  
 251 CGGCGACGTG GTTTCGGGGC AAAGACCCTG TAAATCAGGC GGTGTTGCGG  
 301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC  
 351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTGCG  
 401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCACG  
 451 CTGTTGAGCA ATGCCGCTTC GGTACGCGCG GTGGAAATGT TGGCATGGCT  
 501 GCCGTCGAAA CTCGGTTTCC CTGTCCCCGA TGCGCGGGCG GTCATCGAAG  
 551 GCCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGGTC GGGGCTGCTG  
 601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTGC TGGCTTGGGT  
 651 AGTGTGTAAA ATCCTTTTGA AAACAAGCGA AAACGGATTG GATTTGAAAA  
 701 AGCCCTATTA TCAGGCGGTC ATCCGCGGCT GGCAGAACAA AATCACCAGT  
 751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCACCGA AAATCATCTT  
 801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAG TGGCAGGACG  
 851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT  
 901 GCCACCAATC GGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA  
 951 ACCGGCGCAA CTGCTTATCG GCGTGCGCGC CCAAACGTGT CCGGACCGCG  
 1001 GCGTGTGCG GCAGATTGTC CGACTCTCGG AAGCGGCGCA GGGCGGCGCG  
 1051 TGGGTGACG TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAAA  
 1101 GCTGGAACAT TGGCGTAACG CGCTGGCGCA ATGCGGCGCG GCGTGGCTTG  
 1151 AGCCTGACAG GCGGCGCGAG GAAGGGCGTT TGAAAGACCA ATAA

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pep  
 1 MIDRNRMLRE TLERVAGSF WLWVVAATFA FFTGFSVTYL LMDNQGLNFF  
 51 LVLAVLGMN TLMLAVWLAM LFLRVKVGFR PSSPATWFRG KDPVNQAVLR  
 101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLLV RQYTFNWEST  
 151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRLNGNI ADARAWSGLL  
 201 VGSIAACYGIL PRLLAWVVCK ILLKTSENGL DLEKPYQAV IRRWQNKITD  
 251 ADTRRETQSA VSPKILNDA PKWAVMLETE WQDGEWFEGR LAQEWLQKGV  
 301 ATNREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGA  
 351 VVQLLAEQGL SEDLSEKLEH WRNALAECEG AWLEPDRAAQ EGRLKQD\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETTLERVAGSFWLWVVAATFAFFTGFSTVYLLMDNQGLNFFLVLAVLGMN					
g253	MIDRDRMLRDTLERVAGSFWLWVVASMMFTAGFSGTYLLMDNQGLNFFLVLAVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGFRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGFRFFSSPATWFRGKGPVNQAVLRRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGLVSVLLLLLVQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
g253	SLWLCTLLGLVSVLLLLLVQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m253 . pep	VIEGR	LNGNIADAR	AWSGLLVGS	IACYGILPRL	LAWVVKILLK	TSENGLDLEKPYQAV
g253	VIEGR	LNGNIADAR	AWSGLLVGS	IVCYGILPRL	LAWVVKILLK	TSENGLDLEKTYQAV
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRRWN	QKITDADTR	RETVSAVSPK	IILNDAPKWA	VMLETEWQDGE	WFEGRLAQEWLDKGV
g253	IRRWN	QKITDADTR	RETVSAVSPK	IVLNDAPKWA	LMLETEWQDGE	WFEGRLAQEWLDKGV
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATNREQVA	ALETEL	KOKPAQLL	IGVRAQTV	PDGRVLRQIV	RLSEAAQGGAVVQLLAEQGL
g253	AANREQVA	ALETEL	KQKPAQLL	IGVRAQTV	PDGRVLRQIV	RLSEAAQGGAVVQLLAEQGL
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDDLSEK	LEHWRNAL	AECGA	AWLEPDRA	AQEGRLKDQX	
g253	SDDLSEK	LEHWRNAL	TECGA	AWLEPDRA	VBGRRLKDQX	
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

a253 . seq	1	ATGATCGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
	51	GGGGTCGTTT	TGGTTGTGGG	TGGCGGCGGC	GACGTTTGCG	TTTTTTACCG
	101	GTTTTTCAGT	TACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCTTT
	151	TGGTTTGG	CGGGCGTETT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG
	201	GTTGGCAATG	TGTTCCTG	GCGTGAAAGT	GGGGCGTTTT	TTCAGCAGTC
	251	CGGCGACGTG	GTTTCGGGGC	AAAGACCCTG	TCAATCAGGC	GGTGTGCGCG
	301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
	351	AACGTCGCAC	AGCCTGTGGC	TCTGCACGCT	GCTCGGAATG	CTGGTGTGCG
	401	TATTGTGTCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCAGC
	451	CTGTTGGGCG	ATTCGTCTTC	GGTACGGCTG	GTGGAAATGT	TGGCATGGCT
	501	GCCTGCGAAA	CTGGGTTTTC	CCGTGCCTGA	TGCGCGGECG	GTCATCGAAG
	551	GTCGTCTGAA	CGGCAATATT	GCCGATGCGC	GGGCTTGETC	GGGCGTCTG
	601	GTCGGCAGTA	TCGCCTGCTA	CGGCATCCTG	CCGCGCCTCT	TGGCTTGGGC
	651	GGTATGCAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGCTTG	GATTTGGAAA
	701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCGAT
	751	GCGGATACGC	GTCGGGAAAC	CGTGTCCGCC	GTTTCGCCGA	AAATCGTCTT
	801	GAACGATGCG	CCGAAATGGG	CGGTCATGCT	GGAGACCGAA	TGGCAGGACG
	851	GCGAATGGTT	CGAGGGCAGG	CTGGCGCAGG	AATGCTGGA	TAAGGGCGTT
	901	GCCGCCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
	951	ACCGGCGCAA	CTGCTTATCG	GCGTGCAGCG	CCAACTGTG	CCCGACCGCG
	1001	GCGTGTGCG	GCAGATCGTC	CGACTTTCGG	AAGCGGCGCA	GGGCGGCGCG
	1051	GTGGTGCAGC	TTTGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA
	1101	GCTGGAACAT	TGGCGTAACG	CGCTGACCGA	ATGCGGCGCG	GCGTGGCTGG
	1151	AACCCGACAG	AGCGGCGCAG	GAAGGCCGTC	TGAAACCAA	CGACCGCACT
	1201	TGA				

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

a253 . pep	1	MIDRNRMLRE	TLERVRAGSF	WLWVAAATFA	FFTGFSVTYL	LMDNQGLNFF
	51	LVLAVGLGMN	TLMLAVNLAM	LFLRVKVGRF	FSSPATWFRG	KDPVQNQAVLR
	101	LYADEWRQPS	VRWKIGATSH	SLWLCTLLGM	LVSLLLLLLV	RQYTFNWEST
	151	LLGDSSSVRL	VEMLAWLPK	LGFPVPDARA	VIEGR	LNGNIADAR
	201	WVSGIACYGIL	PRLLA	WVCKILLK	TSENGL	DLEKPYQAV
	251	ADTRRET	VSAVSPKIVL	NDAPKWAV	MLETE	WQDGEWFEGR
	301	AANREQVAAL	ETELKQKPAQ	LLIGVRAQTV	PDGRVLRQIV	RLSEAAQGGG
	351	VVQLLAEQGL	SDDLSEKLEH	WRNALTECGA	AWLEPDRAAQ	EGRLKTNDR
	401	*				

m253/a253 97.2% identity in 395 aa overlap

m253.pep	10	20	30	40	50	60
	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGF	SVTYLLMDNQGLNFFLVLAGVLGMN				
a253	10	20	30	40	50	60
	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGF	SVTYLLMDNQGLNFFLVLAGVLGMN				
m253.pep	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGRFFSSPATWFERGKDPVNQAVLR	LYADEWRQPSVRWKIGATSH				
a253	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGRFFSSPATWFERGKDPVNQAVLR	LYADEWRQPSVRWKIGATSH				
m253.pep	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEM	LAWLP	SKLGFPVPDARA			
a253	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGDSSSVRLVEM	LAWLP	PAKLGFPVPDARA			
m253.pep	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIA	CYGILPRLLAWVCKILLKTS	ENGLDLEKPYQAV			
a253	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIA	CYGILPRLLAWVCKILLKTS	ENGLDLEKPYQAV			
m253.pep	250	260	270	280	290	300
	IRRWNKIDADTRRET	VS	SAVSPKII	LNDA	PKWAVMLETEWQDGEW	FEGR
a253	250	260	270	280	290	300
	IRRWNKIDADTRRET	VS	SAVSPKII	LNDA	PKWAVMLETEWQDGEW	FEGR
m253.pep	310	320	330	340	350	360
	ATNREQVA	ALETELKQKPAQLLIGVRAQ	TV	PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL		
a253	310	320	330	340	350	360
	AANREQVA	ALETELKQKPAQLLIGVRAQ	TV	PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL		
m253.pep	370	380	390			
	SDDLSEKLEHWRNALAECGA	AWLEPDRAAQEGRLKDQX				
a253	370	380	390	400		
	SDDLSEKLEHWRNALTECGA	AWLEPDRAAQEGRLKTNDRTX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcgggtttgat
51  tctggcgcg gcagggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgctt gcactggctt ctttgagaaa cgggccgggc
301 tggacggtat ttctactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggctctgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcgccag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence &lt;SEQ ID 994; ORF 254.ng&gt;:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```



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51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG  
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLS SIAIYIVMGW MVLAVMKSLT  
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF  
 201 VSVYGYVI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)  
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT  
 51 GTACCACGGA ATTGCAGCCG GAAAACAGAA AAGCATTTTG AAAAAACCG  
 101 ACCACTGCAT GATTATATGT CTGATTGCCG GAAGCTACAC ACCGTTTGCA  
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG  
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA  
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG  
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT  
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCCGC ATTACTGCT  
 401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTT  
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGTGACG GTTACGTAAT  
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)  
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI LKKTDHCMYI VLIAGSYTPFA  
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLS IYIYVVMGWM  
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF  
 151 VLGGSITQFV SVYGYVI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGL	MLMLLKTIGH	GDGYRIFSV	VSVYGISLLL	LYLSSSLYHG	IAAGKLKSI
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPG	WTVFSLSWLL	AAAGIAQELT
g254		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPG	WTVFSLSWLL	AAAGIAQELT
	80	90	100	110	120	130
m254.pep		100	110	120	130	140
		IYIYVVMGWM	VLAVMKSLTA	SLPSAGLAWL	LAAGGMLYSV	GIYWFVNDEK
g254		IAIYIVMGWM	VLAVMKSLTA	SLPPAGLAWL	LAAGGMLYSV	GIYWFVNDEK
	140	150	160	170	180	190
m254.pep		160				
		VLGGSITQFV	SVYGYVIX			
g254		VLGGSITQFV	SVYGYVIX			
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq  
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGA GCGGTTTGAT  
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAACCC ATAGGACACG  
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT  
 151 CTGCTCTATT TGAGTTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAACT  
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG  
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

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301 TGGACGGTAT TTCTACTGTC CTGGCTGCTG GCGGCTGCAG GAATCGCACA
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA
401 TTTATATCGT AATGGGCTGG ATGGTCTTGG CGGTAATGAA ATCCCTGACA
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT
501 GTACAGCGTC GGCATTACT GGTGTGTAAG CGATGAAAAA ATCCGACACG
551 GGCACGGAAT CTGGCATCTG TTCGTATTEG GCGGCAGCAT CACCCAATTT
601 GTCAGCGTGT ACGGTTACGT AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

```

a254 . pep
1  MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSLLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

					10				20
30									
m254 . pep									
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL									
a254									
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL									
		20	30	40	50				60
70									
		40	50	60	70				80
90									
m254 . pep									
LKKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS									
a254									
LKKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS									
		80	90	100	110				120
130									
		100	110	120	130				140
150									
m254 . pep									
IVIYVVMGWMVLAVMKSILTASLPSAGLAWLAAGGMLYSVGIYWFVNDKIRHGHGIWHLF									
a254									
IAIYIVMGWMVLAVMKSILTASLPPAGLAWLAAGGMLYSVGIYWFVNDKIRHGHGIWHLF									
		140	150	160	170				180
190									
		160							
m254 . pep		VLGGSITQFVSVYGYVIX							
a254		VLGGSITQFVSVYGYVIX							
		200							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

Computer analysis of this amino acid sequence gave the following results:

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFIGIEAVKNRFAQADRD	I	:	:	:	:
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFIGIEAVENGFAQTGDG	D	V	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GC FDMQLRADGIQGFAHAVHIVFQLGNLAMVGGKKRILGNVF	AAFKPDFF	FADLGN	VGGD	:	:
g255	GG FDMQFRADGIQGF	AHTVHIVFQ	GD LALVGGKKRILGNVF	AAFKPDFF	FADLGN	VGGD
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFF	QPF	FGNGSGSNAGGG	TGGAPAAAAV	VARAVF	VP
g255	FRAEFF	QPF	FGNGSGSGNAGCG	FAGGT	PAAAPV	VARTV
	130	140	150	160	170	180

130            140            150            160            170            180

	189
m255.pep	AALVGIADX
	:
q255	AALVGVADX

```
a255.seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCGTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCCAC GCCTTTGACG
101 GCGGTTGATG CCATCATGGC GTAGCGGATT TCGCGATCGA GCGGGTCGAA
151 TACGGGTTGC CCCAAGCCGA CGGGGACGTT GCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTTGCGCA CGCTGTCCAT ATAGTTTTCC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGAT TTTGGGAAAT
301 GTGTTCCGAC CCTTCAAACC GGATTTCTTT TTCGCCGACT TGGGTAACTG
351 AGGCGGTGAT TTCCGTGCGC AATTTTCTTT TCAACCAATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGCTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGCGGT
501 GGCCCGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA
```

a255.pep

1	VVGQ <b>E</b> ALRGE	FVAVF <b>A</b> AAALR	YAVKTCADFH	AFDGVDAHHG	VGDFGIEAVE
51	YGFAQADGDV	GGFN <b>M</b> QLRAD	GIQGF <b>A</b> HAVH	IV <b>Q</b> LGNL <b>A</b> M	VG <b>G</b> KKRILGN
101	VF <b>A</b> AFKP <b>D</b> DF	FADLGNVGGD	FRA <b>E</b> FFFQ <b>P</b> F	FGNGSGGNAG	GGFAGG <b>T</b> PAA
151	APVVARAVFV	PIGIVGVAGA	EAGGDVAVV	AALVGIAD*	

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVKNRFAQADRD					
a255	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVEYGFQAQADGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFAHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD					
a255	GGFNMQLRADGIQGFAHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFFFQPFNGSGSNAGGGFTGGAPAAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
a255	FRAEFFFQPFNGSGSNAGGGFAGGTAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180

	189
m255.pep	AALVGIADX
a255	AALVGIADX

```
g256.seq
1   atgctcgcgg   tacgcaatcg   ggggtggcac   ggcgagtcg   tccatttcg
51  cagctgcggc   ggcgtagcga   acacgcgcgc   gctgttctac   cacttggggt
101 ataccgcgga   aatcgccctt   gcttggaca   cgctcacgcg   cggttaccgt
151 gaaatatacg   ccgtcggcgt   atcgctgggc   ggcaacgcgc   cggcaaaata
201 tttgggcgaa   cagggcaaaa   aggcattgcc   gcacgctctg   gccgcgcat
251 ccgcccctgt   tgatgcagag   cgggcaggca   gccgcttcga   cagcggcgat
301 acgcgctgc   tctacacgcg   ctacttcctc   cgcacactga   tacccaaag
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351 acgttcgctc caagggttttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcagcact actaccgcca aacttcctgc aaaccgctgc tcaaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgccggcttt gtcagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttagacagt
701 tccgcacaaa caggcgtaaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
  1 MLAVNRGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
 51 EIYAVGVS LG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNAANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
  1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GGCCTAGTCG TCCATTTCGG
 51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151 GAAAtATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTCATCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCTGTTC
601 CAGCCGCGAT ATGGTGGTCA TGTCGGCTTT GTCAGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
  1 MLAVRDRGWH GVVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFARYR
 51 EIYAVGVS LG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNANDP FLPPEALPRA DEVSEAVTLF
201 QPAYGGHVG FVSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

```

          10      20      30      40      50      60
m256.pep  MLAVRDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVS LG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256       MLAVNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVS LG
          10      20      30      40      50      60

          70      80      90     100     110     120
m256.pep  GNALAKYLGEQGKKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256       GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAGSRFDSGITRLLYTRYFLRTLIPKARSL
          70      80      90     100     110     120

          130     140     150     160     170     180
m256.pep  QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKP LLLLNAVNDP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256       QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKP LLLLNAANDP

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	130	140	150	160	170	180
m256.pep	190	200	210	220	230	240
	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

a256.seq

1	ATGCTCGCGG	TACGCGATCG	GGGTTGGAAC	GGCGTAGTCG	TCCATTTCCG
51	CAGCTGCGGC	GGCGTAGCGA	ACACCGCCCC	GGTGTTCIAC	CACTTGGGCG
101	ATACCGCCGA	AATTGCCTTT	ACTTTGGACA	CGCTCGCCGC	GCGTTACCGT
151	GAAATATACG	CCGTCGGCGT	ATCGCTGGGC	GGCAACGCGC	TGGCAAAATA
201	TTTGGGCGAA	CAGGGCGAAA	ACGCGCTGCC	GCAAGCCGCC	GCCGTCATCT
251	CCGCACCCGT	CGATGCAGAG	GCGGCAGGCA	ACCGCTTCGA	CAGCGGCATC
301	ACACGGCTGC	TCTACACGCG	CTACTTCCTC	CGCACACTGA	TACCCAAAGC
351	ACGGTCGCTC	CAAGGTTTTC	AGACGGCATT	TGCCGCAGGG	TGCAAAACAC
401	TGGGCGAGTT	TGACGACCGT	TTCACCGCAC	CGCTGCACGG	CTTTGCCGAT
451	CGGCACGACT	ACTACCGCCA	AACTTCCTGC	AAACCGCTGC	TCAAACACGT
501	TGCCAAACCG	CTGCTCCTGC	TCAATGCCGT	CAACGACCCC	TTCTGCGCGC
551	CCGAAGCGCT	GCCCCGCGCA	GACGAAGTGT	CCGAAGCCGT	TACCCTGTTT
601	CAGCCGACAC	ACGGTGGTCA	TGTCGGCTTT	GTCCGCAGCA	CCGGCGGCAG
651	GCTGCACCTG	CAATGGTTGC	CGCAGACCGT	CCTGTCCTAT	TTGCACAGCT
701	TCCGCACAAA	CAGGCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

a256.pep

1	MLAVRDRGWN	GVVVHFRSCG	GVANTAPVFY	HLGDTAEIAF	TLDTLAARYR
51	EIYAVGVSLG	GNALAKYLGE	QGENALPQAA	AVISAPVDAE	AAGNRFDSGI
101	TRLLYTRYFL	RTLIPKARSL	QGFQTAFAAG	CKTLGEFDDR	FTAPLHGFAD
151	RHDYYRQTSC	KPLLKHVAKP	LLLLNAVNDP	FLPPEALPRA	DEVSEAVTLF
201	QPTHGGHVG	VGSTGGRLHL	QWLPQTVLSY	FDSFRTNRR*	

m256/a256 95.4% identity in 239 aa overlap

m256.pep	10	20	30	40	50	60
	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYX	LGDTAEIAFTLDTFAARYREIYAVGVSLG				
a256	MLAVRDRGWN	GVVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG				
	10	20	30	40	50	60
m256.pep	70	80	90	100	110	120
	GNALAKYLGEQGGKALPQAAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
a256	GNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
m256.pep	130	140	150	160	170	180
	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRH	DYYRQTSCKPLLKHVAKPLLLLNAVNDP				
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRH	DYYRQTSCKPLLKHVAKPLLLLNAVNDP				
	130	140	150	160	170	180
m256.pep	190	200	210	220	230	240
	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

g256-1.seq

1	ATGATTTTGA	CACCGCCGGA	CACGCCCTTT	TTCCTCCGCA	ACGGCAATGC
51	CGACACGATT	GCCGCCAAAT	TCCTGCAACA	CCCCGCACCC	GCATACCGCC

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101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCGG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGGAATG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCAGAGTCG TCCATTTCGG CAGCTCGCGC
301 GGCCTAGCGA ACACCGCCCC GGTGTCTTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTACCCGC GCGTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACGCCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCTGCGCGC CGGAAGCCCT
801 GCCCGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CGGCGGCGAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CTTGTCTTAT TTTGACAGCT TCCGCACAAA
951 CAGCGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```
1 MILTPPDTPF FLRNGNADTI AAKFLOHPAP AYREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVRNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDITLARYR EIYAVGVSLG GNAPAKYLGE
151 QGKKAIPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD RHDYRQTSK PLLKHVAKP
251 LLLNAANDP FLPPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRHLH
301 QWLPQTVLSY FDSFRTNRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```
1 ATGATTTTAA CACCGCCGGA CAGGCCCTTT TTCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCAGCGCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCAGGCG GTAGTCGTCC ATTTCCGCAG CTGCGCGGCG
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGCGGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCGC
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATT GGGCGAACAG
451 GGCAAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAG CGGCTGCTCT
551 ACACGCGCTA CTCTCTCCGC ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTGTC CGCAGGGTGC AAAACACTGG GCGAGTTTCA
651 CGACCGCTTC ACCGCACCCG TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCTTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCGGCGCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CTTGTTCAG CCGGCATAIG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCCT GTCCATTATC GACAGCTTCC GCACAAACAG
951 GCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```
1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVRDRGWHG VVVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 QGFQTAFAAG KTLGEFDDR FTAPLHGFADR HDYRQTSCK PLLKHVAREL
251 LLLNAVNDPF LPPEALPRAD EVSEAVILFQ PAYGGHVGFV SSTGGRHLHL
301 WLPQTVLSYF DSFRTNRR*
```

m256-1/g256-1 93.1% identity in 319 aa overlap

```
10 20 30 40 50 59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
|||||
g256-1 MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
10 20 30 40 50 60

60 70 80 90 100 110 119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVVHFRSCGGIANTAPVYFHLGDTAEIAF
```

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```
|||||:|||||:|||||:|||||:|||||:|||||:
g256-1  LVVLFHGLEGSSRSYAVELMLAVNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
              70      80      90      100     110     120
m256-1.pep 120      130      140      150      160      170      179
          TLDTFAARYREIYAVGVSLGGNALAKYLGEQGGKALPQAAAVISAPVDAEAAGRFRDSCI
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1  ALDTLTARYREIYAVGVSLGGNAPAKYLGEQGGKALPHASAAVSAPVDAEAAGSRFDSCI
              130      140      150      160      170      180
m256-1.pep 180      190      200      210      220      230      239
          TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSC
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1  TRLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSC
              190      200      210      220      230      240
m256-1.pep 240      250      260      270      280      290      299
          KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHL
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHL
              250      260      270      280      290      300
m256-1.pep 300      310      319
          QWLPQTVLSYFDSFRNRRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1  QWLPQTVLSYFDSFRNRRX
              310      320
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```
a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCCGCCGA TCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGGGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCAC TTGGCGGATA CCGCCGAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GCGGAAAACG CGCTGCCGCA AGCCGCCGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCG AACTGATAC CCAAAGCAGC GTCGCTCCAA
601 GGTTTTCAGA CGGCATTTCG CGCAGGGTGC AAAAAGCTGG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCCG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCCG AAGCCGTTAC CCTGTTCCAG CCGACACAGC
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCCT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 GCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```
a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHVGFEV GSTGGRHLHL
301 WLPQTVLSYF DSFRNRR*
```

a256-1/m256-1 95.6% identity in 318 aa overlap

```
10      20      30      40      50      60
a256-1.pep MILTPPDTPPFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m256-1  MILTPPDTPPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60
70      80      90      100     110     120
a256-1.pep VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVVHFRSCGGVANTAPVFYHLGDTAEIAFT
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m256-1  VVLFHGLEGSSRSYAVELMLAVDRGWNGVVVHFRSCGGIANTAPVFYHLGDTAEIAFT
```



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	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGIT					
m256-1	130	140	150	160	170	180
	LDTFAARYREIYAVGVSLGGNALAKYLGEQCKKALPQAAAVISAPVDAEAAGRRFDSGIT					
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHQYRQTSCK					
m256-1	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHQYRQTSCK					
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFGSTGGRLHLQ					
m256-1	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSTGGRLHLQ					
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	310					
	WLPQTVLSYFDSFRTNRRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

```

g257.seq
1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gttttctcgg
151 aaaggtgtcg cgctgggttc cggcgcgagg ctgcgctctg tcggcggtgga
201 cgacagacag gcggcggttt tgggtcaataa ggttttggcg gaagtggcgc
251 gtttggaataa aatgttcagc ctttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggtatt ttttgaact
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

```

g257.pep
1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKVLA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIFT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

```

m257.seq
1  ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GCGGGGgAc. GCGGcGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTTGG
151 AAAGGTGTCT CACTGGGTTC CCGTGCGGa. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAATA ATTGTTTCTG CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCGG TCGGCGGATT TTTTGAAC
351 GKTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

```

m257.pep
1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRDENVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKVLA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLXLXSL AAIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng)

from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60

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```

m257.pep  MGRHFGRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAD
          |||||:||||:||||: ||||| ||| |:|:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGA AVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVGALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
          |||||:||||:||||: ||||| ||||| ||||| ||||| ||||| ||
g257      LRLFGVDDRQAADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC ATTCGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
51  GCGGCGGGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAATAAGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCG CACTGGGTTT CCGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA AATGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGT
301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAAC
351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF LTVA AVAAAG AAVSFLPNPF AADDEKRNKD EKR NENVFFW
51  KGVALGSGAE LRLFGVDDRR AADLVNKKVLA EVARLEKMF S LYREDSLIS
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAX
          ||||| :|||||: |||||
|||
a257      MGRHFGRRRFLTVAAVAAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
          |||||:||||:||||: ||||| ||||| ||||| ||||| |||||
||
a257      LRLFGVDDRRADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |::|
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgcgctcg tcttctgtga
51  cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcggttcagc gcaatgctgc tgctggtgtt gtccgccgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcggtgtt
201 cggttcgtag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttccctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggcggcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgcccc
501 gcttgccctg tacaatgccc caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tgggtgtcgg caggtacgca caacgggcgc gattacgcgc
701 tgttcttccg ccagccgatt ccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgaattaca gcaaaaaagg
801 tttgcagacc ttttttctgg taacctgctt gattgcctcg ctgctgtcga
851 tttttcttgc gctgtgtaag gcaactgtat ttgccgcgct tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagtccgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcca ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctaccctt ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctccctctt ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVVPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLQT FFLVTLIIAS LLSIFLALVM ALYFARRFEV
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVDLG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGOGCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TCGCTGGCG GATTATTTCT
101 GGTGGATTGT TCGGTTTCAGC GCAATGCTGC TGCTGGTGTG GTCCGCCGTT
151 TTGGCACGTT ATGTCAATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTCGCC
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GGCGGCAGAC AACGCCCTCG
401 GCAACGCCGT CCCCGTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAATAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCTGCTT GATTGCCTCG CTGCTGTGCA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCTGTGCA
901 CCCGTCTAT CGCTTGCCGA GGGGCGGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCGTGTG TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

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```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACsTT CAACAAAGCG GCGGAACAGA TTyTGGGGAT GCCGCTTACC
1201 CCCcTGTTGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAAgT GGCGaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCAGC
1501 CCCATCCAGC TTTCGCCCGA ACgGsTGCGG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCTT CGCTCAAATT GGAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGGTTT GCGGCGGACT
1751 TGCCGCGGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

```

m258.pep
  1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS ANLLLVLSAV
 51 LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSINL SKSALNLAAD NALGNAVVPQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQSSLL AEFVAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAANGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

```

              10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSSLADYFWWIVAFSAML LVL SAVLARYVILLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSSLADYFWWIVSFSAM LVL SAVLARYVILLK
              10      20      30      40      50      60

              70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSINL
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSINL
              70      80      90     100     110     120

              130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAVVPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      SKSALDLAADNAVSNVAVPQIDLTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
              130     140     150     160     170     180

              190     200     210     220     230     240
m258.pep  SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      SINPHQFDQPLPDKEHWEQIQOTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI
              190     200     210     220     230     240

```

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAE	LSYSKGLQTF	FLATLLIASLLS	IFLALVMALYF	ARFVE	
	::   :					
g258	PENVAQDAVLIEKARAKYAE	LSYSKGLQTF	FLVTLIASLLS	IFLALVMALYF	ARFVE	
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAE	GAKAVAQGDFSQ	TRPVLRNDE	FGRLTKLF	NHMTEQLS	IAKEADERNRRREEAA
	:					
g258	PILSLAE	GAKAVAQGDFSQ	TRPVLRNDE	FGRLTKLF	NHMTEQLS	IAKEADERNRRREEAA
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGV	VVFDEQGCLKTF	NKAAEQILG	MPLTPWLGSSR	HGW	HGVSAQQSLL
		:	:	:	:	:
g258	RHYLECVLDGLTTGV	VVSYP	LSCCR	TA	VFSTCHSS	PLSYFX
	370	380	390	400		

a258.seq

1	ATGCGCCGTT	TTC <sup>1</sup> TACCGAT	CGCAGCCATA	TGCGCCGTCG	TCCTGTTGTA
51	CGGAC <sup>1</sup> TGACG	GCGGCAACCG	GCAGCACCAG	TTCGCTGGCG	GATTATTCT
101	GGTGGATTG	TGCGTT <sup>1</sup> CAGC	GCAATGCTGC	TGCTGGTGTT	GTCCGCGGTT
151	TTGGCAGCTT	ATG <sup>1</sup> T <sup>1</sup> CATATT	CGTGT <sup>1</sup> TGAAA	GACAGCGCGC	ATCCGCGTATT
201	CGGTT <sup>1</sup> CGCAG	ATTGCCAAAC	GCCTTTCCGG	GATGTTTACG	CTGGTTGCCG
251	TACTGCCCGG	CGTGT <sup>1</sup> TTCTG	TTCCGGCGTTT	CCGCACAGTT	TATCAACGGC
301	ACGATTAA <sup>1</sup> TT	CTGGTTCCG	CAACGATACC	CACGAGGCGC	TTGAACCGCAG
351	CCTCAATT <sup>1</sup> TG	AGCAAGTCGG	CATTGAATCT	GCGCGCAGAC	AACGCGCTTTG
401	GCAACGCCAT	CCCCGTGCAG	ATAGACCTCA	TCCGGCGCGC	TTCCTTGCCC
451	GGGGATATGG	GCAGGGTGCT	GGAACATTAC	GCCGCGACGG	GTTT <sup>1</sup> TGCCCA
501	GCTTGC <sup>1</sup> CCGT	TACAATGCCG	CAAGCGGC <sup>1</sup> AA	AATCGAAAAA	AGCATACCCA
551	CGCACAGCT	CGATCAGCG	TTTCCGGTA	AGGCGCGTTG	GGAAAAATC
601	CAACAGGCGG	GTTCCGGTCAG	GGATT <sup>1</sup> TGAA	AGCATAGGCG	CGCTATTGTA
651	CGCGCAGGGG	TGGCT <sup>1</sup> TCGG	CAGGTACGCA	CAACGGGCGC	GATTACGCCT
701	TGTTTT <sup>1</sup> CCG	TACGCGGTT	CCCAAAGCGG	TGGCAGAGGA	TGCCCTCTTA
751	ATCGAAAAAG	CAAGGCGCAA	ATATGCTGAG	TTAGGTTACA	GCAAAAAAGG
801	TTTGCAGACC	TTTT <sup>1</sup> TCTGG	CAACCTGCT	GAT <sup>1</sup> TGCTCG	CTGCTGTGTA
851	TTTT <sup>1</sup> TCTTG	ACTGGTCATG	GCATGCTATT	TCCGCCGCGC	TTTCGTGCAA
901	CCCGTCTTAT	CGCTTGCCGA	GGGGCGGAAG	CGGGTGGCGC	AGGGCGATT
951	CAGCCAGACG	CGCCCGTGT	TGCGCAACGA	CGAGTT <sup>1</sup> CGGA	CGCTGTACCA
1001	AGTTGTTCAA	CCACATGACC	GAGCAGCTTT	CCA <sup>1</sup> TGCCAA	AGAAGCAGAC
1051	GAGCGCAACC	CGCGCGCGGA	GGAAGCGCTT	AGACATTATC	TCGCAATCGT
1101	GTTGGAGGGG	CTGACCACGG	CGGTGGTGCT	GTT <sup>1</sup> TGACGA	CAAGGCTGTC
1151	TGAAAACCTT	CAACAAAGCG	GCGGAACAGA	TTT <sup>1</sup> TGGGAT	CGCGCTTACC
1201	CCCCTGTGGG	GCAGCAGCCG	GCACGGTTGG	CACGGCGTTT	CGGCGCAGCA
1251	GTCCCTGCTT	CGCGAAGTGT	TTGCCGCGAT	CGGCGCGGCG	GCAGGTACGG
1301	ACAAACCGGT	CCATGTGAAA	TATGCGCGCG	CGGACGATGC	CAAAATCTCG
1351	CTGGGCAAGG	CAACCGTCTC	CGCCGAAGAC	AACGGCAACG	CGGTGGTAA <sup>1</sup> T
1401	GGTGATTGAC	GACATCACCG	TTTTGATACA	CGCGCAAAAA	GAAGCCGCGT
1451	GGGGCGAAGT	GGCAAAACGG	CTGGCACACG	AAA <sup>1</sup> TCCGCA	TCCGCTCACG
1501	CCCATTCCAG	TTTCTGCCGA	ACGGCTGGCG	TGAAATTTGG	CGGGGAAGCT
1551	GGACGAGCAG	GTCGCGCAAA	TCCTGACACG	TTCCAGCCAG	ACCATCATCA
1601	AACAAGTGGC	GGCATTAAAA	GAAATGCTCG	AGGCATTCCG	CAATTACCGG
1651	CGTTCCCTCT	CGCTCAAAAT	GAAAAATCAG	GATT <sup>1</sup> TGAACG	CCTTAATTCGG
1701	CGATGTGTTG	CGATTGTACG	AGACTGTGTC	GTCGCGGTTT	CGTGGCGAAC
1751	TTGCCGGCGA	ACCGCTGATG	ATGGCGGCGG	ATACGACCGC	GATCGCGCAG
1801	GTGCTGCACA	ATATT <sup>1</sup> TTCAA	AAATGCCGCC	GAAGCGGCGG	AAGAAGCCGA
1851	TGTGCCCGAA	GTCAAGGTAA	AATCGGAAGT	GGGGCAGGAC	GGACGGATTG
1901	TCCTGACAGT	TTGCGACAA	GGCAAGGGGT	TCCGGCAGGA	AATGCTGCAC
1951	AATGCCTTCG	AGCCGTATGT	AACGGACAAA	CCGCTTGGAA	CGGGATTGGG
2001	ACTGCCCGTG	GTGAAAAAAA	TCATTGAAGA	ACACGGCGGC	CGCATACAGC
2051	TGAGCAATCA	GAGTACGGGC	GCGCGGTGTG	TCAGAATCAT	CTTGCCAAAA
2101	ACGGTAGAAA	CTTATGCGTA	G		

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
  1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
 51 LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FCVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEFVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAANGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMQ
601 VLNHIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```

      10      20      30      40      50      60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLK
|||||
a258 MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLK
      10      20      30      40      50      60

      70      80      90     100     110     120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
|||||
a258 DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
      70      80      90     100     110     120

      130     140     150     160     170     180
m258.pep SKSALNLAADNALGNAIPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
|||||
a258 SKSALNLAADNALGNAIPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
      130     140     150     160     170     180

      190     200     210     220     230     240
m258.pep SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
|||||
a258 SINPHKLDQFPFGKARWEKIQQAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
      190     200     210     220     230     240

      250     260     270     280     290     300
m258.pep PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
|||||
a258 PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
      250     260     270     280     290     300

      310     320     330     340     350     360
m258.pep PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRREEAA
|||||
a258 PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRREEAA
      310     320     330     340     350     360

      370     380     390     400     410     420
m258.pep RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLT PLWGSSRHGW HGVSAQQSLL
|||||
a258 RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLT PLWGSSRHGW HGVSAQQSLL
      370     380     390     400     410     420

      430     440     450     460     470     480
m258.pep AEFVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
|||||
a258 AEFVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
```

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDQDAQILTRSTDTIIRKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNI FKNAEEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

```

g259.seq
1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgtc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcgga gttctgccc acgacgaaga cgcgcgcacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctg
451 ggcgaaacct atggcgcggt gtccgccgat attttcgagt tgcgcgcggc
501 tttggaaagg cgcgcgttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgtcaat caggcgttga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

```

g259.pep
1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGF
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

```

m259.seq (partial)
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGCGCGGTT CAAAGGCCAA
201 GCGCGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CCGCGGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTCGCCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA .AACATCT TCGmGATGC CTGCCGTTG GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG. .

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

```

m259.pep (partial)
1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVGVG  
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSALEGRAFGLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSALEERRAFKGLKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCCLPFGNGVGVGRRTQSGVAGDFKNIR					
g259	AEYKXHLRRCCLPFGNGVGVGRRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCCGACCGA	TACTTTATGT
51	TTTGATTTC	TTTGCCGGTT	TTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCCGCATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCTTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGTCAAGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCAGC	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCAATTG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCCGCCAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGGAAGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTGC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHKGK	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTDVAVS
151	GETYGRVFAD	IFELSALEG	RAFKGLKLT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					



600

	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKIFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
a259	SARSKAKAEKIFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSALEGRAFGMLKLT					
a259	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSALEGRAFGMLKLT					
	190	200	210			
m259.pep	AEYKXHLRRCLPFGNGVGVGRVTSQSGVAGDFKNIR					
a259	AEYKXHLRRCLPFGNGVGVGRAQSGVAGDFKNIGKVQ					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGTCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGGTT  TTTTGACCGC  GCAAATCTGG  TTCATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGGTCGTG  TCGGTGCGTT  CAAAGGCTAA
201 GGCAGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATACACC
251 CCGTCCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGC  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCACG  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTCGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GCGGAAACCT  ATGGGCGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTCGGCGGC
501 TTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SVRSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALLVKNHGKG  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDVAS
151 GETYGRVFAD  IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGGTT  TTTTGACCGC  GCAAATCTGG  TTCATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGGTCGTG  TCGGCGCGTT  CAAAGGCCAA
201 GGCAGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATACACC
251 CCGTCCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAATACTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCACG  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTCGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GCGGAAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTCGGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAACTGACG  GCGGAATATA
551 AAAACATCTT  CGGCGATGCC  TGCCGTTCCG  AAACGGCGTT  GGAGTTGGGC
601 GCACTCAATC  AGGCGTTGCA  GGAGATTTC  AAAACATCGG  AAAAGTCCAA
651 ACGGATATTT  TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQIL
101 ALLVKNHGKG  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDVAS
151 GETYGRVFAD  IFELSAALEG  RAFKGLKLT  AEYKNIFGDA  CRSETALELG
201 ALNQAALQEIS  KTSEKSRIF  Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALE					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFKGMLKLT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTGACCGC GCAAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GCGTGGCGTG GCGTTCGTG TCGCGCGGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGCGCGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AACCGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC A AACATCCG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQBEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFKGMLKLT					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFKGMLKLT					
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELGALNQLQBEISKTSKSKRIFYX					
m259-1	AEYKNIFGDACRSETALELGALNQLQBEISKTSKSKRIFYX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atgggtgcgg gtgtagtatt cgttgctctt cagccgttct tcagcctgtt
51  tcgagcggtg ttcgagggcg gagtcggtat agtcgaggga gcgcacgatg
101 ccgctgaatg cgacttcttg tccgaggaat ttaccgctat ccggatcggg
151 gatgttttta ttgattcggg aggtcagata acggcccggg tctttcaggc
201 ctttggtgta aaccctggcg cctttggtgt acagcagcct gccttccggg
251 cccgagagca ggcgcggcgc ggcagcggtt tctttgcggg aaacgatttg
301 cgggtgctgc ataaagacgc ggtagaagtt gacatcgatg gcgggaatac
351 cgtatccgga cacttcctta tccggactga ttttgacgac ggggatgccg
401 tctgtctgtt ccaagccgag gcgcgggtcg ccgccaacgt agcgcaacac
451 caatacctgg cccggataaa tcaggtcggg attgtggatt tgatcccggt
501 tcgcgccccca caggggggga ccattgccac gggctgtaca ggtatttggc
551 cgaataaccc cacaggggtg cgcctgttt ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF QPFFSLFRAL FEGGVGIVEG AHDAAECDLF SEEFTRIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGNTVSG HFLIRTFDD GDAVCLFQAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGCTCTT CGGCCGTCTT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGwCA sCGCGGyGC GGCAGCGGTT TCTTTGCGGG AAACGATTTG
301 CGGATGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTG CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCGGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTyCCA CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG
51  DVFIDSVGQV AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFFSLFRALFEDRVGIVEGAHDAAECDLFPEEFTRIRIGDVFIDSVGQV					
	:     :					
g260	MGAGVVFVVFQPFSSLFRLAFEGGVGIVEGAHDAAECDLFSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAPFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG					
	: : :     :					
g260	TARFFQAFGVNPGAFGVQQPAPFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVRINQVGIVDLIPVRVPQ					
g260	HFLIRTFDDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260 GICPKYPTGCRPV  
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq  
1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT  
51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG  
101 CCGCTGAATG CCACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT  
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC  
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG  
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGTT TCTTGCGGG AAACGATTTG  
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCEATG CCGGGAATAC  
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG  
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCT CCGTCAACGT GCGGCAACAC  
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT  
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTTGCC  
551 CGAAATGCCC CACAGGTGT GGCCTGTTT GA

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep  
1 MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG  
51 DVFIDSVGQV AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL  
101 RVPKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH  
151 QYLQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV\*

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG DVFIDSVGQV					
a260	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG DVFIDSVGQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL RVPKDAVEV DIDGGNTVSG					
a260	AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL RVPKDAVEV DIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH QYLQINQVG IVDLIPVRVP QAAXIATGCT					
a260	HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH QYLQINQVG IVDLIPVRVP QAAXIATGCT					
	130	140	150	160	170	180
m260.pep	GICPKCPTGCRPVX					
a260	GICPKCPTGCRPVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq  
1 atggagcttg ggcataatcgt attccttggtg ctttgcgcg cttcagacgg  
51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag  
101 ctgggcatc cgcggcagcc gccgacgata cccttgtagc aggtgtgggt  
151 ctgttcgagg atgtagtcca acacgccccat ttcgtccgccc aacgccccag  
201 tttgcgcctt ggtcaggtag atcagcggcg tgtggatttg aaaatcgtag  
251 tccatcgcca gattaagggt aacgttcagt gatttgacga acacgcccgc  
301 gcagtcggga tagcccgaaa aatcgggttc gcacacgccc ccgatgatgt  
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc  
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc  
451 gatggcgagg gtttcgatgg cggcggtttc gtccatcagg gcgttgtagc  
501 taacttgccg catcaggctc aaatcgagta cggtttgact gacacccaaa  
551 tcctgcgcga tccactctgc gcgttcacgc tcgacggcat gcggttgccc  
601 gtatcggaag gtgatgggtt ggacgttttc gcgcccgtag gtttgattg

604

651 cctgaatcag gcaggtcggtc gaatcctgac cgcccagaaa gatgaccaag  
701 gctttttggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep  
1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG  
51 LFADVVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA  
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF  
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP  
201 VSEGDGLDVF APVGLDCLNQ AGGRILTARE DDQGLV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq  
1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG  
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTTCGCG CAAGATACAG  
101 CTCGGGCATT CGCGcCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT  
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCACG  
201 TTTGCGCCTT GGTGAGATAC ATCAGCGGCG TGTGGATTTG AAAATCATAG  
251 TCCATCGCCA AATTAACGGT AACGTTTCATC GATTTGACAA ACACGTCGCG  
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT  
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC  
401 gCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC  
451 GATGGCGGCG GTGTCGICCA TCAGGGCATT GTGCGTAATC TGCCGCATCA  
501 GgCTcAAGTC GAGTACGTT TGTGACGC CCAAATCCTG CGCAATCCAG  
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT  
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGSCAGG  
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep  
1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG  
51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA  
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF  
151 DGGGVVHQGI VRNLP HQAQV EYGLFDAQIL RNPAGTFQLD GMALPVLESN  
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGL LV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVVQHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHAHARDDVPYP					
g261	FVRQRPRLRLGQVHQRRVDLKIIVHRQIKGNVHGFDEHAAVGIARKIGFAHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGIIRNAVFGSFDGGGV----VHQGIVRNLPHQAVQVEYGLF					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAITFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
g261	DTQILRDPLCAFQLDGMALPVSEGDGLDVFAFVGLDCLNQAGGRILTAREDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAATAC ATCAGCGGCG TGTGGATTTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTC GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA SGTATTGCGA ACGCCGTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTGTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGCGCT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC GTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHGFQKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	AHARDDVPYP			
a261	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVT	AVGIAGEVGF	AHARDDVPYP			
	70	80	90	100	110	120
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV	EYGLFDAQIL			
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV	EYGLFDAQIL			
	130	140	150	160	170	180
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgccaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggtttatc cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccgcgaag tcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagctctcgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttggcggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcaccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

q263.pep

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIQVLANA PEALAFYQEV  
51 GKLNAANSLT AGEVEVIRII AVR TNQCSFC VAGHTKLATL KKL LSEQSLN  
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDDELNAF LEAGYNRQQA  
151 VEVVMGVALA TLCNYANNLA QTEINPKLOA YA\*

m263.seq (partial)

```

1      GCAGCAGGCG AATTTGACGA TGCCAAACTC GGC CGCTCG CCGCTTCAC
51     CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCGA TGCGGGCTAC AACCAGCAGC AGGACGTCGA AGTCGTGATG
151    GGGCT.AsyC TgGCCAACCTT GTGCAACTAC GTCAACAACC TCGGACAAAC
201    CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

```

m263.pep (partial)

1 GCAGCAGGCG AATTGACGA TGCCAACTC GGC GCGCTCG CCGCTTCAC  
51 CCAAGCCGTA ATGGCGAAAA AAGGCGGGT ATCCGACGAG GAACTCAAAG  
101 CATTTTTCGA TGCGGGCTAC AACCAGACT AGGACGTCTGA AGTCGTGATG  
151 GCGCT.AsyC TgGCCAACCT GTGCACATC GTCAACAACC TCGGACAAAC  
201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

from *N. gonorrhoeae*:

m263/q263

```

                                     10      20      30
m263.pep                        AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
                               |||:|||||||:|||||:|||||:
g263      QCSFCVAGHTKLATLKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD
           80      90      100     110     120     130


           40      50      60      70
m263.pep    ELKAFFDAGYNQQAVEVMGVXLATLCNVNVLGQTEINPELQAYAX
            ||::||::|||:|||||:|||||:|||:|||:|||:|||
g263      ELNAFLAEGYNRQQAVEVMGVVALATLCNYANNLAQTEINPKLQAYAX
           140     150     160     170     180

```

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCCTCGAA	ACGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCC	CCCGAAGCCT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGCTCA	ACGCCGCCAA	CAGCCTGACC	GCCGGCGAAG	TCGAAGTAAT
201	CCAGATTATT	GCGCGCCGCA	CCAACCAATG	CGGCTTCTGC	TGTGGCAGGG
251	ACACCAAAC	CGCAACCCTG	AAAAAACTCC	TTTCCGAACA	ATCCGTCAAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCGGCC	TTTACCCAA	CCGTAATGGC	AAAAAAAGGC	GCGGTATCCG
401	ACGAGGAAT	CAAAGCATTT	TTTGATGCGG	GCTACAACCA	GCAGCAGGCA
451	GTCGGAATCG	TGATGGGCGT	AGCCTTGCGA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCCGA	ATTGCAAGCT	TACGCCTGA

a263.pep

```

1 MARLTVHTLE TAPEAAKARV EAVLQNNNGFI PNLIGVLSNA PEALAFYQEV
51 GKLNAANSLT AGEVEVIQII AARTNQCGFC VAGHTKELATL KLLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA_
151 VEVVMGVALA TLCNYVNNLG OTEINPELOA YA*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	<u>QTASADAVVK</u>	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGG	FHGRKTSGE	RYDMNAFTAA	HKTLPISYV
101	RVTNTKNGKS	VIVRVNDRGP	KSNRIIDVS	KAAAQKLGFV	NQGTAVHKIE
151	QIVPGQSAVP	AENKIDIFDL	FSFGTEHAQ	AYLNQAAQNF	AVSSSGTNLS
201	VEKRRYEYVV	KMGPTSOER	AAEAGAAARG	MVRAVLTAG*	



608

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDI FIDLKSFGEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENKDI FIDLKSFGEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFQSQERAAEAEQA RGMVRAVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPFASQERAAEAEQA RGMVRAVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

```

1   TTGACTTTAA CCGAAAAAC CCTTTTCCTC CTCACCGCCG CATTCCGGCAT
51  ACATTCTTTT CAGACGGCAT CCGCCGACGC AGTGGTCAGG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAA ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGCGGGCAGG TTTCACGGGC GCAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC CGCTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAAAT GGGCTTTGTC AACCAAGGGA CGGCGCACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCGETT GCCGAAAACA AAGACATCTT
501 CATCGACTTG AAATCTTTTG GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CAAAACCTG GCTTCATCGG CATCAAACCC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTGCCTC
651 GCAGGAACGC GCCGCCGAGG CCGAAGCTCA GCGCGCGGGT ATGGTTCGGG
701 CGGTATTAAAC CGCCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

```

1   LTLTRKTLFL LTAAFGIHSF QTASADAVVR AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGR FHGRKTSgge RYDMNAFTA HKTLPISYV
101 RVNTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAAQKLG FVNQGT AHVKIE
151 QIVPGQSAPV AENKDI FIDL KSFGEHEAQ AYLNQAAQNL ASSASPNLS
201 VEKRRYEYVV KMGPFASQER AAEAEQA RGMVRAVLTAG*

```

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	50
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	50

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	70	80	90	100	110	120
m264.pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264.pep	FHGNRIIDVSKAAQKLGFEVNGTAHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAQKLGFEVNGTAHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264.pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFTSQERAAEAEQAARGMVRVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFASQERAAEAEQAARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```
m265.seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGCTG ATGATTTTGT CTTGTTTGT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTGTATGTT
201 CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTGGGCTTC GCGGCGCGT TCCTGCGAGG TAAACGGTCC
351 CATTTGACG ACGTATTCGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```
m265.pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFIKF AFVNRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265.pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIKF AFVNRGLENVDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI - FALVNQGLKNGDINKVSNNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
g265	TYSX					
	120					

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

```
a265.seq
1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... ..GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

```
a265.pep
1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQF AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*
```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANA	AAFSAWARLMIL	SCLLCWCAACP	WSSSPCPSWW	ASAGAEMLS	SAVAAEV
a265	MSVILPPTRANA	AAFSAWARLMIL	SCLLCWCAACP	WSSSPCPSWW	ASAGAEMPIS	AVAAAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFI	XFAFVN	RGLNV	DINKV	SNNRQ	PAVNTARTIPR
			:	:	:	
a265	KRRRLKFI	---FAPAKYL	XXCLKDVK	AGHQPAVNT	ARTIPR	ASASAARSCEANGPIL
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

```
g266.seq
1   agttcagacg gcatacgccg cgacaatgcc caaacagaaa gcccatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tgttcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgacg gagctggcgg caggtttcgc gctgaccgcc
201 tctcttgccg acatcctcga atcccggtgc ggagcggtac acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgtttcgt gcggcggtat tttgggcaca cgcgcaacag ggaataa
```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

```
g266.pep
1   MQFRRHRRRO CPNRKPIMTA SMYILLVLAL IFANAPFLT TRLFVAAALKR
51  KHFGHHLIEL AAGFALTASL AYILESRAGA VHNQWFEFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTGCGCGTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CGGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTGG CGTTTCCATG TTTTGTGTGG CGGTATTTTT GGCACACGCG
351 CAACAGGGAA TAG
```

611

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      LIELAAGFALTAVLAYILES RAGAVHNDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          60      70      80      90      100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTG CTGCTTGCC
101  TGATTTTTC CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATT CCGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTT TGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC GTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  ||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTKLFGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90      100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```

1	atgcaagtcg	ccttttttct	cgccgtggtg	ttcaaaaata	tgggtttcca
51	caatcgcatt	ggtcgggcag	gcctcttcgc	agaaaccgca	gaagatgcac
101	ttggctcagg	cgatgctcga	acgcttggtg	cggcgggtgc	cgctcttcgg
151	tctctccgat	tcgatgtgtg	tcgcaccttc	cggacacacc	cgctcgacac
201	atttacacgc	gatgcagcgt	tcctctccgt	tcggaaaaacg	gcgttgccgg
251	tcgacagccg	ggaaacgcac	ggattgcggc	gtttctctct	cgggaaaaata
301	aatgtgtctt	ttgcgggcaa	aaaagttttt	gagcgttacg	cccatgcctt
351	tcaccacgtc	qccaaqcaga	aaqattttta	ctaa	

g267 . pep

m267.seq

m267.pep

m267/g267

a267.seq

1	GTGCAAGTCG	CCTTTTCTTCT	CGCGGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCTTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGCGCGCTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TGCGCAATGC	GGGGCAAGC	GCTTCCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	CGCTTGC CGC
251	TGCAGACCGC	GGAAACGCAC	GGATTGCGCG	GTTTCTCTTT	CGGGAAAATA
301	AATCGTGTCT	TTGCGGGCAA	AAAAGTTTTC	GAGCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTCFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLEFAVRI	PPLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
	:::	:::				
a267	GANGFTQFTRDAAFLAVWIT	TALRVQTAETHGLRRFLFGK	INRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tggtaaact ggtccgagac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgctgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccagcga
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaaacgc cgactttttt gaacctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cggttgacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgagggg
651 ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcgcagaaa acatggaaaa gcggtatgga caagatctgt gccaaacatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaacgag cagaaacgga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTEKTD
101 SSKLKCEAAL KLDVPDDVVD YAVANQSIG NSHKKTPDF EPYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAEEA TAQEAREAE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAESET FNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

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```

51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151 AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAACCG TCACAGAAAA CATGGAAGAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401 AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1  ..MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAARVS EWEERYKLSR
51  XQFEQFWKGL POTVQNKLOP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||||:||||:||||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKORNEKLEAAETAQEAERE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAQEALGREQEAARVSEWEERYKLSRSQFEQFWKGLPQTVQNKLOPSQKTWKSMD
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g268      AEEAAAQEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1  ATGGCACTGA TTAAAGAGCC GTTGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAGAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1  MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTVQNKLOA SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEAAAQEALGREQEAARVSEWEERYKLSRXQFEQFWKGL
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
a268      MALIKEPLDKAKQRNEELEAAEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

	10	20	30	40	50	60
m268.pep	70	80	90	100	110	120
	PQTVQNK	LQPSQKT	WKS	GMDKICANNAKAEGKTPNGIKFSELACKTA	KTEARLEELHNRK	
a268	PQTVQNK	LQASQKT	WKS	GMDKICANNAKAEGETPNGIKFSELACKTA	ETEARLEELHNRK	
	70	80	90	100	110	120
m268.pep	130	140				
	KALIDEM	KREADXKELSKRLX				
a268	KALLDEM	AREADKELPKRLX				
	130	140				

m268-1.seq

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.ppt

m268-1/q268 82.3% identity in 164 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

1	GTGCAATCCC	GATATGATGG	TTTGCATAAA	TTTAAACATA	TATGTTCCGC
51	AGCTATGGCA	AGCTGTTAAG	AGCGCTTGGA	CAAGACGGAA	CAAGGAAGAC
101	AAGAACTTGA	ACGGCAGGAA	GAGCGCGCG	CGAGGAGGC	ATTGGTGCG
151	GAGCAGGAAG	TCGACCGCGT	ATCCGATATGG	GAAAGACGCT	ACAAGCTGTC
201	GCGCAGCGAG	TTCGAGCAGT	CTCGGAAGG	ATTGCTCAA	ACCGTACAGA
251	ATAAGCTGCA	AGCCTCACAG	AAAACATGGA	AAAGCGGAG	GGATAAAATC
301	TGTGGCAACA	ATCGGAAGC	TGAAGGTTGA	ACGCCAAACG	GCATAAAATC
351	CAGCGAAGCT	GCATGCAAAA	CGCGCGAAGC	CGAGACACGC	TTGGGAAGAG



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401 TGCACAACCG TAAAAAGCC CTTCTGACG AAATGGCCAG GGAAGCGGAC  
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep  
 1 VQSRDGLHK FKHCISAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR  
 51 EQEVDVRSEW EERYKLSRSE FEQFWKGLPQ TVONKLOASQ KTWKSGMDKI  
 101 CANNAAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD  
 151 KKELPKRL\*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCISAAMALIKEPLDKAKQRNEELEAAEAAAQALGREQEVDRVSEW					
m268-1	VQSRDGLHKFKHCISAAMALIKEPLDKVQKQRNEELEAAEAAAQALGREQEAARVSEW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEKTPNGIKFSEL					
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq  
 1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc  
 51 cagcccttgg atttgggcgg tgggtgtggg gtggtcgcgg tcggcttttt  
 101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttgccg  
 151 gtttcgccgt gggactttat ccggaacacg gcttcgcccc aggtgtcggc  
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc  
 251 cgcccggtgc cattttgctg tccaatcgcg gggtaaaaa accgttgctc  
 301 ttttaagtcg cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc  
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep  
 1 MVWRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA  
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS  
 101 FKSPSVQVDV SALLCLSLRS S\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq  
 1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC  
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTGT  
 101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCTGC GTTGATGGTT  
 151 TCGCGGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTGCGCGGC  
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC  
 251 CTGTGCGCCAT TTTGCTGTCC GAGCGCGGGG TTA AAAAGCC GTTGTGCTTT  
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT  
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep  
 1 MVWRVNCAAT AVLIFSSSPW IWA AVVWWSR SALSCKPCAT CPRPAPALMV  
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF  
 101 KFSSVQVDT S ALLCLSLRSS \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
           |||||
g269      MVWRVNCAATAALIFSSSPWIWAVVWWSRSASFCKPCASLDASSAPALAVSPWDFIRNT  60

m269.pep  ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSPKFSSVQVDTSAALLCLSLRS  119
           |||||
g269      ASPKVSAAALMHSEKTRALGRFSAPPVAILLSNRGVKKPLSPKSPSVQVDTSAALLCLSLRS  120

m269.pep  SX  121
           ||
g269      SX  122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51  CAGCCCTTGG ATTTGGGCGG CCGTGTGGGT GTGGGCGCGG TCTGCTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCGCGT CCAGCGCGCC GGCCTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGCGCG TTTTCGTCGC
251 CGCCTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTGTGCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVVWWAR SALSWRFCAS VPASSAPALT
51  VSPWDFIQNT ASPKVSAAAL HSEKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269.pep  10 20 30 40 50 59
           MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
           |||||
a269      10 20 30 40 50 60
           MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSWRFCASVPASSAPALTVSPWDFIQNT

m269.pep  60 70 80 90 100 110 119
           ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSPKFSSVQVDTSAALLCLSLRS
           |||||
a269      60 70 80 90 100 110 120
           ASPKVSAAALMHSEKTRALGRFSSPPVAILLSGRGVKKPLSPKFSSVQVDTSAALLCLSLWS

m269.pep  120
           SX
           ||
a269      120
           SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gactgctgc tgactgcctt
51  tgccgccttc aagctcggtt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg agggttgca cgtgccggac
151 ggaagccgtg tccgcgccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cagcgccccg ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcatt cgctgcccgc tctgtgtcga
351 aggcaggcgc gattttacgg cgacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

618

g270.pep  
 1 MNKNRLLLLL ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ  
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq  
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca . CAGCCGC  
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCgGTTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA  
 301 cCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCTGA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep  
 1 MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ  
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng)

from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRLLLLL AALLLAF AAVKLVLLQWWQA XQPQAVAAQC DLTEGCTLPD GSRVRAAAVS					
g270	MNKNRLLLLL AALLLAF AAVKLVLLQWWQA XQPQAVAAQC DLTEGCTLPD GSRVRAAAVS					
	10	20	30	40	50	60
m270.pep	TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ PSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ PSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
m270.pep	TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ PSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ PSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
m270.pep	DFTADITIGS RTFQTAFTAE X					
g270	DFTADITIGS RTFQTAFTAE X					
	130	140				
m270.pep	DFTADITIGS RTFQTAFTAE X					
g270	DFTADITIGS RTFQTAFTAE X					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq  
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC  
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA  
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCTGA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep  
 1 MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

**m270/a270 99.3% identity in 140 aa overlap**

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALLL	IAFAAVK	LVLLQW	WQAXQP	QAVAAQC
a270	MNKNRKL	LLAALLL	IAFAAVK	LVLLQW	WQAXQP	QAVAAQC
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDI	YIEHAP	AGTEQV	SISFSM	KNMDMG	FNRYMFE
a270	TKKPFDI	YIEHAP	AGTEQV	SISFSM	KNMDMG	FNRYMFE
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADIT	IGSRTF	QTAFTA	EX		
a270	DFTADIT	IGSRTF	QTAFTA	EX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcggatggc	gaggatttgg	gcgacggggg	taacgttgtg
51	tatgggtcagt	ccgtgtcccg	cgttgacgac	caagcccaaa	tcgcccgcga
101	aatgcgcgcc	gttttgatg	cgctcgaaact	gcctgatttg	ttcggcgtgg
151	ctttgtgctg	cggcatatgc	gccgggtgtgc	agctcgacaa	cgggcgcgcc
201	gacatcacgg	gcggcttggg	tttgctgtgc	gtcggcatcg	ataaacaagg
251	acacgcgtat	gcccgctcgc	gtcaggattt	tggcgaattc	ggcgattttt
301	tcctgttgcg	ccaatacgtc	caaaccgcct	tcggtcgtga	tttcctgcgc
351	tttttcaggc	acgatgcaca	cgtcttccgg	catcacttta	agcgcgtttt
401	cgagcatttc	ttccgtcaac	gccatttcaa	ggttcaggcg	cgtgcggatg
451	gcgtttttga	cggcaaatac	atccgcgtct	ttgatgtggc	ggcggctctc
501	gcgcaggtgc	atggtaatca	ggtctgcacc	gtgcgtttcg	gcaaccagtg
551	ccgcctccac	ggggtcggga	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTL	CMVS	PCPAL	TTKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LCASAYAPVC	SSTTGAP	TSR	AAWICL	SSAS	INKDTR	MPAS	VRILANS	AI
101	SCCANTSKPP	SVVISCR	FSG	TMHTSS	GITL	SAFSSIS	SVN	AISRFR	VRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIRSAP	CVS	ATSAAST	GLG	*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTcagTt	CGCGGATGgc	GAGGATTtGg	GCGATGGGGG	TAACGTtGTg
51	TATGGTcAGT	CCGTGTCCGg	CGTTGACGAc	CAAGCCCAAA	TCGCCGgCGA
101	AATGCGCGCC	GTTTTGgATG	CGCTCGAACT	GCCTGATTtG	TTCCGGCGTGG
151	CTGCGCGCGT	CGCATACGc	GCCTGTGTGc	AGCTCGACAA	CGGGCGCGCC
201	GACATCACGG	GCGGCTTGGa	TTTGCCTGTC	GTCGGCATCG	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTCG	GTCAGGATtT	TGGTGAACCC	GGCGATtTTT
301	TCCTGTTGCG	CCAATACGTC	CAAACCGCCT	TCGGTCGTGA	TTTCCTGACG
351	TTTTTCAGGC	ACGATGCACA	CGTCTTCCGG	CATCACTTTC	AAAGCGTtTT
401	CCAACATTTC	TTCCGTCAAC	GCCATTTCAA	GGTTCAGGCG	CGTGCGGATG
451	GCGTTTTTGA	CGGCAAAACG	GTCCGCGTCT	TTGATGTGGC	GGCGGTCTTC
501	GCGCAGGTGC	ATGGTAATCA	AATCCGCACC	GTGCGTtTCG	GCAACCAAGT
551	CCGCCTCCAC	GGGCTGGGA	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTL	CMVS	PCPAL	TTKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LRASAYAPVC	SSTTGAP	TSR	AAWICL	SSAS	INKDTR	MPAS	VRILVNP	AI
101	SCCANTSKPP	SVVISXRFSG	TMHTSSGITF	KAFSNISSVN	AISRFRVRM				
151	AFLTANTSAS	LMWRRSSRRC	MVKSAPCVS	ATSAASTGLG	*				

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271 . pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 . pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPSPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTS KPSPSVVISXRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271 . pep	TMHTSSGITLFAFSNISSVNAISRFRVRMAFLTANTASLMWRRSSRRCMVIRSAAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTASLMWRRSSRRCMVIRSAAPCVS					
	130	140	150	160	170	180
	190					
m271 . pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271 . seq

```

1  ATGTTCAAGT  CGCGGATGGC  GAGGATTTGG  GCGATGGGGG  TAACGTTGTG
51  TATGGTCAGT  CCGTGTCGGG  CGTTGACGAC  CAAGCCCAAA  TCGCTGGCAA
101 AATGCGCGCC  GTTTTGGATG  CGCTCGAACT  GCCTGATTTG  TTCGGCGTGG
151 CTGCGCGCGT  CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201 GACATCACGG  GCGGCTTGGG  TTGCCTGTC  GTCGGCATCG  ATAAACAAGG
251 ACACGCGTAT  GCCGCGCTCG  GTCAGGATT  TGGTGAATTC  GGCAATTTTG
301 TCTTGTTGCG  CCAATACGTC  CAAGCCGCCT  TCGGTGCTGA  TTTCTGACG
351 TTTTCCGGC  ACGATGCACA  CGTCTTCCGG  CATCACTTTA  AGCGCGTTTT
401 CGAGCATTT  TTCCGTCAAC  GCCATTTCAA  GGTTCAGGCG  CGTGCGGATG
451 GCGTTTTTGA  CAGCAAACAC  GTCCGCGTCT  TTGATGTGGC  GGCGGTCTTC
501 GCGCAGGTGC  ATGGAATCA  GGTGGCACC  GTGCGTTTCG  GCAACCAAGT
551 CCGCCTCCAC  GGGGCTGGGA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271 . pep

```

1  MFSSRMARIW  AMGVTLCMVS  PCPALTTKPK  SLAKCAPFWM  RSNCLICSAW
51  LRASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDTRMPAS  VRILVNSAIL
101 SCCANTS KPP  SVVIS*RFSG  TMHTSSGITL  SAFSSISSVN  AISRFRVRM
151 AFLTANTSAS  LMWRRSSRRC  MVIRSAAPCVS  ATSAASTGLG  *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271 . pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 . pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPSPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTS KPSPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pcp	TMHTSSG	ITFKAFS	NISSVNA	ISRFRVR	MAFLTAN	TASASL
a271	TMHTSSG	ITLAFSS	ISSVNA	ISRFRVR	MAFLTAN	TASASL
	130	140	150	160	170	180
	190					
m271.pcp	ATSAAST	GLGX				
a271	ATSAAST	GLGX				
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

```

g272.seq
1  atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaagggttcc gacctgtttg tgacgacca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgcg atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtcca atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgct caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttcgcg tgaacaaacg cgggctgggt atttttgcg
401 gcggcaccgg ctccgggcaa tcgacttcgc tcgcctcgct taccgactac
451 cgcaatgaaa attcggttcg acacatcatc accatcgaag atccgatcga
501 gtttgcctac gaacacaaaa actgcacatc taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggttg aaaatacgct gcgtcaggcg
601 cgggatgtga tccttatcgg cgaatccgcg gaccgtgaaa caatggacta
651 cgccatcgcc ttgcccgaac cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctgcaccgca tcatcaactt cttcccgag
751 gagcgcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatctcgcaa cgctcgttc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga ttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtag agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

```

g272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMMT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDLELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

```

m272.seq
1  ATGACCGCAA AGGAAGAAGT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTCG TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCCTGAC GGCgGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAaaaaaACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCAGCGC GAGGTCGGCG

```

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551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTCCCCGAG
751 GAGCGGCGCG AACAAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCAAA CGCCTCGTTC CGCGAGACGG CGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCtGA TTTCGGAGTT GATTCACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAAATCCG ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CaaAGTTyCA GCCCCGATTT
1101 GGNACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1 MTAKBELFAW LRHMxQNKGs DLFVTHFFP AMKLDGKI TR ITDEPLTAEK
51 CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RTITSKIPKF ESLNLPPVLK DVALKKRGLV IFVGGTGSgK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCII TQR EVGVD TENNM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLyQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QsXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/q272

	10	20	30	40	50	60
m272.pep	MTAKEELFAWLRHMxQNKGsDLFVTHFFPAMKLDGKI TRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKGsDLFVTHFFPAMKLDGKI TRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALV FRTITSKIPKESLNLPPVLK					
	70	80	90	100	110	120
m272.pep	130	140	150	160	170	180
g272	DVALKKRGLVIFVGGTGSgKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCII TQR					
	130	140	150	160	170	180
m272.pep	190	200	210	220	230	240
g272	EVGVD TENWMAALKNTLRQAPDVILIGEIR DRETMDYAIAFAETGHLcMATLHANSTNQA					
	190	200	210	220	230	240
m272.pep	250	260	270	280	290	300
g272	LDRIINFFPEERREQLLTDL SLNLQAFISQRLVPRDGGKGRVAAVEVLLN SPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
g272	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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```

                370
m272.pep      QSXSPDLXLLX
                || :||| |||
g272          QSSDPDLELLX
                370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51 CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGCGAAAAA
151 TGTATGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCATTAA CCAACAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCTGTCGG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAACCTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCIGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTCGGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTC TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCCACCAAC ACCTTTACCA ATTGTATGAA AAAGCGGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAATGCCG ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTIGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51 CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPPVLK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHL CMA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMO TFDQHL YQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

                10      20      30      40      50      60
m272.pep      MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
                ||||| :|||||
a272          MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
                10      20      30      40      50      60

                70      80      90      100     110     120
m272.pep      AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVERTITSKIFKESLNLPPVLK
                ||||| :|||||
a272          AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIFKESLNLPPVLK
                70      80      90      100     110     120

                130     140     150     160     170     180
m272.pep      DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
                ||||| :|||||
a272          DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
                130     140     150     160     170     180

```



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	190	200	210	220	230	240
m272 . pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272 . pep	LDRIINFPEERREQLLDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFPEERREQLLDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272 . pep	GNIHEIKEVMKKSTTLGNQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGNQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272 . pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```
g273 . seq
1  atgagtccttc aggcggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcacgc ttttcctgcc gtttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcgcca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacgggttaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgccgctga aatcaaggcg
351 gtttgagaag tgttccnacc gcgccgcccg tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccctg ctttttggtt ttcaagcagt
501 tttttcttac gcgtaa
```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```
g273 . pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRRARWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCCR VPLKSRREFK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```
m273 . seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTTCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTCAAT
251 GTTGTTCCTT AATGCTTAAA AACCCGCTG TCCGTGCAAC CGTTTTAAGG
301 CGGCAAAATG CAAAATTGT TTGCGGCGGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTGTGC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTGTGTWTC AAGCAGTTT
501 TTCTTACGCG TAA
```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```
m273 . pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCCR VPLKSGRFEK CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY *
```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTFFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFEAGTFPFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRQIAKFVCGRVPLKSGRFEG					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRALCALCAGVICRSPAKSPRTRFAEFPHCLVSYGVYLPFVXQAVFSYAX					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1  ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAAATA
51  CAACGAAAT  CAGGAAAACG GCGGTAAAGC TCATAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAAC
151 CCATTACCG  TTTTCCTGCC GCTTTTGTG GCTTTTAAA TAAAGGATGA
201 TGCCGGAAG  CAGCGCGGCA GCCGCGCCG ACATTAGCAT AATGTTTATT
251 GTTGTTCCTT AACGGTTAAA AACCGGCCG TCCGTGCAAC CGTTTAAAG
301 AGGCGGTAAA TCACAAAGTT TGTGGCGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAA GGGCATGATG CACTGCCCG TGTGCCGAT ATTATTTGTC
401 GCTCACCTGC AAAATTGCCA AGAACGCGT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT CATACGCGT TTGCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP PSRTAQYNEN QENGGAHKQ GQSGKHADRR QDIGVFQGTG
51  PFTVFLPLFV AFEIKDDAGK QGRSRARH*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL FVQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTFFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFQGTGTFPFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRQIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRALCALCAGVICRSPAKSPRTRFAEFPHCLVSYGVYLPFVXQAVFSYAX					
a273	GHDALPRV-PDIICRSPAKLPTRTFAGFPHCLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTTCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGCGGc ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCCCT
351 TCCGCGCGCC AACCACTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTCGATTTG
451 ACCCCGATGG ACAAACCTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAKVFGV GEPDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAAACATAT CGACATCCAG CTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGCGGc GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCCCT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAKVFGV GEPDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAKVFGVGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLPPA					
m274	DMNAKVFGVGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNATESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGCGC GCGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTTG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVIA SVAMFFVAQQ HATDLVTDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
a274	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
a274	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESXX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESXX					
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESXX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESXX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggacgaga tgatgcgggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgctcaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgctctt ttcaaaatgg cgcgggcat
201 ggcgacgcgt tgccgctgtc cgcggataaa gttgctgccc ttgatccga
251 tgggctggtg cagtccgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggcttgga ggcggacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggacg ttttcaaaaca ggggtgctgc aaacaggaaat acgtcttggg
401 agacgagggc gaattgggcg cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcggg
501 cagaagggtg acgacgggtg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctctg atgtcgaggt tgaagttgtc gagggtttg
601 atgccgtctg aacgggtatc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgcgga gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcggcga ggaacatcgt ctgcataagg
751 atgctgatgt tggcaaggct tttgatggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgcgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

628

```

1  MILPPSMTMM RSADSTVVRW WATMPVRFSS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

```

m276.seq
1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCCGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GCGGACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGA GGGCGAACAG GACTTCGGCT TCGCCGCGT CGGGACGCGT
351 GTATCGGACG TTTTCAAACA GGGTGTGCTC AAACAGGAAT ACGTCTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCACT CGAGTTGAT GTCCGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCT ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCCACACGC TCGGTGCGCA GCGTGCCCTT GTCCTGTTTC GCGGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

```

m276.pep
1  MILPSSITMM RSAPSMVVRW WATMPVRFSS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GELSLRLCRL
101 AWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng)

from *N. gonorrhoeae*:

```

m276/g276
      10      20      30      40      50      60
m276.pep  MILPSSITMMRSAPSMVVRW WATMPVRFSS IRRSSACWTRRSDSLSNALVASSNNNIGAS
          ||| |:||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
g276      MILPSSMTMMRSADSTVVRW WATMPVRFSS IRRSSACWTRRSDSLSNALVASSNNNIGAS
          10      20      30      40      50      60

      70      80      90      100     110     120
m276.pep  FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSLRLCRLAVWRANRTSASPASGRLYRT
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g276      FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSLRLCRLAAWRADRTSASPASGRLYRT
          70      80      90      100     110     120

      130     140     150     160     170     180
m276.pep  FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGRRLTTVDLPLPER
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g276      FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGRRLTTVDLPLPER
          130     140     150     160     170     180

      190     200     210     220     230     240
m276.pep  PTRATRSPLCMSRLKLSRALMPSERYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g276      PTRATRSPLCMSRLKLSRALMPSERYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP
          190     200     210     220     230     240

```

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

a276.seq

```

1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGCG AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTTCA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTGTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCTTT GTCCTGTTG GCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCG CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCACATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

a276.pep

```

1  MILPSSITMM RSAPSMVVR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKRGSRL TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgcgc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtagat cgccaagcgt
101  tcgatgccgt aggtaatctt gccgagtacg ggcgtgcaat cgataccgcc
151  gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201  cttcccagcc caaacccac gcaccgaggg tggggtttcc ccagtcgtct
251  tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgagc
301  ggagtcgaga tagaggtctt ggatattggc gggggcgggg ttgagggcga
351  cttggaattg gtaatagtgt tgcaggcggg tggggttgtc gccgtagcgg
401  ccgtcttttg ggcggcggtt ggggttgga ctagcgccaa accaagggtc
451  gggggccgagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501  cttccatgtc gaagggttg atgacgggtg agcctttgtc tgcccagaag
551  gtttgcagtt tgaagatgat ttgttggaag gtaagcatgg cttattgttc
601  gataaaataa aggttttatt ttactgttcc catagccgct tgaatagatt
651  tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG YFHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101  GVEIEVL D I G G G F E G D L E L V I V L Q A V G V V A V A A V F G A A A G L D V G G K P R L
151  GAERAQAGGG MGCAGTDFHV EGLDDGA AFV CPEGLQFEDD LLEGKHGLLF
201  DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101  CGCAGCAGCC AGTCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
151  GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201  GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251  ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301  GTCGATGCCG CCGACTTGTT GGAAATAGGT AACTGGGTT ACTTCCATGC
351  CGTTGAGCCA GACTTCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401  TCCAGTCGT CTTCGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451  CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501  GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551  TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601  AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651  TGCCGGCACC GACTTCCATG TCGAAGGTT GGATAGCGGT GCAGCCTTTG
701  TCTGCCAGA ATGTTTCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751  GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPVG I AVFEVVGGLL
51  DFVLVVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101  VDAADLLEIG KLG YFHAVEP DFPAQT PRAE GGVFPV VFDK ADVVDFGIDA
151  QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201  KPRLGARCAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251  GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30  
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH

631

```

                                     :||||| :||:|||||:||||:||||
m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAVGDGVAVERFCPNEVVDFYTLQVH
           30      40      50      60      70      80

           40      50      60      70      80      90
g277.pep   ROAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAFEPDFPAQTPRTEGGVFPVVFDDKADV
           |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      ROAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEPDFPAQTPRAEGGVFPVVFDDKADV
           90      100     110     120     130     140

           100     110     120     130     140     150
g277.pep   DFGIDAQFAQGVEIEVLDIGGGFEGDLELVIVLQAVGVVAVAVFGAAAGLDVGGKPR
           |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      DFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQAVGVVAVAVFGAAAGLDVGGKPR
           150     160     170     180     190     200

           160     170     180     190     200
g277.pep   GAERAQAGGGMGCAGTDFHVEGLDDGAAFVCPEGLQFEDDLLEGKHGLL
           ||| |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1   ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCAGTTCGT CTTCGACAAA GCGGATGTCG TGCACTTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTGCAG TTTGAAGATG ATTGTGTTGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1   MPRFEDKLVG RQEGGVVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFLVHVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDD ADVVHFGVDA
151 QFAQGVEIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

           10      20      30      40      50      60
m277.pep   MPRFEDKLVGRQEGGVVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAV
           |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      MPRFEDKLVGRQEGGVVFFGKQAFGLRFVVVELAQQPIGIAVFEVVGGLDFVLVHVAV
           10      20      30      40      50      60

           70      80      90      100     110     120
m277.pep   GDGVAVERFCPNEVVDFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEP
           : :|:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120

           130     140     150     160     170     180

```



632

```

m277.pep    DFPAQTPRAEGGVFPVVFADKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVQLQA
a277        DFPAQTPRAEGGVFPVVFADKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVQLQA
            130      140      150      160      170      180

m277.pep    VGVVAVAAVFGAAGLDVGGKPRLGAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPCECLQ
a277        VGVVAVATVFGAAGLDVGGKPRLGAECAQTGGGMGCAGTDFHVEGLDDGAAFVCPCECLQ
            190      200      210      220      230      240

m277.pep    FEDDLLEGKHGLX
a277        FEDDLLEGKHGLX
            250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1   ttgcgtgcaa tcacgcccg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaat acggccggta
151 caggtaaccg tgtcgccctc tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtcgcgct ccagggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatcg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1   LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1   TTGCGCGCAA TCACGCCCGG TGCGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GCGCGCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1   LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPOVRTSFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDL DRDFQLAVET LIQHLHLQAD
201 LFGVQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

633

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVV	LIGPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC				
m278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYPNTTAPTESRSR	FIAPKPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPRVLTSAFT			
m278	SYPNTTAPTESRSR	FIAPKPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPQVRTSAFT			
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGLS	CMKTLIRHSRVQSTQFALYRQIQNLITHFNF				
m278	DRFSILALIKSLISAGLS	CMKTLIRHSRVQSTQFALYRQIQNLITHFNF	YAANQLRFDF			
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFV	QGRIGTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

```

1  TTGCGCGCAA TCACGCCCCG TGCGATTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTCG CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCCTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTCA CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTCGCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTGC GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSPNTTAPT ESRSRFIAPK KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LEVQGRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
a278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC				
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNTTAPTESRSR	FIAPKPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPQVRTSAFT			
a278	SCSPNTTAPTESRSR	FIAPKPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPRVRTSAFT			
	70	80	90	100	110	120

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	130	140	150	160	170	180
m278 .pep	DRFSILALIKSLISAGLS	CMKTLIRHSRVQGTQF	FALYRQIQNLITHFN	FYAANQLR	EDF	
a278	DRFSILALIKSLISAGLS	CMKTLIRHSRVQGTQF	FALYRQIQNLITHFN	FYAANQLR	EDF	
	130	140	150	160	170	180
	190	200	210	220		
m278 .pep	DRDFQLAVETLIQHLH	QLADLFVQGRIGTVND	GRFDMVEX			
a278	DRDFQLAVETLIQHLH	QLADLFVQGRIGTVND	GRFDMVEX			
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279 .seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagttttgctg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgctg ttggctcggg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gtgcctgca atcacgactt gtccgggcga
201 gttgaagtgt acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcctct tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaa ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279 .pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAALPA ITTCPELKL TASTTSPCAD SAQICLTSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279 .seq

```

1  ATAACGCGGA TTGCGGCTG CTGATTTCA ACGGTTTCA GGGCTTCGGC
51  AAGTTTGTGCG GCGGCGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CCGGCAGCGG CAGGGCGCGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGCGGCGGCG GTTGCTGCA ATCACGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCACAAA TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCGGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279 .pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAALPA ITICPELKL TASTTSLWAA SAQMALTSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N.gonorrhoeae*:

	10	20	30	40	50	60
m279 .pep	ITRICGCLISTVFRASASLSAAGFIRLQWE	CTDTGSGRARLAPASLAAAMARPTAALPA				
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWE	CTDTGSGRARLAPASLAAAMVRPTAALPA				
	10	20	30	40	50	60
	70	80	90	100	110	120

m279 . pep  
ITICPGELKLTASTTSLWAASQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSTLTA  
|| ||||||| | : ||||| : |||||||  
g279  
ITTCPGELKLTASTTSPCADSAQICLTCSKKPKMAAIAPTPCGTADCISSARRRSTLTA  
70 80 90 100 110 120

130 140 150  
m279 . pep  
SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX  
||| || ||||||| ||||||| |||  
g279  
SAKSNSAATSAVYSPRLCPATAAGVLPTTSKX  
130 140 150

a279.seq

```
1 ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNNA GGGCTTCGGC
51 GAGTTTGTCTG GCGGCGGGTT TCATGAGGCT GCAATGGGAA GTTACNGACA
101 CNGGCAGCGG CAGGGCGCGT TTGGCGCCGG CTCTCTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGC ATTGCTGCA ATCACGATT GTCCGGCGCA
201 GTTGAAGTTG ACGGCTTCAA CCACTTATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCCGAATAG
```

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	<u>ARSTAAALPA</u>	<u>ITTCPGELKL</u>	<u>TASTTSSCAD</u>	<u>SAQICFTCSS</u>	<u>SKPRIAATAP</u>
101	<u>TPCGTADCIS</u>	<u>SARXRTSLTA</u>	<u>SAKSNAAPAT</u>	<u>SAVYSPXLCF</u>	<u>ATAAGVLPPA</u>
151	SE*				

		10	20	30	40	50	60
m279.pep		ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA					
		:					
a279		MTXICGCLISTVXFRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m279.pep		ITICPGELKLTASTTSLWAASQAQMALTCSSSKPRIAAIAPTFCGTADCISSARRRSTLTA					
a279		ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTFCGTADCISSARXRSTLTA					
		70	80	90	100	110	120
		130	140	150			
m279.pep		SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279		SAKSNAPAATSAVYSPXLCPATAAGVLPPASEX					
		130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Ouakvi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgcgga
151 gccaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagcaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccaaa acgtcgctga aaccctgata aaggccgata ccgaaggcaa
501 agttttattat caacaacgct tgggcaacta ccaaatagcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaaat cgtccctgc cgccaaacgc
601 aaagtctctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaaaacaagt cgccgcatc atccgcaaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcacgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADIQRAV KQSKVSYAEA
101  TKGIQPLKAE EGGHHHDHHD HDHDHDHDEGH HHDHGEYDPH VWNDPVLMDS
151  YAQNVAETLI KADPEGKVYY QRLGNYQMQ LKKLHSDAQA AFNAVPAAKR
201  KVLGTGHDFAF YGMNRYNLSF IAPQGVSSSE EPSAKQVAAI IRQIKREGIK
251  AVFTENIKDT RMVDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNVE
301  ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACCTCAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGTCTCA CCGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCCTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CTTTTCTCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACGCGCCCC
851 CAGACACCTA CATCGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADVQRAV KQSKVSYTEA
101  TKGIQPLKAE EGGHHHDHHD HDHEGHHHDH GEYDPHVWND PVLMSAYAQN
151  VAKALIKADP EGKVVYQORL GNYQMLKKL HSDAQAAFNA VPAKRKVLV

```

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAAIIRQI KREGIKAVFT  
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN  
 301 AMKQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)  
 from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSFILGDAKQIGGERVSIQSLVGANQDTHAYHM					
	: : :     : : :     : : :     : : :     : : :     : : :					
g280	MKHLKLTLIAALLATAATAAPLPVVTFSFILGDAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDH-					
	: : :     : : :     : : :     : : :     : : :     : : :					
g280	TSGDIKKIRSAKLVLLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
	: : :     : : :     : : :     : : :     : : :     : : :					
g280	HDHDHDHEGHHHDHGEYDPHVWNDPVLMSDYAQNVAETLIKADPEGKVYYQORLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI					
	: : :     : : :     : : :     : : :     : : :     : : :					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSSAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	: : :     : : :     : : :     : : :     : : :     : : :					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNVE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

```

1  ATGAAACACC CCAAACCTCAC CCTTATCGCC GCATTGCTGA CCACTGCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTCAGCATT TTAGCGGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGCGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGATTAA CGGCTTAGGA CTTGAAGCTG
251 CCGACATCCA ACGTGCCGTC AAACAGAGCA AAGTATCCTA TGCCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGCGG GACACCATCA
351 CGACCACGAT CATGACCACG ACCATGACCA CGAAGGACAC CACCACGACC
401 ACGGCGAATA TGACCCCCAC GTCTGGAACG ACCCCGTCCT TATGTCCGCC
451 TATGCCCAAA ACGTCGCCGA AGCCCTGATA AAGGCCGACC CCGAAGGCAA
501 AGTTTATTAT CAACAACGCT TGGGCAACTA CCAAATGCAG CTCAAAAAAC
551 TGCACAGTGA CGCACAAGCC GCATTTAATG CCGTCCCTGC CGCCAAACGC
601 AAAGTCCTGA CCGGGCACGA TGCCCTTTCC TATATGGGCA AACGTTACCA
651 TATCGAATTC ATCGCCCCAC AAGGTGTGAG CAGCGAAGCC GAGCCTTCAG
701 CCAAACAAGT CGCCGCCATC ATCCGACAAA TCAAACGCGA AGGCATCAAA
751 GCCGTATTTA CCGAAAATAT CAAAGACACC CGCATGGTTG ACCGCATCGC
```

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG  
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA  
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep  
 1 MKHPKLTLLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG  
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA  
 101 TKGIQPLKAE JEEGHHHDHD HDHDHDHDEGH HDHGEYDPH VWNDPVLMSA  
 151 YAQNVAEALI KADPEGKVYY QORLGNYQMQ LKKLHSDAQA AFNAVPAAKR  
 201 KVLTHDAFS YMGKRYHIEF IAPQGSSEA EPSAKQVAAI IRQIKREGIK  
 251 AVFTENIKDT RMDVRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNIK  
 301 ALTNAMKQ\*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLLIAALLTASATAAPLPVVTSFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
a280						
	10	20	30	40	50	60
	70	80	90	100	110	120
m280.pep	TSGDIKKIRS AKLVLLINGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280						
	70	80	90	100	110	120
	130	140	150	160	170	
m280.pep	HDH----EGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
a280						
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEF IAPQGSSEA EPSAKQVAAI					
a280						
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIK AVFTENIKDTRMDVRIAKET GNVVSGKLYS DALGNAPADTYIGMYRHNIK					
a280						
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
a280						
	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq  
 1 atgcactacg ccctcgcatc cgtctctgc ctgtccctca gcgcgcacc  
 51 cgctcgcgta ttctctgta tgcgcgtat gacctgata ggcgacgat  
 101 tgagccacgc cgtctgccc ggtgccgccc tcggctacat gtttgcggc  
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgccgccc gtatgctgat  
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg  
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc  
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc  
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg  
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa  
 451 agcatagacc cccttttctt caagtccgtc aacggcaaa ggcggctttg





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g281	VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGLWHVIFLILVVMNLV	130	140	150	160	170	180
m281.pep	SGFOALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTAALLCGLSGLLISYHIEIPSGP	190	200	210	220	230	240
g281	SGFOALGILMSVGIMMLPAITARLWARMGTLILLSVLIALFCGLIGLLISYHIEIPSGP	190	200	210	220	230	240
m281.pep	AIILCCSVLYLFSVILGKEGGILT	250	260				
g281	AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

a281.seq	1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGCACC
	51	CGTCGGCGTA	TTCCTCGTCA	TGCGCCGTAT	GAGCCTGATA	GGCGACGCAT
	101	TGAGCCACGC	CGTCCTGCCC	GGTGCCGCGG	TCGGCTACAT	GTTTGCCGGC
	151	TTAAGCCTGC	CCGCCATGGG	TTTGGGCGGC	GTAGCCGCAG	GTATGCTGAT
	201	GGCACTGCTT	GCCGACTCG	TCAGCCGCTT	CACCACCCTG	AAAGAAGATG
	251	CCAACCTTGC	CGCCTTTTAT	CTCAGCAGCC	TCGCCATCGG	TGTAGTCCTC
	301	GTCAGCAAAA	ACGGCAGCAG	CGTCGATTTC	CTCCACCTCC	TTTTCGGCTC
	351	CGTACTTGCC	GTCGATATTC	CTGCCCTGCA	ACTCATCGCC	GCCGTATCCA
	401	CCCTCACACT	GCTTACCCTT	GCCGTCATCT	ACCGCCCGCT	CGTACTCGAA
	451	AGCATCGACC	CCCTGTTTCT	CAAATCTGTC	GGCGGCAAAG	GCGGGCTTTG
	501	GCACGTCCTC	TTTCTCGTCC	TGGTCGTCAT	GAACCTCGTA	TCCGGCTTTC
	551	AAGCCCTCGG	CACACTCATG	TCCGTCGGAC	TTATGATGCT	GCCAGCCATT
	601	ACCGCCCGCC	TATGGGCGAA	GCACATGGGC	GCACTCATCC	TCCTATCCGT
	651	TCTGACAGCC	CTGCTGTGCG	GCTTGAGCGG	ACTGCTCATT	TCCTACCACA
	701	TCGAAATTCC	TTCCGGTCCC	GCCATCATCC	TCTGTTGCAG	CGTCCTTTAT
	751	CTCTTTTCCG	TCATACTCGG	CAAAGAAGGC	GGCATTCTGA	CCAAATGGCT
	801	CAAAAACCAC	CGCCACCACA	CCACCTGA		

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

a281.pep	1	MRYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG
	51	LSPAMGLGG	VAAGMLMALL	AGLVSRTTL	KEDANFAAFY	LSSLAIGVVL
	101	VSKNGSSVDL	LHLLFGSVLA	VDIPALQLIA	AVSTLTLLTL	AVIYRPLVLE
	151	SIDPLFLKSV	GGKGLWHVL	FLVLVVMNLV	SGFOALGTLM	SVGLMMLPAI
	201	TARLWAKHMG	ALILLSVLTA	LLCGLSGLLI	SYHIEIPSGP	AIILCCSVLY
	251	LFSVILGKEG	GILTKWLKNH	RHHTT*		

m281/a281 99.2% identity in 264 aa overlap

m281.pep	10	20	30	40	50	60
	MRYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG	LSPAMGLGG
a281	10	20	30	40	50	60
	MRYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG	LSPAMGLGG
m281.pep	70	80	90	100	110	120
	VAAGMLMALL	AGLVSRTTL	KEDANFAAFY	LSSLAIGVVL	VSKNGSSVDL	LHLLFGSVLA
a281	70	80	90	100	110	120
	VAAGMLMALL	AGLVSRTTL	KEDANFAAFY	LSSLAIGVVL	VSKNGSSVDL	LHLLFGSVLA
m281.pep	130	140	150	160	170	180
	VDIPALQLIA	AVSSLTLLT	LAVIYRPLV	LESIDPLFLK	SVGGKGLWH	VFLVLVVMNLV
a281	130	140	150	160	170	180
	VDIPALQLIA	AVSTLTLLT	LAVIYRPLV	LESIDPLFLK	SVGGKGLWH	VFLVLVVMNLV

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgacg ggcggtgcgc tattgaaggt
201 tttgggcata agcgtcggtt cgtttcaggt cggcggcggg attttgggtc
251 tgcctgacgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggagcatt gccgtcgtgc ccacgcacat accgatcacc atcgggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatcgcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattcccgc aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAUVS
201 VEIIVSGLKT IFFQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCCGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGCTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGETCAG CCGCTGCTG GCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAUVS
201 VEIIVSGLKT IFFQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng)  
from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALS	SLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI				
g282	MGLGMEIGKLIVALLVLINPFSALS	SLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI				
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISM	MNGNDNPAKQNLGAQPETGQARPARNAGAI				
g282	GGALLKVLGISVGSFQVGGGILVLLIAISM	MNGNDNPAKQNLGAQPETGQARPARNAGAI				
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGACCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GCGCGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGT CGTTTCAGGT CGGCGGCGGA ATTTTGGTGT
251 TGCTGATTGC CATTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGTGCGACGG
551 GGCTGACGAT TTTAAACCGT ATCATGGGTA TGATGCTGGC GCGGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAATG AATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

```

1  MGLGMEIGKL IVAFVLINP FSALS SLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRL GATGLTILNR IMGMLAAVS
201 VEIIVSGLKM IFPQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALS	SLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI				
a282	MGLGMEIGKLIVAFVLINPFSALS	SLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI				
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282.pep	GATGLTILNRINGMMLAAVSVEIIVSGLKTIFPQLAGX					
a282	GATGLTILNRINGMMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1  atgaactttg ctttatccgt catcacattt accctgcgct ctttctgcgc
51  cgtcccgccg gccggaaccg ccgtctttac ttggaaagac ggcgggcgga
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgtcca aaccaaaccg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaatata
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1  MNFALSVITF TLASFLEVPVP AGTAVFTWKD GGGNSYSDDVP KQLHPDQSQI
51  LNLRLTQTKP AVKPKPAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1  ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCTTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAACCTGCG GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGCG ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGCG CGGATTTCAG AAATGAACCT
351 GAAGCGGTG GGAATTCAG ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1  MNFALSVIML TLASFLEVPVP AGAAVFTWKD GGGNSYSDDVP KQLHPDQSQI
51  LNLRLTQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKEENC RISKMLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLEVPVPAGAAVFTWKDGGGNSYSDDVPKQLHPDQSQILNLRLTQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDDVPKQLHPDQSQILNLRLTQTKP					
	10	20	30	40	50	60

```

              70      80      90      100      110      120
m283.pep      AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV
              |||| | :  :| :||| : |||| |||||:||||| ||||| ||||| |||||
g283          AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKIIAETERQNKEENCRISKMNLKAV
              70      80      90      100      110

              130      140
m283.pep      GNSNAKNKDDLIRKYNNVAVNKYCRX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g283          GNSNAKNKDDLIRKYNNVAVNKYCRX
              120      130      140

```

a283.seq

```
1  ATGAAC TTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGAGCCG CCGTCTTTAC TTGGAAGGAC GGGCGCGGCA
101 ACAGCTATTG GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAACCTCTG GCAGCGCCCA AACCAAACCG GCGGTCAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACGGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACCTGC CGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GGAATTCAA ATGCAAAAAC CAAGGATGAT TTGATTCCGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA
```

a283.pep

1	MNFALSVIML	TLASFLEVP	PP	AGAAVFTWKD	GGGSYS	SDVP	QQLHPDQSQI
51	LNLRTQTKP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEKKRIAE		
101	TERONKEENC	RISKMNKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*		

	10	20	30	40	50	60
m283.pep	MNFALSVMILTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
a283	MNFALSVMILTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDCAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
a283	AVKPAQADAGKRTDCAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	130	140				

g284.seq.

```
1 atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51 aggttggggc ttagcgggtt ttgtaacggc attcgtcttt gccctgcaaaa
101 gagtcgccgg ctttgcggtt gcccttgaag ccttcgccgg ttttttgaag
151 actgtctttt ttaaagcctt cttctttgaa accttcgccg cgcggtttgc
201 cgccgaagcc ttctttgccc ggtttatgat cgccgcgcgc gccgcgggat
251 ttctatcgc cccagccgcc ttgccccttc ggcttgccgc ctgcggattt
301 cggtttgcgg gccggtccca tgccttcgat ggtcagttcg gccagtttgc
351 cgtaatatga tttttcgatt ttgtggacct tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgg tgcgcgcgat
451 cgcgttgacg tagtcttcgc cctgttttcg caggtcgtaq tttatgacct
```

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```

501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaatttttg agcggccttt acgcaaatcc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggccgcaaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttgg-gga cgtgaaaaatc
701 acacattggt cgatgttggc atcgcgcagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatcgctgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcttt ggtcagtttg
851 cgcgcagatt tgccgactgc gccgtcccaa gtggcgagaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51  TVFLKAFFLE TFAARFAAEA FFARFMIAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGKRNRT RAACAAGAPD
151 AVDVVFLRFR QVVYDVGNNG RYVNTACGNV GGNONFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREGG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LLEDFALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1  ATGCCGCTCG AACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT SCCTGCAAAA
101 GAATCGCCGG CTTTGCGTTT GCCTTTGAAG CCTTCGCCGG TTTTTTTGAA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTTTATGAT CGCCGCGCCA ACCGCGCGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGGCG GTCGGTTCCA TGCCTTCGAT GGTCACTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTCCGCCCT GCGCGGCCGG TCGCGCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TCGCGCGAAA CCTTTTTCGT
651 ACAGTTTATC CGCAATGACT TCGGTCATGG CTTTGGTGGA CGTGAAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATT CAGGCTCTTT GGTCACTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCCTTG CTTCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CACTTTTGCC GCTTTGCATC AGGTCCATCA GACGCGCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCGGACG ATGCTGACGG TCGGGAACCA ACGCATATTT
1151 TTGGCATAAG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGCGCTTT GCCCGGTTTT TCGCTGCGTT
1251 TGTCAGTTT TTGCAAAGTC GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51  TVSLKAFFLE TFAARFAAEA FFARFMIAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGKRNRT RAACAAGAPD
151 AVDVVFLRFR QVVVDNVGNNG RYVDTACGNI GGNONFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFEGG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LLEDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQATAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQRV FLDSLRSQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

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	10	20	30	40	50	60
m284.pep	MPSETRNRFQ TALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFQ TALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAPAGFP IAPAAFAFRLAACGFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDV FVHFGKRN RNTAACAGAPDAVDVVFRLFRQVVVDNVGNRGYVDTACGNI					
g284	FFDFVDFDV FVHFGKRN RNTAACAGAPDAVDVVFRLFRQVVVDNVGNRGYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNF AAAFTQI HQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNF AAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGRHFGGRENHTLV DVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDRVFCQFARQFADRAVPSGGEQXS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFFDRVFCQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQTFKINFAALHQVHQ TARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGCTCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGSTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCSTTT  GCCTTTGAAG  CCTTCGCCGG  TTTT TTTGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTCG
201 CGCCGAAGCC  TTCTTTGCTC  GGTATTATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 GCGTTTGGCG  GTCGGTTCCA  TGCCTTCGAT  GGTCA GTTCG  GGCAGTTTTC
351 GGTTAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TGCGCCCGAT
451 GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGGCCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GCGGCGGAAA  CCTTTTTCGT
651 ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701 ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801 GGTCTGTCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCA GTTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCT  TCCGCGCTGG  CTTTCGACGAT  GGTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001 CGGGCGAAAT  CGACTTTGCC  GCTTTCATC  AAGTCCATCA  GACGGCCCGG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101 CGAACGATGC  ACCACGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151 TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCGGCCA  ATTCGCGGGT
1201 CGGCGTCAAC  ACCAACGCGC  GCGGCGCTTT  GCCCGGTTTT  TCGCTGCGTT
1251 TGGTCAGTCG  CTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNREQ  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

```

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```

51 TVSLKAFFLE TFAARFAAEA FFAREMI AAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFAHFD GQFGQFSVNV FFDFVDFDVF VHFGKRNNT RAACAAGAPD
151 AVDVVFRFLFR QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQO LFFDFALVVH AFDDDFRVF GQFARQFADR AVPSGGEQOS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNO HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFAREMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFAHFDGQFGQFSVNV					
a284	TFAARFAAEAFFAREMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFAHFDGQFGQFSVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGKRNNTRAACAAGAPDAVDVFRQLFRQVVVDNVGNGRYVDTACGNI					
a284	FFDFVDFDVFVHFGKRNNTRAACAAGAPDAVDVFRQLFRQVVVDNVGNGRYVDTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAAFQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAAFQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDDDFRVFGQFARQFADRAVPSGGEQOS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDDDFRVFGQFARQFADRAVPSGGEQOS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFAALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNHQFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSSTRAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

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g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

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151  tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcggggt
201  gtaccaaatc cgttcctggt tcggcgtaaa ctttcctcc caaaacctca
251  aaggcacact gctcgacggc ttcgacggcg acaactggte gatagaaacc
301  gagggggagc accttaaaat cagccgcttc cgcttcgctg gaaaccgtc
351  cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401  tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451  ggccctgccg acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501  cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacctctt
551  atctcgaacg cctcaacggc gcataccggt acgaccgtaa agggcacggc
601  ctcgacctga aggcgcgga cagccgtgg agcagttcgt cggggtcagc
651  ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701  aaggcggatt cgaagcgaa accatacaca gtacggcgcg gctgagcggc
751  agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801  ccttcggga aaatccgtca tccaccgtt tgccgaatca ttggataaaa
851  cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901  gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgccatccc
951  gtcgttttca gacggcatcg cgctggaagg ctgcctcgat ttgaaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tcccgcctcg tcaggttttg
1051 ggcggccttg tcatccggca ggacggcacg gtgcataatc gcaataacgc
1101 cgccgccctg ctcgacggg gcggcatcag gctgtcgggc aaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaatcc cgtcggcgcg
1201 gaagacgtgc tgcaaacgc gttcaaaagg aggttggacg gcagcatcgg
1251 catcgcgcc acgaccgcct cgcccaaaat ctcttggcaa ctcggcaccg
1301 gcacggcacg cacggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtgtt cgacacggtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct alctcgagct gtttaagac cgctgtctca
1451 agctggacat ccgttcccgc gcattcgacc ctccgcgat cgatccgcaa
1501 tttccggcag gcaatatcaa cggttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt tttgcccggt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcgcgc ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
1701 cggcggtctt ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttacc ccgtttcggt ttcggaactc cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgatgt ggacggcggc atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggaacagcg gcagacatcc
1901 gttcgctcga ttttaccctc aaaggctcac ccggcacaa gcccccgatg
1951 cgcgccgata tcaaggcgcg ccgcctttcc ctgtcggggc gcggcgcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcgcg cagcaccgca
2051 tccgcacaca cgccgccatg acgctggacg gcaaacggtt caaactcgat
2101 ttggacgctt caggcgcat caacagggaa cttaccgat ggaaggcag
2151 catcggcac ctcgacatcg gcggcgcat caacctcaa ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tgcggcaaat
2251 tggcaggcaa tgggcggcag cctcaacctg caacactttt cttgggacag
2301 gaaaaccggc atatcggcaa aaggcggcgc acgcggcctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgctta cgggcacaa cgcgcgggct acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgctttc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcggaagg attaacgcg atttgggcat
2601 cggcaacgcc ttcggcggca atatggcaaa tacaccgctc ggcgcgagga
2651 ttacagcctc ccttcccgcac ttgggcgcat tgaagccctt tctgcccgcc
2701 gccgcgcaaa acattaccgc cagcctgaat gcctccgcgc aaatcggcg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaat caacggcaat atcaccgtcg ggcaaacgct ctcttcgat
2851 accgcacctt tgggcggcag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccgc tcggacaaac cgtcaaaagg agcctgaatg
2951 ccgccgtaac cctcggcggc agcatcgccg acccgcaact gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgctcgctt cgcatattgc aggcaggaaa tgggtaatcg
3101 acagcctgaa attccggcac gaaggacgg cggaactctc cggcacggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcgcgcgcg tgttcgacaa
3201 ataccgcatc ctgtcccgcc ccaaccgcgc cctgacggtt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgac aggggctggt cggttcgcaa aaatcctcga tgccgtccgt
3351 cggcgacgat gtcgtcgat tggcggaagt caagaaagag gcggcgcat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcaaccgc

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649

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3451 ttctccggct acggcgcgga cgttaccata ggcgcgaaac tgacctgac
3501 cgcgcaaccg ggcggaatat tgcgtggggt gggcacggtc cgcgtcatca
3551 aagggcggtta caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgcgga
3651 acgcccgcctt tccccgcgtg gtgcgggctg ggaatatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcactct caaccgtgcc ggcagcgcca gcagcgcgga
3801 caatgcccgc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacag tgctgacctg
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accgctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcggcgcgcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacgacaa agggaaataa

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This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
1  MTDTTPTD TD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSERM RRLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSGSASVGL LKPPALDPA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSPS DGIALEGSLO LENTKAGFAD RINGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSPRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPC TFNGVPIACS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFTDLDSG TARNLHIGKA ADIRSLDFTL KGSFGTSRPM
651 RADIKGGRLS LSGGAHVVDV AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFCK PPFENHLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD
951 TAPLGGRLNL TVADAEAFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILONG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 SMENSVDPDV IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP OKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGGD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GKKLTTLTAQP GGNVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVAGAVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNAAL LSAAAGALLA QINDRIGLV BDLGFTSKRS
1301 RNAQTGELNP AEQVLTGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLFGSDKK DSAGNGKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

```

m285.seq
1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAATGCCC TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCG3CG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAAAT CAGCCGCTTC CGTTCGCGT GGAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG CTTGACGGC
751 AGCCTGAAGG ATGTGCGCGC GAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCGTTC TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTC ACGGCGATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCG TCAGGTTTTA
1051 GCGCGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGCGCGC
1201 GAAGACGTAC TGCAAAACGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACSACCGCCT CGCCCAAAAT CTCTTGGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACG CTTGCGCAT CGATCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGCGAGT GCGGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGGC CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAAACAGAA
1701 GCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAGC
1751 CCGATTATC CCGTTTCGGT TTCGACTCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 TTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGCGGT
2001 TGTGATACG GCGGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCAT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAA
2251 TGGCAGGCAA TGGGCGGCGC CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GGCGACTGGG ATGTGCGCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGT
2501 TGAACGCAAT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGGCGC TTTGCGGCGG ATTAACGCGC ATTTGGGCAT
2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GGCGGCAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 TCCGCGCAA ACATTACCGG CAGCCTGAAT GCGCGCGCGC AAATCGGCGG
2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGG AGCCTGAATG
2951 CCGCGCTAAC CCTCGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACCTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGTAATCG
3101 ACAGCCTGAA ATTCGGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
3151 GGTATGGAAG ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CTGACGGTT TCCGGCAACA
3251 CCGGCTGCG CTATTCGCGC CAAAAGGCA TATCCGTTAC CGGCATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTGCGAA AAATCCTCGA TGCCGTCCTG
3351 GCGGACGAT GTCTGCTAT TAGGCGAAGT CAAAAAGAG GCGCGGCGC
3401 CGTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCGGCT ACGGCGCGGA CGTTACATA GCGGCAAAAC TGACCTGAC
3501 CGCCCAATCG GCGGAAGCG TACGGGCGGT GGGCAGGTC CCGTCATCA
3551 AAGGCGTTA TAAGCATAAC GGGCAGGATT TGACATTAC CAAAGGCAG
3601 GTCTCCTTTG TCGGCGCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
3651 ACGCGCCTT TCCCGGTCG GTGCGGGCGT GGAATATTG GCGAGCCTCA
3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGC GGCAGCGGCA GCAGCGGCA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAATCA
3851 ACGACCGCAT CCGGCTG3TG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT
3951 CCGCAAAACA CTGACCG3CA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCC3TC AACTGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTG TCGGCGGCG AGCTGACATA

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651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG  
4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep  
1 MTDAPTDT PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV  
51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET  
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPPL  
151 SLPDSIDLPA AVYLDREFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR  
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG  
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF  
301 VPSLPDAGLN FDLTAIPSF3 DGIALEGLSD LENTKAGFAD RNGIPVRQVL  
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA  
401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN  
451 GQRKLVLDTV NIAAGQGSIT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ  
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL  
551 PRAAVDLRLG RNIKTGGG GKKGDRLNLN ITAPDLRFG FGLAGSLNVR  
601 GHLSGDLDDG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI  
651 RADIKGSRLS LSGGAADVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD  
701 LDASGGINRE LTRWKGSIGI LDIGGAFLNK LQNRMTLEAG AERVAASAAN  
751 WQAMGGSNLN QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN  
801 GWDVAVYGRN ARGYLNISRO SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI  
851 LLDGGAREFR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA  
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD  
951 TAPLGGRLNL TVADADEVFN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS  
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV  
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI  
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKEE AAPLPVNMN LTLDLNDGIR  
1151 FAGYGADVTI GSKLTTLTQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT  
1201 VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSLNSPRITL TANEPMSKED  
1251 KLSWLIINRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS  
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI  
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDAPTDTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	:     :     :     :     :     :     :     :     :     :					
g285	MTDTTPTDTPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	:     :     :     :     :     :     :     :     :					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTTPKEERPPSLPDSIDLPAAVYLDREFETGKISMKGAFDK					
	:     :     :     :     :     :     :     :     :					
g285	RRSLHITDISAGDIAIVTKPTTPKEERPPQGLPDSIDLPAAVYLDREFETGKISMKGTFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	:     :     :     :     :     :     :     :     :					
g285	QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

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g285						
	TIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF					
	250	260	270	280	290	300
m285.pep	310	320	330	340	350	360
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT					
g285						
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT					
	310	320	330	340	350	360
m285.pep	370	380	390	400	410	420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG					
g285						
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG					
	370	380	390	400	410	420
m285.pep	430	440	450	460	470	480
	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD					
g285						
	TTASPKISWQLGTGTARTDGS LPIASDPANEQRKLVFDTVNISAGEGSLTAQGYLELFKD					
	430	440	450	460	470	480
m285.pep	490	500	510	520	530	540
	RLKLDIRSRAFDPSRIDPQLPAGNINGS INLAGELAKEKFTGKMRFLPGTFNGVPIAGS					
g285						
	RLKLDIRSRAFDPSRIDPQFPAGNINGS IHLAGELAKEKFTGKMRFLPGTFNGVPIAGS					
	490	500	510	520	530	540
m285.pep	550	560	570	580	590	600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR					
g285						
	ADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR					
	550	560	570	580	590	600
m285.pep	610	620	630	640	650	660
	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGS PDTSRPIRADIKGSRLS					
g285						
	GHLSGDLGGIRTFFETDLSGTARNLHIGKAADIRSLDFTLKGS PGTSRPMRADIKGGRSL					
	610	620	630	640	650	660
m285.pep	670	680	690	700	710	720
	LSGGAAVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKLDLDASGGINRELTRWKSGSIGI					
g285						
	LSGGAAVVDTAGLTLEGTGAQHRIRTHAAMTLDGKPFKLDLDASGGINRELTRWKSGSIGI					
	670	680	690	700	710	720
m285.pep	730	740	750	760	770	780
	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSINLQHFSWDKKTGISAKGGAHGL					
g285						
	LDIGGAFNLKLQNRMTLEAGAEHVAASAANWQAMGGSINLQHFSWDRKTGISAKGGARGL					
	730	740	750	760	770	780
m285.pep	790	800	810	820	830	840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK					
g285						
	HIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYLNISRQSGDAVLPGGQALGLNAFSLK					
	790	800	810	820	830	840
m285.pep	850	860	870	880	890	900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFPLPA					
g285						
	TRFQNDRIGILLDGGARFGRINADLGIGNAFGGNMANTPLGGRITASLPDLGALKPFPLPA					
	850	860	870	880	890	900
m285.pep	910	920	930	940	950	960
	AAQNITGSLNAAQIGGRVGS PSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN					

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|||||:|||||
g285 AAQNITGSLNASAQIGGRVGSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRLNL
      910      920      930      940      950      960

      970      980      990      1000     1010     1020
m285.pep TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
|||||:|||||
g285 TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
      970      980      990      1000     1010     1020

      1030     1040     1050     1060     1070     1080
m285.pep SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
|||||:|||||
g285 SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
      1030     1040     1050     1060     1070     1080

      1090     1100     1110     1120     1130     1140
m285.pep SGNTRLRYSPPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
|||||:|||||
g285 SGNTRLRYSPPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
      1090     1100     1110     1120     1130     1140

      1150     1160     1170     1180     1190     1200
m285.pep LTLDLNDGIRFAGYGADVTIGGKLTLTAQSGGSVRGVGTVRVIKGRYKAYQDLDITKGT
|||||:|||||
g285 LTLDLNDGIRFAGYGADVTIGGKLTLTAQSGGSVRGVGTVRVIKGRYKAYQDLDITKGT
      1150     1160     1170     1180     1190     1200

      1210     1220     1230     1240     1250     1260
m285.pep VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
|||||:|||||
g285 VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
      1210     1220     1230     1240     1250     1260

      1270     1280     1290     1300     1310     1320
m285.pep GSGSSGDNAALSAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
|||||:|||||
g285 GSGSSGDNAALSAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
      1270     1280     1290     1300     1310     1320

      1330     1340     1350     1360     1370     1380
m285.pep LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
|||||:|||||
g285 LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
      1330     1340     1350     1360     1370     1380

      1390
m285.pep DSAGNGKGKX
|||||
g285 DSAGNGKGKX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

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a285.seq
1 ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAATGCGG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGCTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGCACGGAA GCGGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAACCGTC
351 CGAACTGATG CGCCGACGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTA AAGAAGAACC CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAAGC GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCGA CAGCCGCTGG AGCAGTTCGT CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA  
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC  
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG  
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA  
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGECTTC  
901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC  
951 GTCGTTTTC A GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGGA AAAACA  
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCG TCAGGTTTTA  
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAG GTGCATATCG GCAATACGT  
1101 CGTCGGCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA  
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG  
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTGAGACG GCAGCATCGG  
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCGGCATCG  
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCGCGCAAAAC  
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG  
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA  
1451 AGCTGGACAT CCGTTCCCGC GCATTCGACC CTTGCGCCAT CGATCCGCAA  
1501 CTTCGGCAG GCAATATCAA CGGCTCAATA AACCTTCCCG GCGAACTGGC  
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG  
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT  
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTA AACAGA  
1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC  
1751 CCGATTATC CCGTTTCGGT TTCGGA CTG CCGGGTCTTT AAATGTACGC  
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA  
1851 CTTTCCGGC GCGGCGCGCA ACCTGCACAT CCGCAAGCGC GCAGACATCC  
1901 GTTCGCTCGA TTTCACGCTC AAAGTTTCG CCGACACAAG CCGCCCGATA  
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTGCGGCG GAGCGGAGGT  
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACC GCA  
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT  
2101 TTGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG  
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC  
2201 GTATGACGCT CGAAGCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAAAT  
2251 TGGCAGGCAA TGGGCGGCG CCTCAACCTG CAACACTTTT CTTGGGATAA  
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG  
2351 AGTTGCAAAA TTTCTTCAAA CCGCCCTTCG AACACAATCT GGTTTTAAAC  
2401 GGCGACTGGG ATGTGCGCTA CGGGCGAAAC GCGCGCGGCT ACCTCAATAT  
2451 CAGCCGCAA AGCGCGGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT  
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC  
2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCGC ATTTGGACAT  
2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA  
2651 TTACCGCCTC CTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC  
2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG  
2751 ACGGTCGCG TCTCCGTCCG TCAATGCCGC CGTCAACGCG AGCAGCAACT  
2801 ACGGGAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT  
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT  
2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG  
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCG ATCCGCACTT GGGCGGCGAG  
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT  
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG  
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACTCTC CGGTACGGTC  
3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCGACAA  
3201 ATACCGCATC CTGTCCCGCC CCAACCGCGC CTGACGGTT TCCGGCAACA  
3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCGTTTAC CGGGATGATT  
3301 AAAACGGATC AGGGGCTGTT CGGTCGCAA AAATCCTCGA TGCCGTCCGT  
3351 CGGCGACGAT GTCGTGCTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC  
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC  
3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAC TGACCCTGAC  
3501 CGCCCAATCG GCGGAAGCG TGCGGGGCGT GGGCACGCTC CGCGTCATCA  
3551 AAGGCGGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG  
3601 GTCTCTTTG TCGGCGCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA  
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAATATTG GGCAGCTCA  
3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGA AAAAGAC  
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA  
3801 CAATGCGCC CTGTCCGAG CCGCGGCGC GCTGCTTGCC GGGCAAAATCA  
3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC  
3901 CGCAACGCGC AAACGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

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3951 CCGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTG CCGTATCGG CAGCCGTTCG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
1 MTDAPTDTPT PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWLAGE AGLRFGLYQI PSWFGVNIS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRLHTEIS AGDIAIVTKP TPKPEERPPL
151 SLPDSIDLPA AVYLDREFETG KISMGAFFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLD LENTKAGFAD RINGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSIT AQGYLELEFD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYERHIL
551 PRAAVDLRLG RNIKTGDDG GKKGDRLNLN ITAPDLRFRG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDV ADMLLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGINRE LTRWKGSI LIDIGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
801 GDWDVAYGRN ARGYLNSRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLLP
901 AAQNTIGSLN AAAQIGGRVG SPSVNAAVNG SSNYKINGN ITVQSRSD
951 TAPLGGRLNL TVADAIEVFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKEE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGLTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNSKKG*

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m285/a285 99.4% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
a285	MTDTAPTDTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	10	20	30	40	50	60
m285.pep	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
a285	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
a285	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
m285.pep	RRLHTEISAGDIAIVTKPTPKPEERPPLSLPDSIDLPAAYVLDREFETGKISMGAFFDK					
a285	RRLHTEISAGDIAIVTKPTPKPEERPPLSLPDSIDLPAAYVLDREFETGKISMGAFFDK					
	130	140	150	160	170	180
m285.pep	RRLHTEISAGDIAIVTKPTPKPEERPPLSLPDSIDLPAAYVLDREFETGKISMGAFFDK					
a285	RRLHTEISAGDIAIVTKPTPKPEERPPLSLPDSIDLPAAYVLDREFETGKISMGAFFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					



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a285	TIHSTARLSGSLKDVRAELAI	DGGNIRLSGKSVIH	PPAESLDKTL	EEVLVKGF	NINPSAF
	250	260	270	280	290 300
	310	320	330	340	350 360
m285.pep	VPSLPDAGLNFDLTAIP	SFSDGIALEGS	LDLENTKAG	FADRNGIP	VQRQVLGGFVIRQDGT
a285	VPSLPDAGLNFDLTAIP	SFSDGIALEGS	LDLENTKAG	FADRNGIP	VQRQVLGSFVIRQDGT
	310	320	330	340	350 360
	370	380	390	400	410 420
m285.pep	VHIGNTSAALLGRG	GIRLSGKIDTEK	DILDNLNIGINS	VGAEVDLQ	TAFKGRLDGSIGIGG
a285	VHIGNTSVALLGRG	GIRLSGKIDTEK	DILDNLNIGINS	VGAEVDLQ	TAFKGRLDGSIGIGG
	370	380	390	400	410 420
	430	440	450	460	470 480
m285.pep	TTASPKISWQLGIG	TARTDGLAIASD	PANGQRKLVLD	TVNIAAGQGS	SLTAQGYLELFKD
a285	TTASPKISWQLGIG	TARTDGLAIASD	PANGQRKLVLD	TVNIAAGQGS	SLTAQGYLELFKD
	430	440	450	460	470 480
	490	500	510	520	530 540
m285.pep	RLKLDIRSRAFDPS	SRIDPQLPAGN	INGSINLAGEL	AKEKETGKMR	FLPGTFNGVPIAGS
a285	RLKLDIRSRAFDPS	SRIDPQLPAGN	INGSINLAGEL	AKEKETGKMR	FLPGTFNGVPIAGS
	490	500	510	520	530 540
	550	560	570	580	590 600
m285.pep	ADIVYESRHLPRAA	VDLRLGRNIIK	TGGGFGKKGD	RNLNITAPDL	SRFGGLAGSLNVR
a285	ADIVYESRHLPRAA	VDLRLGRNIIK	TGGGFGKKGD	RNLNITAPDL	SRFGGLAGSLNVR
	550	560	570	580	590 600
	610	620	630	640	650 660
m285.pep	GHLSGDLGGIRT	FETDLGAARNL	HIGKAADIRSL	DFTLKGSPDT	SRPIRADIKGSRLS
a285	GHLSGDLGGIRT	FETDLGAARNL	HIGKAADIRSL	DFTLKGSPDT	SRPIRADIKGSRLS
	610	620	630	640	650 660
	670	680	690	700	710 720
m285.pep	LSGGAAVVDTADL	MDGTGVQHRIR	THAAMTLDGK	PFKFDLDASG	GINRELTRWKSIGI
a285	LSGGAEVVDTADL	MDGTGVQHRIR	THAAMTLDGK	PFKFDLDASG	GINRELTRWKSIGI
	670	680	690	700	710 720
	730	740	750	760	770 780
m285.pep	LDIGGAFLNKLQNR	MTEAGAERVAAS	AANWQAMGGS	LNQHFSWDKKT	GISAKGGAHGL
a285	LDIGGAFLNKLQNR	MTEAGAERVAAS	AANWQAMGGS	LNQHFSWDKKT	GISAKGGAHGL
	730	740	750	760	770 780
	790	800	810	820	830 840
m285.pep	HIAELHNFFKPPF	EHNLVLNGDWD	VAYGRNARGYL	NISRQSGDAVL	PGGQALGLNAFSLK
a285	HIAELHNFFKPPF	EHNLVLNGDWD	VAYGRNARGYL	NISRQSGDAVL	PGGQALGLNAFSLK
	790	800	810	820	830 840
	850	860	870	880	890 900
m285.pep	TRFQNDRIGILLD	GGARFGRINADL	GIANAFGGNMA	NAPLGGRITAS	LPDLGALKPFLPA
a285	TRFQNDRIGILLD	GGARFGRINADL	GIANAFGGNMA	NAPLGGRITAS	LPDLGALKPFLPA
	850	860	870	880	890 900
	910	920	930	940	950 960
m285.pep	AAQNITGSLNAAAQ	IGRGVSGPSVNA	AVNGSSNYGK	INGNITVGQSR	SFDTAPLGGRNLN

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a285	AAQNITGSLNAAAQIGGRVGSPPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRRLNL
	910 920 930 940 950 960
m285.pep	TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSADPHLGGSSINGDKLYYRNQTQGIILDNG
a285	TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSADPHLGGSSINGDKLYYRNQTQGIILDNG
	970 980 990 1000 1010 1020
m285.pep	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
a285	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
	1030 1040 1050 1060 1070 1080
m285.pep	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPSVGDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPSVGDVVVLGEVKKEAAAPLPVNMN
	1090 1100 1110 1120 1130 1140
m285.pep	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
a285	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
	1150 1160 1170 1180 1190 1200
m285.pep	VSVFVGPLNDPNLNIRAERRLSVPVAGVEILGSLNSPRITLTANEPMSKDKLSWLIILNRA
a285	VSVFVGPLNDPNLNIRAERRLSVPVAGVEILGSLNSPRITLTANEPMSKDKLSWLIILNRA
	1210 1220 1230 1240 1250 1260
m285.pep	GSAGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNAQTGELNPAEQVLTVGKQ
a285	GSAGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNAQTGELNPAEQVLTVGKQ
	1270 1280 1290 1300 1310 1320
m285.pep	LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
a285	LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
	1330 1340 1350 1360 1370 1380
m285.pep	DSAGNGKKGX
a285	DSAGNSKKGX
	1390

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAACATTT CCTCCCAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCGG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CGGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGCCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCTTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTGGGCGG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCGTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTCT GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCAAGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTGACA CCGTCAACAT CTCCGCGGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATTT CGACCTTCG CGCATCGATC CGCAATTTC
1401 GGCAGGCGat atCAACGGTT CGATTCTCT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTTGTTAC GAGTCCCGCC ACCTTCCCGG
1551 CCGCGCGGTC GATTGCGGT TGGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCITCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGG GATTGAGCG GCGGCATCCG AACCTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTCT
1801 CTCGATTTTA CCTCAAAGG CTCACCCGGC ACAAGCGGCC CGATGCGCGC
1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GCGCGGCGCG GCGGTGTCTG
1901 ATACCGCGCG CCTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGACGGCAAA CCGTTCAAAC TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CGATGGAAG GGCAGCATCG
2051 GCATCTCTGA CATCGCGGCG GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACCCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTTGG GACAGGAAA
2201 CCGCATATAT GGGAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGGAACAC AATCTGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAC
2401 GCATTTTCTT TGAACGCGG CTTTCAAAC GACCGCATCG GAATCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACCGCTTCGG CGGCAATATG GCAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTTGAG CUCTTTCTGC CGGCCGCGG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCCTC CGCGCAAATC GCGGACGGG
2651 TAGGCTCTCG GTCCGTCAAT GCCGCCGTCA ACGGTAGCAG CAACTACGGG
2701 AAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGG
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTT CGGCGAGCAT CGCCGACCCG CACTTGGGCG CAGATATCAA
2901 CGCGGACAA GCTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACCGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTACGAT
3051 GGAACACAGC GTGCCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCTGTCT CCGCCCAAC CGCGCGCTGA CGGTTTCCGG CAACACCCCG
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAATA
3201 TGATCAGGGG CTGTTTCGTT CGCAAAAATC CTCGATGCCG TCCGTCCGGG
3251 ACCATGTCGT CGTATTGGG GAAGTCAAGA AAGAGGCGG GGCATCGCTC
3301 CCCGTCRATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CCGCTACGGC GCGGACGTTA CCATAGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGCGG AAATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGG
3451 CGTTACAAAG CATACGGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTCCGG CCGCTCAACG ACCCAAACCT GAACATCCG CCGGAACGCC
3551 GCCTTTCCCC CGTCGTGCG GCGGTGAAA TATTGGGAG CCTCAACAGC
3601 CCGCGCATTA CGTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACC GTGCCGCGAG CGGCAGCAGC GGCACAATG
3701 CCGCCCTGTC CGCAGCCGCA GCGCGCTGCG TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCGCGCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCCGCG CCATACAGG
3951 GGTGGCCCGT ATCGGCAGCC GTTCGTGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCCTCTTC GGTTCGGACA AAAAGACTC CGCAGGAAAC
4051 GGCAAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:  
g285-1.pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLIDGFDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPKPE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAAYRYD RKGHRDLKA ADTPWSSSSG SASVGLKPPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGDN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLLENTK
301 AGFADRNIGP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDNLNIGI NSVGAEDVLQ TAFKGRDLGS IGIGGTTASP KISWQLGTGT
401 ARTDGLAIA SDPANEQRKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPG RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGTARNL IIGKAADIRS
601 LDFTLKGSFG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASANWQAMG GSLNLQHFWS DRKTGISAKG GARGLHIAEL
751 NHFFKPPFEH NLVLNGDWDV AYGHNARGYL NISROSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNASHAI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVSO SRSFDTAPLG GRNLNTVADA EAFRNLFPVG QTVKGSINAA
951 VTLCGSIADP HLGGSINGDK LYYRNQTOGI ILDNGLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDVVVLG EVKKEAASL
1101 PVNNMLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR VGTVRVIRK
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDLGEF TSKRSRQAOT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AECQSVKLIYR LTRAIQAVAR IGSRSSGSEL TYTIRFDRLE GSKKDSAGN
1351 GKGA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTC TTGTTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAC CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGCT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG CGGCGCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA CGGCGAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAAAT CGTCATCCAC CCGTTTGGCG AATCATTGGA TAAACATTG
751 GAAGAAATAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGAC TGAATTTGCA CCTGACCGCC ATCCCGTCGT
851 TTTACAGACG CATCGCGCTG GAAGGTTTCG TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCGCTCAGG TTTTAGCGCG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAA TATAGGCATC AACTCCGTCG CGCGGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 CGCGCACGCG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 CGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCAT TCGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTACAG AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CGGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCCGCGCT GATTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGCGAC CGGCTTAACC TCAATATCAC CGCACCGCAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGT GATTGGACG CGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGCGCGCGC CGGCAACCTG CACATCGGCA AGGCGGCGAG CATCCGTTCC
1801 CTGATTTTCA CGCTCAAAGG TTCGCCGAC ACAAGCGGCC CGATACCGGC
1851 CGACATCAAA GGCAGCGGCC TTTGCTGTC GGGCGGAGCG CGCGTTGTCG
1901 ATACCGCGCA CCGTATGCTG GACGGCACGG GCGTGACGCA CCGCATCCGC
1951 ACACACCGCG CATGACGCT SGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGGCG SCATTCAACC TCAAGTGCAG AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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660

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTCCATAT CCGCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACCGCGA
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2351 GGCAAAAGCG CGATGCCGTA TTGCCCGCGG GGCAGGCTTT GGGTTTGAAC
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2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCTTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAAAT GCGCGACGGG
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2701 AAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
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2901 CCGCGACAAA CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGTA CGGTCGGTAT
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3151 CTGCGCTATT CCGCGCAAAA AGGCATATCC GTTACCGGGA TGATTAACAA
3201 GGATCAGGGG CTGTTCGTT CGCAAAATC CTGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGCG GGCACCGCTC
3301 CCGGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGCGCG AAGCGTACGG GCGGTGGGCA CGGTCCGCT CATCAAAGG
3451 CGTTATAAGG CATACGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CCGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGG GCGGTGAAA TATTGGCAG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGCTC ATCCTCAACC GCGCCGCGAG CCGCAGCAGC GGCAGCAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGG TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGCGAAACC GGCAGAACTCA ACCCCGCGCA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CCGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 CCGGAACAGT CCGTCAAACT GATTACCGG CTGACCGCGC CCATACAGGC
3951 GGTGCGCGT ATCGGCGGCC GTTCGTGCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAGACTC CCGCGGAAAC
4051 GGCAAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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1  LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFCDGN WSIETEGADL KISRFRPAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEKGTIHST ARLSGSLKDV RAE LAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFN I NPAAFPVSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP RVQLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDNLIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 UHSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHL SG DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKSGPD TSRPIRADIK GSRLSLSGGA AVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGS LNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGO SRSDTAPLG GRNLTVADA EVFRNPLPVG QTVKGS LNAA
951 VTLLGGS IADP HLGG SINGDK LYRNRQTQGI ILDNGLSLRSH IAGRKWIDS
1001 LKFRHECTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTQDQ LFGSQXSMP SVGDVVVLG EVKKEAAPL
1101 PVNNMLTIDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSVPGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRFS GSKDKDSAGN
1351 GKCK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

661

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m285-1	LKLSAALLSVLILAVCF LGW IAGTEAGLRFG LYQIPSWFGVNISSQNLKGTLLDGF DGDN
	10 20 30 40 50 60
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	WSIETEGADLKISRFRFAWKPS ELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS
m285-1	WSIETEGADLKISRFRFAWKPS ELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS
	70 80 90 100 110 120
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m285-1	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAAADTPWSSSSG
	130 140 150 160 170 180
g285-1.pep	190 200 210 220 230 240
	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH
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	190 200 210 220 230 240
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	PFAESLDKLTLEEVLVKGFENINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK
m285-1	PFAESLDKLTLEEVLVKGFENINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK
	250 260 270 280 290 300
g285-1.pep	310 320 330 340 350 360
	AGFADRNGIPVRQVLGGFVIRQDGT VHIGNTS AALLGRGGIRLSGKIDTEKDILDNLIGI
m285-1	AGFADRNGIEVRQVLGGFVIRQDGT VHIGNTS AALLGRGGIRLSGKIDTEKDILDNLIGI
	310 320 330 340 350 360
g285-1.pep	370 380 390 400 410 420
	NSVGAEDVLQTAFAKGRLDGSIGIGGTTASPKISWQLGTGTARTDGS LAIASDPANEQRKL
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	370 380 390 400 410 420
g285-1.pep	430 440 450 460 470 480
	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRAFDPSTRIDPQFPAGDINGSIHLAGE
m285-1	VLDTVNIAAGQGS LTAQGYLELFKDRLLKLDIRSRAFDPSTRIDPQLPAGNINGSINLAGE
	430 440 450 460 470 480
g285-1.pep	490 500 510 520 530 540
	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD
	490 500 510 520 530 540
g285-1.pep	550 560 570 580 590 600
	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRT FETDLSGTARNLHIGKAADIRS
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRT FETDLSGAARNLHIGKAADIRS
	550 560 570 580 590 600
g285-1.pep	610 620 630 640 650 660
	LDFTLKGSPGTSRPMRADIKGGRLSLSGGA AVVDTAGLTLEGTGAQHRI RTHAAMTLDGK
m285-1	LDFTLKGSPGTSRPIRADIKGSRLSLSGGA AVVDTADLMDGTGVQHRI RTHAAMTLDGK
	610 620 630 640 650 660
g285-1.pep	670 680 690 700 710 720
	PFKLDDASGGINRELTRWKSGSIGILDIGGAFNLKLNRM TLEAGAEHVAASAANWQAMG
m285-1	PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLNRM TLEAGAEHVAASAANWQAMG
	670 680 690 700 710 720
g285-1.pep	730 740 750 760 770 780
	GSLNLQHFSWDRKTGISAKGGARGLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL
m285-1	GSLNLQHFSWDRKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL

662

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAQNTGSLNAAQIGGRVGSFVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAQNTGSLNAAQIGGRVGSFVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSDTAPLGGRLNLTVADEAFRNFLPVGQTVKGSNAAVTLGSSIADP					
m285-1	KINGNITVGQSRSDTAPLGGRLNLTVADEAFRNFLPVGQTVKGSNAAVTLGSSIADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYQDLDITKGTVSFVGPLNDPNLNIRAERRLSPVAGAVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYQDLDITKGTVSFVGPLNDPNLNIRAERRLSPVAGAVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKKGK					
m285-1	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

```

1 CTGAAGCTGT CGGCGGCACT SCTGTCTGTT CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG CTCGCCGGCA CGGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATCGCGCG CAGCCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCACAGAG ATAGACCTGC CTGCCGCGCT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAACAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGCGGCAAT ATCCGCTCT
701 CGGGAAAAAT CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGTCTCG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTATAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 CGGGAACATG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGGA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATRAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAATTTTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCCGTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTTCGGCA AAAAGCGGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGC GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCA CGCTCAAAGG TTCGCCCGAC ACAAGCCGCC CGATACGGCG
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGCGGAGCGG GAGGTTGTCC
1901 ATACCGCCGA CCTGATGCTC GACGGCACGC CCGTGCACCA CCCATCCGCG
1951 ACACACGGCG CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGCGG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCGTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTGCG CCGCCGCGCG
2601 GCAAAACATT ACCGCGAGCC TGAATGCCGC CGCGCAAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAAGC GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG CGGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CGGGGACAAA CTCTATTACC GCAACCAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAATTTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCGGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCGCTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 GCTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CCGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAT TATTGGGAG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAT AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GCGCCGGCAG TGCGAGCAGC GGCACAAATG
3701 CCGCCCTGTG CGCAGCCGCC GCGCGCTGCT TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCCGCGCA ACAGGTGCTG ACCGTGCGCA
3851 AACAACGTAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTTCGCCGT ATCGGCAGCC GTTCGTGGG CGGCAGCTG ACATACACCA
4001 TACGTTTCGA CCGTCTCTCC GGTTCGGACA AAAAAGACTC CGCGGAAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:



664

## a285-1.pep

1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG  
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA  
101 IVTKPTPKPE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL  
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG  
201 GLEGKTIHST ARLSGSLKDV RAEALIDGDN IRLSGKSVIH PFAESLDKTL  
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK  
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLRGG IRLSGKIDTE  
351 KDILDNLIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT  
401 ARTDGSALAI SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL  
451 DIRSRAFDPG RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV  
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIK TDGGFGKKGD RLNLNITAPD  
551 LSRFGEGLAG SLNVRGHLG DLDGGIRTFE TDLGSAARNL HIGKAADIRS  
601 LDFTLKGSPI TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHFIR  
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRN  
701 TLEAGAERVA ASANWQAMG GSLNLQHFESW DKKTGISAKG GAHGLHIAEL  
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN  
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNN ANAPLGGRIT  
851 ASLPDLGLTK PFLPAAQNI TGSNLAAQI GGRVGSPPSVN AAVNGSSNYG  
901 KINGNITVGO SRSFDTAPLG GRNLNIVADA EVFRNPLPVG QTVKGSNLAA  
951 VTLGSSIADP HLGGSINGDK LYRNQTQGI LLDNGSLRSH IAGRKWVIDS  
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR  
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAAPL  
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG  
1151 RYKAYQDID ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS  
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAQIND  
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGQLTGKL YIGYEYSISS  
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN  
1351 SKGK\*

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPKPEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPKPEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELADGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELADGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
m285-1	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGCCIRLSCKIDTEKDILDNLIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGCCIRLSCKIDTEKDILDNLIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGSALAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGSALAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	LTACGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGSIN	LAGE	
m285-1	VLDTVNIAAGQGS	LTACGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGSIN	LAGE	
	430	440	450	460	470 480
a285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHL	PRAAVDLRLGRNI	IKTDGGFGKKGD		
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHL	PRAAVDLRLGRNI	IKTDGGFGKKGD		
	490	500	510	520	530 540
a285-1.pep	RLNLNITAPDLSRFGFGLAGSLNVRGHL	SGDLGGI	RTFETDLSGAARNLHIGKAADIRS		
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHL	SGDLGGI	RTFETDLSGAARNLHIGKAADIRS		
	550	560	570	580	590 600
a285-1.pep	LDFTLKGS	PDTSRPIRADIKGSRLSLSGGAEVVD	TADMLDGTGVQHRIRTHAAMTLDGK		
m285-1	LDFTLKGS	PDTSRPIRADIKGSRLSLSGGAEVVD	TADMLDGTGVQHRIRTHAAMTLDGK		
	610	620	630	640	650 660
a285-1.pep	PFKFDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
m285-1	PFKFDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
	670	680	690	700	710 720
a285-1.pep	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
	730	740	750	760	770 780
a285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
	790	800	810	820	830 840
a285-1.pep	ANAPLGGGRI	TASLPDLGTLKPFLPAAQ	ONITGSLNAAQIGGRVGS	PSVNAAVNGSSNYG	
m285-1	ANAPLGGGRI	TASLPDLGTLKPFLPAAQ	ONITGSLNAAQIGGRVGS	PSVNAAVNGSSNYG	
	850	860	870	880	890 900
a285-1.pep	KINGNITVGQSR	SFDAPLGGRLNLTVA	DAEVFRNFLPVGQTVKGS	LNAAVTLGGS	IADP
m285-1	KINGNITVGQSR	SFDAPLGGRLNLTVA	DAEVFRNFLPVGQTVKGS	LNAAVTLGGS	IADP
	910	920	930	940	950 960
a285-1.pep	HLGGSINGDKLYYRNQTQGI	ILDNGSLRSHIAGRKWVIDSLKFRHEGTAELS	SGTVGMENS		
m285-1	HLGGSINGDKLYYRNQTQGI	ILDNGSLRSHIAGRKWVIDSLKFRHEGTAELS	SGTVGMENS		
	970	980	990	1000	1010 1020
a285-1.pep	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRL	RYSPQKGISVTGM	IKTDQGLFGSQKSSMP		
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRL	RYSPQKGISVTGM	IKTDQGLFGSQKSSMP		
	1030	1040	1050	1060	1070 1080
a285-1.pep	SVGDDVVVLGEVKKAAAPLPVNMNLTLDLNDGIRFAGY	GADV	TIGGKLT	LTASGGSVR	
m285-1	SVGDDVVVLGEVKKAAAPLPVNMNLTLDLNDGIRFAGY	GADV	TIGGKLT	LTASGGSVR	
	1090	1100	1110	1120	1130 1140
a285-1.pep	GVGTVRVIKGRYKAYQDLDITKGT	VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS			
m285-1	GVGTVRVIKGRYKAYQDLDITKGT	VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS			
	1150	1160	1170	1180	1190 1200

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSKDKLSWLILNRAGSGSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKKGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

```

g286.seq
1  atgcagaaca ccggtaccat gatgatcaaa cgcaccgccc tgctcctgcc
51  ggctttatatt ttctttccgc acgcatacgc gcctgcgccc gacctttccg
101 aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaaacc caaattcccc gtccgcacgc acacgcagga
201 cagtgaaatc aaagatatgg tcgaagaaca cctgcgcgtc atcacgcagc
251 agcaggaaga ggttttgat aaggaacaga cgggattcct tgccgaagaa
301 qcaccggaca acgttaaaac aatgctccgc agcaaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacgggtg cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
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501 ctggcagcag ccggttaggca gcgatttcga tcaggacagt tyggaaaaca
551 gcaaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601 aagctcgcca acacccgggc ggccgtcaac cccgataccg ccaccgcccga
651 ttgaaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcacccg cacacagcgt taccccaagc aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgtgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcattattc cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaag tcagcgtaac
901 cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggaacaaac gcctacgact attacaacct cttcaacaaa
1001 ggctataatc gctcgtcgt ctgggatatg gacaaatacg aaaccacgct
1051 tgccgcggcg atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaaacgcgc
1151 ttctccggcg gcattctgga tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaaatccc cgctcggatg
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1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tattttctca cgcccgaaaa caaaaaactc
1451 ggcacgttca tcatacgcg acaagcgggt tacaccgttg cacgcgacaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcggc cgctcttccg
1551 tgccgcgtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

```

g286.pep
1  MONTGTMMIK PTALLLPALF EFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVL D KEQTGFLAEE
101  APDNVKTMLR SKGYFSSKVS LTKEDGAYTV HITPGPRTKI ANVGVAI LGD
151  ILSDG NLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201  KLG NTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251  RFQPGTPYDL DLLLDFQ QAL EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301  RGQTPQTRNR HPFRFGIRFG RQNRLLRLQP LQRLYRLGR LGYQIRNHA
351  CRRHQPA AQL SGQLLDKQRF LQPF DHEKPR KTRLLRRILV CARPRGHRCQ
401  AGGGISRRRP ENPRLGCRFG QQPRHDADRL LETPAAQORA APRKRPLPRR

```

451 QNRDDEFGHIP VLHRANPHLC PRRFLHARK QKTRHVHHTR TSGLHRCTRQ  
501 CRCLGADV P QRRRVFRARL RT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq  
1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC  
51 GGCTTTTATT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG  
101 AAAACAAGGC GCGGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACACC  
151 GAATCAGTCA AATTAAACC CAAATTCCTCC GTCTCATCG ACACGCAGGA  
201 CAGTGAATC AAAGATATGG TCGAAGAACA CTGCGCGCTC ATCAGCGAGC  
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA  
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACGACG  
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC  
401 CCGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGCGGAC  
451 ATCCTTTTCA AGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA  
501 CTGGCAGCAG CCGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA  
551 GCAAACTTTC CGTCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC  
601 AAGTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA  
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GCGACTTTG  
701 AAATCACCAG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGGC  
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA  
801 ACAGGCGCTC GAACAAACG GGCATTATTC CCGCGCGTCC GTACAAGCCG  
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC  
901 GAGGTCAAAC GCCACAACT CGAAACGGC ATCCGCGCTC ATTCGGAATA  
951 CCGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG  
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT  
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CCGGGCAACT ACTGGACAAG  
1101 CAACGTTTCC TACAACCGTT CGACCACCA AAACCTCGAA AAACCGCCT  
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGCAT CGATGCCAGG  
1201 CTGGGGCGG AATTCTCTGC AGAAGGCCGG AAAATCCCG GCTCGGCTGT  
1251 CGATTGGGC AACAGCCAGC CCACGATGCT GACCGCTCT TGGAAACGCC  
1301 AGCTGCTCAA CAACGTGCTG CATCCGAAA ACGGCCATTA CCTCGACGGC  
1351 AAAATCGGTA CGACTTTGGG CACATTCTTG TCTCCACCG CGCTGATCCG  
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCGAAAAC AAAAACTCG  
1451 GCACGTTTCA CATACGCGGA CAAGCGGTT ACACCGTTGC CCGCGACAAT  
1501 GCCGACGTTT CTTACGGGCT GATGTTCCGC AGCGCGGCG CGTCTTCCGT  
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCG AACGGATCGG  
1601 TCCTGCCCCA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG  
1651 TTTACGCGCA CCTTTCCGG CCGGTTGTTC CACGATATGG GCGATGCCG  
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC  
1751 GCTGGTTCAG CCCGCTTGC CCGTTTCCT TCGACATCG CTACGGGCAC  
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep  
1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT  
51 ESVKLKPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAE  
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAIGD  
151 ILSGNIAYE YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPIA  
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA  
251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDRLQG DRVPVKSVT  
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYSVSV WMDKYETTL  
351 AAGISQPRNY RGNWYTSNVS YNRSTTONLE KRAFSGGVWY VRDRAGIDAR  
401 LGAEFLAAGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG  
451 KIGTTLGTFL SSTALIRTSR RAGYFFTPEN KKLGTFFIRG QAGYTVARDN  
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP  
551 FTRLSGAVF HDMGDAAANE KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH  
601 SDKKIRWHIS LGTRF\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLPALFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
g286	MQNTGTMMIKPTALLPALFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
g286	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTOAAVNPDATADLNWVVDVSGRPIAFGDFEITGTQR					
g286	WENSKTSVLGAVTRKGYPLAKLGNTRAAVNPDATADLNWVVDVSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDLDDLDFQQALEQNGHYSYGASVQADFRL-QGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDLDDLDFQQALEQNGHYSYGASVQADFRLPRGFRPRQSQRN					
	250	260	270	280	290	300
	300	310	320	330	340	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAVDYNNLFNKGYIGSVVWMDKYETTLAAGISQPRN					
g286	RGQTPQTRNRHPPRFGRFGRQNRRLRLQLQRLYRLGRLGYQIRNHACRRHQPAAL					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

```

a286.seq
1  ATGCACGACA CCCGTACCAT GATGATTAAA CCGACCGCCC TGCTCCTGCC
51  GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GGCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCAGACAC
151 GAATCAGTTA AATTAAAACC CAAATTCCTC GTCCGCATCG ACACGCAGGA
201 TAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCGAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCACCGGACA ACGTTAAAAC AATGCTCCGC AGCAAAGGCT ATTTAGCAGC
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCT GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAATA
501 CTGGCAGCAG CCGGTAGGCA GTGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAAACTTC CGTCCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ACACCCGGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCCC CATCGCCTTC GCGGACTTTG
701 AAATTACCGG CACGCAGCGT TACCCGAAC AAATCGTCTC CGGCTTGGCG
751 CGCTTCCAAC CGGGCAGGCC CTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCCTCT GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAAGCT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGCGCG CATCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AGTTTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGATAT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC

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669

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1351 AAAATCGGTA CGACTTTGGG CGCATTCTCG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGCGCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTTCGGG CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTCTCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

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This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
1  MHDTRTMMIK PTALLLPALF FFFHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAYTV HITPGPRTKI ANVGVAIGD
151 ILSDGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDTATADLN VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA L EQNGHYS GAS VQADFDR LQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYYNL FNKG YIGSVV WMDKYETTL
351 AAGISQPRNY RGN YWTENV S YNRSTQNL E KRAFSGGIWY VRDRAGIDAR
401 LGAEFLA EGR KIPGSDIDL G NSHATMLTAS WKRLNNNLV HPENGHYLDG
451 KIGTTLGAFL SSTALIRTS A RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLGSAVF HDMGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

m286/a286 98.7% identity in 615 aa overlap

10 20 30 40 50 60
m286.pep MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP
a286 MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP
10 20 30 40 50 60

70 80 90 100 110 120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
a286 VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
70 80 90 100 110 120

130 140 150 160 170 180
m286.pep LTEKDGAYTVHITPGPRTKIANVGVAIGDILSDGNLA EY YRNALENWQQPVGSDFDQDS
a286 LTEKDGAYTVHITPGPRTKIANVGVAIGDILSDGNLA EY YRNALENWQQPVGSDFDQDS
130 140 150 160 170 180

190 200 210 220 230 240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLN VVDSGRPIAFGDFEITGTQR
a286 WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLN VVDSGRPIAFGDFEITGTQR
190 200 210 220 230 240

250 260 270 280 290 300
m286.pep YPEQIVSGLARFQPGMPYDLDLLDFQQA LEQNGHYS GASVQADFDR LQGDRVPVKVSVT
a286 YPEQIVSGLARFQPGTPYDLDLLDFQQA LEQNGHYS GASVQADFDR LQGDRVPVKVSVT
250 260 270 280 290 300

310 320 330 340 350 360
m286.pep EVKRHKLETGIRLDSEYGLGGKIAIDYYNLFNKG YIGSVVWMDKYETTLAAGISQPRNY
a286 EVKRHKLETGIRLDSEYGLGGKIAIDYYNLFNKG YIGSVVWMDKYETTLAAGISQPRNY
310 320 330 340 350 360

370 380 390 400 410 420

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670

m286.pep	RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLEAGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLEKRAFSGGIWIYVRDRAGIDARLGAEFLEAGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH
a286	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTREX
a286	SDKKIRWHISLGTREX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

1	atgtttaaac	gcagtgat	tgcaatggct	tgtatttttc	ccctttcagc
51	ctgtgggggc	ggcggtegcg	gatcgcccga	tgtcaagtcg	gcggaacacgc
101	cgtaaaaacc	ggccgcccc	gttggtgctg	aaaatgccgg	ggaaggggtg
151	ctgccgaaag	aaaagaaaga	tgaggaggca	gcgggcggtg	cgccgcaagc
201	cgatacgag	gacgcaaccg	ccggagaagg	cagccaagat	atggcggcag
251	tttcggcaga	aaatacagcg	aatggcggtg	cggaacaac	ggacaacccc
301	aaaaatgaag	acgcgggggc	gcaaaatgat	atgccgcaaa	atgccgcgca
351	atccgcaaat	caaacaggga	acaaccaacc	cgccggttct	tcagattccg
401	cccccgctc	aaacctgcc	cctgcgaatg	gcggtagcga	ttttggaagg
451	acgaacgtg	gcaattctgt	tgtgattgac	ggaccgtcgc	aaaatataac
501	gttgaccac	tgtaaaggcg	attcttgtaa	tggtgataat	ttattggatg
551	aagaagcacc	gtcaaaatca	gaatttgaaa	aattaaagta	tgaagaaaaa
601	attaagcgat	ataaaaaaga	cgagcaacgg	gagaattttg	tcggtttggt
651	tgctgacag	gtaaaaaagg	atggaactaa	caaatatata	atcttctata
701	cggacaaaac	acctactcgt	tctgcacggt	cgaggaggtc	gcttccggcc
751	gagattccgc	tgattcccgt	caatcaggcc	gatacgtgta	ttgtggatgg
801	ggaagcggtc	agcctgacgg	ggcattccgg	caatatcttc	gcgccggaag
851	ggaattaccg	gtatctgact	tacggggcgg	aaaaattgcc	cggcgcatcg
901	tatgccctcc	gtgtgcaagg	cgaaccggca	aaaggcgaaa	tgcttggttg
951	cacggccgtg	tacaacggcg	aagtgtgca	ttccatatg	gaaaacggcc
1001	gtccgtaccc	gtccggaggc	aggtttgccg	caaaagtcga	tttcggcagc
1051	aaatctgtgg	acggcattat	cgacagcggc	gatgatttgc	atatgggtac
1101	gcaaaaattc	aaagccgcca	tcgatggaaa	cggctttaag	gggacttgga
1151	cggaaaatgg	cggcggggat	gtttccggaa	ggttttacgg	cccggccggc
1201	gagggaagtgg	cgggaaaata	cagctatcgc	ccgacagatg	ctgaaaaagg
1251	cggattccgc	gtgtttgccg	gcaaaaaaga	tcgggattga	

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

1	MFKRSVIAMA	CIFPLSACGG	GGGSPDVKS	ADTPSKPAAP	VVAENAGEGV
51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNP
101	KNEDAGAQN	MPQNAAESAN	QTGNNQFAGS	SDSAPASNPA	PANGGSDFGR

671

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151 TNVGNSSVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGNTKYI IFYTDKPTR SARSRRSLPA
251 EIPLIPVNOA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGG
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVDDGIIDSG DDLHMGTOKF KAAIDGNGFK GTWTENGSGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGGFG VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTGT CCCTTTCAGC
51  CTGCGGGGGC GCGGTGGCG GATCGCCGA TGTCAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCT GTTGTTCGT AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTGGCA GCGGGGCAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTGAGATCC CATCCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGGAA GGGTTGATT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAT CAGAATTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTGCGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATT TCGATGGGGA AGCGGTCAGC CTGACGGGCG
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCGAG
1201 TTTGCCGCAA AAGTCGATT CGGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGCAT GATTTCGATA TGGGTACGCA AAAATTCAA GCCGCCATCG
1301 ATGGAACGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGCGA
1451 AAAAAGAGCA GGATTGA

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This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1  MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSPKPAAP VVSEKETEAK
51  EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMAANA
151 DGMQGGDPSA GGQNAGNTAA QGANQAGNNQ AAGSSDPIPA SNFAPANGGS
201 NFGRVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIIFYKPK PTSFARFRRS
301 ARSRRSLPAE MPLIPVNOAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAELPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTOKF KAAIDGNGFK GTWTENGSGDV
451 SGKFYGPAGE EVAGKYSYR PTDAEKGGFG VFAGKKDRD*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEAK
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVAENAGEVLPKEKKDEEA
          10      20      30      40      50      60

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672

m287.pep	50	60	70	80	90	100	109
	KEDAPQAGSCGQGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT						
g287	AGGAPQADTQD--ATAGEGSDMAAVSAENTGNGGAATTDNPKNECAGAQNMPQNAA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDFNMLAGNMENQATDAGESSQPANQPDMAAADGMQGDPSAGGQNAGNTA						
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNIITLTHCKGDS						
g287	-ESANQTGNNQPAGSSDSA PASNPAPANGGSDFGRTNVGNVVIDGPSQNIITLTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP						
g287	CNGDNLLDEEAPSKSEFEKLSDEEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFAFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT						
g287	KPPT-----RSARSRRSLPAEIPVNPQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVLDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYR						
g287	KSVLDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSGRIFYGPAGEEVAGKYSYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGGFGVFAGKKEQDX						
g287	PTDAEKGGFGVFAGKKDRDX						
	420	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

```

a287.seq
1  ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51  CTGTGGGGGC GCGGTGGCG GATCGCCCGA TGTTAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAATGAT ATGCCGCAAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGC ACAACCGCA
451 AACCAACCGG ATATGGCAAA TGCGGCGGAC GGAATGCAGG GGGACGATCC
501 GTCGGCAGGG GAAATGCGG GCAATACGGC AGATCAAGCT GCAAATCAAG
551 CTGAAAACAA TCAAGTCGGC GGCTCTCAAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACTGTT ACACATTGTA
701 AAGACAAAGT ATGCGATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA

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```
801 AGACGAGCAA CGAGAGAATT TTGTCGTTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CCGGATTCAG GCGTTCTGCA CCGTCGAGGC GGTCGCTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTGAGCCTG ACGGGGCATT CCGGCAATAT CTTGCGGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG
1101 ATCGTATGCC CTCAGTGTGC AAGCGGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGTACAAC GCGGAAGTGC TGCATTTCCA TATGAAAAAC
1201 GGCCGTCCGT CCCCGTCCGG AGGCAGGTTT GCGGCAAAAG TCGATTTCCG
1251 CAGCAAATCT GTGGACGGCA TTATCGACAG CCGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGAAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGGA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGCGCGATT CGGCGTGTTC GCCGCAAAA AAGAGCAGGA TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

a287.pep

```
1 MFKRSVIAMA CIVALSCGG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMQDDPSAG ENAGNTADQA ANQAENNQVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDSGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRSLPAEM FLIPVQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGDD LHMGTQKFKA VIDNGGFKGT
451 WTENGGDVVS GRFYGPAGEE VAGKYSYRPT DAEKGGFVGF AGKKEQD*
```

m287/a287 77.2% identity in 501 aa overlap

```
10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSKPAAPVSE-----KETE
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 MFKRSVIAMACIVALSCGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDVAQNMPQNAAGT
|||| :| |:::||||| |||||:::||||:| ||||| |
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADT
70 80 90 100 110

110 120 130 140 150 160 169
m287.pep DSSTPNHTPDENMLAGNMENQATDAGESSQPANQPDMANAAGMQDDPSAGGQNAAGNTA
||||| ||| : :| ||| |||||:||||| ||||| ||||| :|||
a287 DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAAGMQDDPSAG-ENAGNTA
120 130 140 150 160 170

170 180 190 200 210 220 229
m287.pep AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDS
|:|||| |||:::|:| :|| :|||:||||:|:| :|: |:|:|||||
a287 DQAANQAENNQVGGSQNPASSTNPNATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV
180 190 200 210 220 230

230 240 250 260 270 280 289
m287.pep CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDKNDKFVGLVADSVQMKGINQYIIFYKP
|: :||||| :||||| :||:||||| : :||||| |: :| |:|:||||
a287 CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKD
240 250 260 270 280 290

290 300 310 320 330 340
m287.pep KP--TSFARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 KSASSSSARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
300 310 320 330 340 350
```

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	350	360	370	380	390	400
m287 . pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSCGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287 . pep	GSKSVVDGIIDSGDDLHMGTKQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVVDGIIDSGDDLHMGTKQKKAVIDGNGFKGTWTENGSGDVSGRFGYPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287 . pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggtg cgcccttacc gcaccttttc
201 acccttgccct gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgccg ttaaccggca ttctaccctg
301 cggagcccggt actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccg tccaatacgg
501 ctttgggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288. pep
1  MHTQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288. seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTIACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCgGTTTg CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288. pep
1  MHTQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180

m288.pep	DTX
g288	DAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCCCT GTGCTGCCAA AGCAGCCATC GCGGTTTTC CTTTCTGTTC
251 CACTTTCCTG CCGTTACCG CGCCGCGCCG TTAACCGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACAGGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGCTTT AATGCGTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1210; ORF 288.a&gt;:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
		:		:		:

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```

a288      PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADVFVACAQVF
           130      140      150      160      170      180

m288.pep   DTX
           ::
a288      NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```

g290.seq
1  atggcaaaaa tgatgaaatg ggcggctgtt ggcggcggtcg cggcgggcagc
51  gggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt cgccgtccaa cctggtatcg gtcggcgcg caggcttcggg
201 gcagattaaa aagctttatg tcaactcgg gcaacaggtc aaaaaggggc
251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
351 tgcattgggc agcgcggaaa aaaaatataa gcgtcaggcg gcgttggtga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 gccgcgccca aagccaatgt tgcgagttg aaggctttaa tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga tttgggctac acgcgcatta
551 ccgcgacgat ggacggcacg gtggtggcga ttcccggtga agaggggcag
601 actgtgaacg cggcgcgatc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggatacg
751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 gtcgggcggc tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgccg ttcgtttgtg ccgaatccg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaatcgac ggtgtgaaaa atgtgttgct
951 tattccgtcg ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg
1001 tgttgggtgc ggacggcaag gcagtggaac gcgaaatccg gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc ggggtgaaag agggggacaa
1101 agtggctcgc tcgaaataaa ccgcgcgccg gcagcaggaa agcggcgaaac
1151 gcgccctagg cggcccgccg cgccgataa

```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```

g290.pep
1  MAKMMKWAAY AAVAAAAYWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQQV KKGDLIAEIN STTQNTIDM
101 EKSLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTMSGG YNSSTDASN AVYYYARFV PNPDGKLTATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```

m290.seq (partial)
1  ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTGCA
101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GCAAACGTAT
151 CAGGCGAAGC TGGTGTCCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTAATCAG ACAGAGCAAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGAAGAG GGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GCGGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCTG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCTTCG TTTGTGCCGA

```

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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGA AAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGTGTG GGTGCGGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1 ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
 51 QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSDTA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTVE
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                         VSVGAQASGQIKILYVKLGQVKKGDLIAE
                                         |||
g290      PQAAYTEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE
          30      40      50      60      70      80

m290.pep          40      50      60      70      80      90
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||:||||: |||
g290      INSTTQNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATSKEDLESAQD
          90     100     110     120     130     140

m290.pep          100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPEEGQTVNAAQST
          150     160     170     180     190     200

m290.pep          160     170     180     190     200     210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||
g290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          210     220     230     240     250     260

m290.pep          220     230     240     250     260     270
GGYNSSDTASNAVYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
|||
g290      GGYNSSDTASNAVYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
          270     280     290     300     310     320

m290.pep          280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKVVISEITAAEQQESGERALGG
|||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTVEVKSGLKEGDKVVISEITAAEQQESGERALGG
          330     340     350     360     370     380

m290.pep      PPRRX
              ||||
g290          PPRRX
              390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GGCGGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTCAAGGCG GGCGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACCTCG GCAACAGGTT AAAAAGGCGG
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAAC GTATCAGGCG AAGCTGGTGT CCGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTCTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTTGGGTGC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCCGCCG CGCGGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAIV AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTMMSSGG YNSSTDASN AVYYYARFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAREIRTMG
351 RDSMNTEVKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```

                                     10      20      30
m290.pep                               VSVGAQASGQIKILYVKLGQOVKKGDLIAE
a290      POAAYITETVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQOVKKGDLIAE
          30      40      50      60      70      80

          40      50      60      70      80      90
m290.pep  INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
a290      INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD
          90     100     110     120     130     140

          100     110     120     130     140     150
m290.pep  AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
a290      ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
          150     160     170     180     190     200

          160     170     180     190     200     210
m290.pep  PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPLTMMSS
a290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPLTMMSS
          210     220     230     240     250     260

          220     230     240     250     260     270
```

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```

m290.pep    GGYNSSTD TASNAVYYAR SFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
             |||||||
a290        GGYNSSTD TASNAVYYAR SFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
             270      280      290      300      310      320

             280      290      300      310      320      330
m290.pep    KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
             :|||||
a290        KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
             330      340      350      360      370      380

m290.pep    PPRRX
             |||||
a290        PPRRX
             390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1  atgaaaacca agttaatcaa aatcttgacc ccctttaccg tctgcccgt
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgccgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttggacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaa gcaaatcccc ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaaaac acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAASLKR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAGG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTYVSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFFVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHFPQK AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTGTA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTG ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCATTG CCGGCTGCA CCCCAGATGC GCGCGCAAGG
551 CGCAATCTT ATGGTGTGAG CCCGACCGCG CCAAGCGGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTCCT GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG GCGACCCAAA GCGGTACAG CCCGATGCC

```



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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence &lt;SEQ ID 1220; ORF 292&gt;:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAALKAR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238. aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP	PAVKAESAGKSVAAALKARLEKTYSAQDL				
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAES	AVKAESAGKSVAAALKARLEKTYSAQDL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGY	MFVGELINIDTRKNLTEERAADLNKIDF				
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGY	MFVGELINIDTRKNLTEERAADLNKIDF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCK	RLHEFEKMTDVTVYSFMMPIAGLHPDA				
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCK	RLHEFEKMTDVTVYSFMMPIAGLHPDA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTSLGEQFGFN	GTPTLVFPNG			
g292	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTSLGEQFGFN	GTPTLRLPQR			
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGCGCC
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGTTTAA
501 CAGCTTTATG ATGCCATTG CCGGCTGCA CCCCAGTACC GCGCGCAAGG
551 CGCAAAATCTT ATGGTGTGAG CCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATCCG GGTCCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

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This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
251  QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep     MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR LEKTYSAQDL
a292          MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR LEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep     KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
a292          KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep     ASPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
a292          ASPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep     ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
a292          ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep     RSQSGYSMP QLEEIIRKNQX
a292          RSQSGYSMP QLEEIIRKNQX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atcgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtcctggtc
 51  gggttcgggct gtcagaacat catcgaaacc ctttctctgc gcgttacgac
101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcggg tgcggcggtt caagtcgaat cggcggaacg gtggcgtgaa
201  gccgttgaaa aaaccttatac tggcgagggg ggcggaatgc agatgcaggc
251  gcccggtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgaggcggt gcgggaagcg gtatgcggac atcgggggag atagtatac
351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca ccgccttgt cggcggcgtg
451  ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgcgcg
501  cgaggcgccg cgcgaaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601  actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVWSVRA VRTSSNRFPA ALRRYSARFP TIFPKPAGTP
 51  WRRVRRFKSN RTRGVKPLK KPYLARGAEC RCRRAWTALS HNIAERARES
101  PRRCGKRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVCGV
151  FFEVLVLSVL HTGRVSRER REVEKAMS YRVRMPFAVG LLFARGTLES
201  TAAACP...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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m294.seq  
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC  
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC  
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT  
 151 TGGCATCGGG TCGCGCGGT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA  
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC  
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG  
 301 CCGAGGCGGT GCGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC  
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG  
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG  
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCTCG  
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTGAGGG  
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG  
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG  
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT  
 701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC GGTGCGTTGG  
 751 TCGAAATACA TACACGCCGT CGTCTTTACC CATATGCTGC TGATTGTCTT  
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep  
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRRYSAFQP TIFPKPADTP  
 51 WHRVRRFKSN RMRGGKPLK KPYRPRGGG RCRRRAWTALS HNIARARES  
 101 PRRCGKRYAD IGGSDTIRI RVERLEHRMS IYAVAHIVHL YCAIAFVGGV  
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPEFVVG LLFASGIVMA  
 201 ANYLSLIGE PFATSGTML TLKILLAFSV LAHFAIAVVK MARSTLTGVW  
 251 SKYIHAVVET HMLLIVFLAK AMFYISW\*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSA	AVWSVRAVRTSS	NRFFAALRRY	SAFRPTIFPK	PAGTPWHRV	RRFKSN
m294	MRITCAPMSLLSA	AVWSIRVVRTSS	NRFFAAPFRY	SAFQPTIFPK	PADTPWHRV	RRFKSN
	10	20	30	40	50	60
g294.pep	RRTRGVKPLK	KPYLARGAEC	RCRRRAWTALS	HNIAERARES	SPRRCGKRY	ADIGGSDTIRI
m294	RRMRGGKPLK	KPYRPRGGC	RCRRRAWTALS	HNIAERARES	SPRRCGKRY	ADIGGSDTIRI
	70	80	90	100	110	120
g294.pep	RVFRLEHRMS	IYAVAHIIHLY	CATAFVGGV	FFEVLSVLHT	GRVSREAR	REVEKAMSYR
m294	RVFRLEHRMS	IYAVAHIVHLY	CAIAFVGGV	FFEVLSVLHT	GRVSREAR	REVEKAMSYR
	130	140	150	160	170	180
g294.pep	AVRVMPEFVVG	LLFARGTLE	STAAACP			
m294	AVRVMPEFVVG	LLFASGIVMA	ANRYLSILGE	PFATSGTML	TLKILLAFSV	LAHFAIAVVK
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq  
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC  
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC  
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT  
 151 TGGCATCGGG TCGCGCGGT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA  
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGAG GCGGAATGC AGATGCAGGC  
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG  
 301 CCGAGGCGGT ACGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC  
 351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG  
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG  
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCTCG  
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTGAGGG  
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG  
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG  
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

683

```

701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

```

a294.pep
  1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAPFR TIFPKPAGTP
 51 WHRVRRFKSN RRTRGKPLK KTYRPRRAEC RCRRTALS HNIAERARES
101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYLSILGE PFATSGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

```

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	RTSSNRFPA	AFRRYSAPFR	TIFPKPADT	PWHRVRRFKSN	
a294	MRITCAPMSLLSAAVWSIRV	RTSSNRFPA	AFRRYSAPFR	TIFPKPAGT	PWHRVRRFKSN	
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGG	CRRAWTALSHNIAERARES	PRRCGKRYADIGDSDTIRI			
a294	RRTRGKPLKKTYRPRRAEC	RCRRARTALSHNIAERARES	PFERYGKRYADIGDSDTIRI			
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVH	LYCAIAFVGGV	FFEVLVLSVLHTGRVS	REARREVEKAMSYR		
a294	RVFRLEYRMSIYAVAHIVH	LYCAIAFVGGV	FFEVLVLSVLHTGRVS	CEARREVEKAMSYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMFVVGLLFASGIVMA	ANRYLSILGE	PFATSGTMLTLKILLAF	SVLAHFAIAVVK		
a294	AVRVMFVVGLLFASGIVMA	ANRYLSILGE	PFATSGTMLTLKILLAF	SVLAHFAIAVVK		
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVVF	THMLLIVFLAKAMFYISW				
a294	MARSTLTVGWSKYIHTVVF	THMLLIVFLAKAMFYISW				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

```

g295.seq
  1 atgctcggga tggcgcgga cgacggccag cagggcacg ccgcgatatt
 51 gttgccacgc cgcacagcgt tttccgcct cgtcttcgcc ccgataaacg
101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
151 ctgccccgcc agcggtttca tgtcttcaga cggcatcagg tcgtatttgg
201 tattgccgca cactgcacg gatgccgcgc ccaatttcgc caaccgcgcc
251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
301 acggatcagg cggcggaact tcagataacc gttcagcgat tttccgaca
351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgcgc gcattccttc
401 atcagattgg gccagatttc ggtttccatc aaaatgcga acatcgggcg
451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
501 agcggcattg cgcacggga aacagaactt gcgcggtttc ccgtcccgtc
551 ggggtcatct cgtcatcag cagcggcgca tcgggaaaac gccgccgcaa
601 ctgcgcgtatc aagggtctgg cggcacgcgt ttctccgacc gaaacggcgt
651 gtatccaaac cgcgcggta acgggattcg gatgcggcct gccgaaacgc
701 tcgtccctat cgcgccgta tgccggggca cttccggagc gtttgtccaa
751 ataacgccgt atccatatcg gcgcaagcag ccacaataca tcataaagcc
801 attggaacat cttctatatt cctgcaaac aaatgccgtc cgaacggctc
851 ggacggcatt tcggcaacgg aatcaaatat cgtag

```

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

684

## g295.pep

```

1  MLGMAHDDGQ QGIAAILLPR ROQFFRLVFA PINARAAAIG NRPASDAFFK
51  LPRQRHFHVR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLR QTARQRSGCCG
101 TDQAADFQIT VQRFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSQAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

## m295.seq

```

1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTCC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTCAAAA
151 CTGCCCCGCC AGCGTTTTC TCTGTTCGGA CGGTATGATG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGCGCGCAGG
301 ACGGATCAGG CGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC
401 ATCAGGTGGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCGGCG AAAAAGTCC GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGCAATG CGCATCGGGA AACAGAACTT GCGCGGTTT CCGCCCGTC
551 GGGGTCACTC GCGTCATCAG CAGCGGCGCA TCGGGAAC GCGCCGCAA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT CCGCCCGATA TCGCGGGGCA CTTCCGAGC GTTGTCCAA
751 ATAACGCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGGCC
801 ATTGGAACAT CTTTCTATT CCTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGCAACCG AATCAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

## m295.pep

```

1  MLGMAHDDQ QRIAAILLPR ROQFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRHFHFR RYDVVFGLAA HLHGCRAQFR QPRRIRLCLR QTARQRSGGR
101 TDQAADFQIT VQRFFRQPRI RQKQRHTRAP AFPHQVGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRGLRHQ QRRIGKTPPQ
201 LAYQGLGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSQAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV XTVQTAFRQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
	MLGMAHDDQ	QRIAAILLPR	ROQFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRHFHFR
g295	MLGMAHDDGQ	QIAAILLPRR	QOQFFRLVFA	PINARAAAHG	NRPASDAFFK	LPRQRHFHFR
	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
	RYDVVFGLAA	HLHGCRAQFR	QPRRIRLCLR	QTARQRSGGR	TDQAADFQIT	VQRFFRQPRI
g295	RHQVVFGLAA	HLHGCRAQFR	QPRRIRLRLR	QTARQRSGCC	TDQAADFQIT	VQRFFRQPRI
	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
	RQKQRHTRAP	AFPHQVGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
g295	RQKQRHTRSP	AFLHQIGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
	PPRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRIRL	AETLVPMRPI
g295	PSRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRMRL	AETLVPMRPV
	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
	CRGTSQAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
g295	CRGTSQAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTAFRQR	NQIS
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1   ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACS
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTC TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCCGACTT TCAGATAACC GTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCG ACATCGGGCG
451 GTGTTCCGCG AAAAAGTGG GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCCTC
551 GGGGTCATCT GCGTCATCAG CAGCGCGCGA TCGGGAAC GCTGCCGCAA
601 CTCGCGTATC AAAGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCGATA TGCAGGGGCA CTTCCGAGC GTTGTGTTAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGCC
801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGT CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1   MLGMAHDDQ QGIAAILLPR RQQFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQREHLFR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLC QTARQSRGGR
101 TDQAADFQIT V*RRFRQPRI RQQRHTRAP AFLHQIGPDF GFHQAETHRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLFQ
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMAHDDQ	QRIAAILLPR	RQQFFRLVFT	PINARAAAHG	NRNPASDAFFK	LPRQREHLFR
a295	MLGMAHDDQ	QGIAAILLPR	RQQFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQREHLFR
	10	20	30	40	50	60
	70	80	90	100	110	120
m295.pep	RYDVVFGLAA	HLHGCRAQFR	QPRRIRLRLC	QTARQSRGGR	TDQAADFQIT	VQRFFRQPRI
a295	RHQVVFGLAA	HLHGCRAQFR	QPRRIRLRLC	QTARQSRGGR	TDQAADFQIT	VXRFFRQPRI
	70	80	90	100	110	120
	130	140	150	160	170	180
m295.pep	RQQRHTRAP	AFPHQVGP	DFGFHQAETHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
a295	RQQRHTRAP	AFPHQVGP	DFGFHQAETHRA	VFAQKLPYPR	FFVIRKIAAL	CIRKQNLRGF
	130	140	150	160	170	180
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTP	PQLAYQGLGG	TRFSDNRGVYP	NRAGNGIRIRL	AETLVPMRPI
a295	PSRRGHLRHQ	QRRIGKTP	PQLAYQGLGG	TRFSDNRGVYP	NRAGNGIRIRL	AETLAPMRPI
	190	200	210	220	230	240
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
a295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	RTVRTAFRQR	NQISX
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1   ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

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```

51  GCTTGCCGTT TCGATTATTC TGGTGTcgcG GGCATACATT GcTtcgacag
101 aggggaccga gcgcgtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTTGGg gcggcaacgG CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGGcatt tGCCTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCGA
351 CGGCAGTGCG CGCGAAGTGC AGTTTtttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTcGC TTTGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCATG CCGTGCGCCT GCTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGCGGCA
701 CAACCCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCATATTAT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACCGCAT TTCTTCGCGG TTCGGCTACC
851 GATGCGACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACCGCGACT TGAGCGCGTT TTCGAGGCA
1051 CAAGGCATATG TCGCGGCGCG CGAGGTATC GGTTTTGTG GTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGAGGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGGCG GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

g297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGS A REVQFFDDED GERNLVALEK KGGIWRRSAS
151 DADMKVLP LPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQQVA AGDILAEV KGGTTHQAFY YRSDKEGGGG
251 GNYDDEGRV LQEKGGFNIE PLVYTRISSP FGVRMHPILH TWRLHTGIDY
301 AAPQGTFPVR SADGVITFKG RKGGYGNAMV IRHANGVETL YAHLSAFSA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPSV ALPTPELTQA
401 DKAFAAQAQK KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

m297.seq

```

1  ATGGCTGTCT TCCCACTTTC GGCAARACAT CGGAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTcgcG GGCATACATT GcTTCGACAG
101 AGAGGACGGA CGCGCTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TCGGTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCGA
351 CGCGGGCGCG CGCGAAGTGC AGTTTtttaC CGACGAAGAC GGCAGCGCA
401 ATCTGGTcGC TTTGAAAAG AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACCGCGACT TGAGCGCGTT TTCGAGGCA
1051 GAAGGCATATG TCGCGGCGCG CGAGGTATC GGTTTTGTG GTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGAGGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGGCG GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

m297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PORVEQNLP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGS A REVQFFDDED GERNLVALEK KGGIWRRSAS
151 EADMKVLP LPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

```

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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG  
 251 GNYDEDEKLV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY  
 301 AAPQGTTPVRA SADGVITFKG RKGGYGNAVMI RHANGVETL YAHLSAFSQA  
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA  
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD \*

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSII	LVSAAYIASTERT	VRPQRVEQNLP	PLSWGSGVQT		
g297	MAVFPLSAKHKYALRALAVSII	LVSAAYIASTEGT	VRPQRVEQKL	PPLSWGNGVQT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEA	VPQPGDSLADVL	ARSGMARDEI	ARITEKYGG	EADLRHLRAD	QSVHVLVGGDGGA
g297	AYWVQEA	VPQPGDSLADVL	ARSGMARDEI	ARITEKYGG	EADLRHLRAD	QSVHVLVGGDGSA
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFT	DEGGERNLVALEK	KGGIWRRS	ASEADMKV	LPTLRSVV	KTSARGSLARAEVPV
g297	REVQFFT	DEGGERNLVALEK	KGGIWRRS	ASDADMKV	LPTLRSVV	KTSARGSLARAEVPV
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIF	AGRFSLDGLKEG	DAVRLMYD	SLYFHGQQA	AGDILAAEVV	KGGTRHQAFY
g297	EIRESLSGIF	AGRFSLDGLKEG	DAVRLLYD	SLYFHGQQA	AGDILAAEVV	KGGTTHQAFY
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGG	GNYDEDEKVL	QEKGGFNIE	PLVYTRISS	PFGYRMHPIL	HTWRLHTGIDY
g297	YRSDKEGGGG	GNYDEDEKVL	QEKGGFNIE	PLVYTRISS	PFGYRMHPIL	HTWRLHTGIDY
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGT	PVRASADGVIT	FKGRKGGYG	NAVMI RHANG	VETLYAHLSA	FSQAEGNVRGGEVI
g297	AAPQGT	PVRASADGVIT	FKGRKGGYG	NAVMI RHANG	VETLYAHLSA	FSQAQGNVRGGEVI
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRST	GPHLHYEARING	QPVNPVSV	ALPTPELTQ	ADKAFAAQK	QKADALLARLR
g297	GFVGSTGRST	GPHLHYEARING	QPVNPVSV	ALPTPELTQ	ADKAFAAQK	QKADALLARLR
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCCGC	GGCATAACATT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGCAGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTCAAGACG	GCATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GGCGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTGG	TCGGCGGCGA
351	CGGCGGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCGC	TTTGGAAGAAA	AAAGGCGGCA	TATGGCGGCG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTT	GCCGACGCTG	CGTTCGGTGC	TGGTCAAAAC
501	GTCGGCGCGC	GGTTCGCTGG	CGCGGGCGGA	AGTGCCCGTC	GAAATTCGCG



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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCCCTT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTCTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACSATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGCTCT ATACGCGCAT TTCTTCGCCG TCGGCTACC
851 CTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 CCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGC CGCGCGCG CGAGGTCATC GGT TTTGTCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGC GCGCATC AATGGGCAGC
1151 CCGTCAATCC TGT TTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 EACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1 MAVFPLSAKH RYALRALAV SIILVSAAYI ASTERTERV RQRVEQKLPE
51 LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGG EAD
101 LRHLRADQSV HVLVGGDGGG REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGYRMHPILH TWRLHTGIDY
301 AAPQGT PVRA SADGVITFKG RGGYGNVAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
401 EKAAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHRYALRALAVSIILVSAAYIASTERTERV RQRVEQKLPELSWGGSGVQT					
a297	MAVFPLSAKHRYALRALAVSIILVSAAYIASTERTERV RQRVEQKLPELSWGGSGVQT					
	10	20	30	40	50	60
m297.pep	AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGG EADLRHLRADQSVHVLVGGDGGG					
a297	AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGG EADLRHLRADQSVHVLVGGDGGG					
	70	80	90	100	110	120
m297.pep	AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGG EADLRHLRADQSVHVLVGGDGGG					
a297	AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGG EADLRHLRADQSVHVLVGGDGGG					
	130	140	150	160	170	180
m297.pep	REVQFTDEDGERNLVALEKKGGIWRRSASEADMKVLP LRSVVVKTSARGSLARAEVPV					
a297	REVQFTDEDGERNLVALEKKGGIWRRSASEADMKVLP LRSVVVKTSARGSLARAEVPV					
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSL YFHGQQAAGDILAAEVVKGGTRHQAFY					
a297	EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSL YFHGQQAAGDILAAEVVKGGTRHQAFY					
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGNYYDEDEGKVLQEKGGFNIEPLVYTR ISSPFGYRMHPILHTWRLHTGIDY					
a297	YRSDKEGGGGNYYDEDEGKVLQEKGGFNIEPLVYTR ISSPFGYRMHPILHTWRLHTGIDY					
	310	320	330	340	350	360
m297.pep	AAPQGT PVRASADGVITFKGRGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
a297	AAPQGT PVRASADGVITFKGRGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					

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	370	380	390	400	410	420
m297. pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297. pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298. seq

```

1  ATGAAAACT  TTCCTTCCCT  TTTCCCTCC  ATACTGATGT  CTGCCCTGAT
51  TGCCGTGTGG  TTCAGCCAAA  ACCCCATCAA  CGCCTACTGG  CAGCAGACCT
101 ACCACCGCAA  CAGCCCGCTC  GAACCGCTTG  CCGCTACGG  ATGGTGGCGG
151 AGCGGAGCGG  CGTTGCAAGA  AAACGCTAC  GCCCTTTCAG  ACGGCATCAA
201 AACCTTCCTG  TCCGGCGAAA  cgcgcgcac  ggCTCAAGAC  GCGGTTTCGG
251 CAGATATGCC  GCCTGAAGCC  GCCGCATCCG  AAGCCGCCCC  GCCGGCCGGC
301 GGAACAGAAT  GGAACAAGG  CACCGAAGCC  GCCGCCGTCC  GCAGCGGCGA
351 CAAAGTCTTT  TTCGCCGAG  ATTCGCTGAT  GCAGGCGGTT  GCGCTTTCG
401 TGCAAAAAAG  CCTGAAACAG  CAATACGGCA  TCGAATCCGC  CAACCTCAGC
451 AAACAAAGCA  CGGGGCTTTC  CTATCCCTCA  TTCTTCGACT  GGCCGAAAAC
501 GATTGAAGAA  ACCTTGAAAA  AACATCCCGA  AATCAGCGTA  CTCGCCGTCT
551 TCCTCGGCCC  GAACGACCCG  TGGGATTTC  CCGTCGGCAA  ACGTACCTC
601 AATTCGCTT  CCGACGAATG  GCGCAAGAA  TACCTGAAAC  GCGTCGACCG
651 CATCCTTGA  GCGCACACA  CGCACCGCGT  CCAAGTCGTC  TGGCTCGGCA
701 TCCCTACAT  GAAAAAGTC  AAGCTCGACG  GTCAGATGCG  CTACCTCGAC
751 AAAGTCTTT  CGGAACACTT  GAAAGGCAAA  ATCATCCTGA  TTCCACCGC
801 GCAAACTG  AGCGCGGGA  AAGgcGCTA  CACCGATTCC  GTCACGTC
851 ACGGCAAA  CGTCCGCTAC  CGCAGTAAGG  ACGGCATACA  CTTTACCGCC
901 GAAGACAAA  AACTGCTGGC  GGAATAATA  ATGAAAAAA  TCGTTTTGA
951 ACCGAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298. pep

```

1  MKNFLSLFAS  ILSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWR
51  SGAALQENAY  ALSDGIKTF  LSGETPPTAQD  GGSADMPPEA  AASEAAPPAG
101 GTEWKQTEA  AAVRSGDKV  FFGDSLQGV  APFVQSLKQ  QYIESANLS
151 KQSTGLSYPS  FFDWPKTIE  TLKKHPEISV  LAVFLGPNDP  WDFPVGKRYL
201 KFSDEWAQE  YLKRVDRI  LAAHTRVQV  WLGIPLYMKV  KLDGQMYLD
251 KILSEHLK  LILIPTAQL  SGGKGRYTD  VNVNGKPVRY  RSKDGIHFTA
301 EGQKLAEKI  MEKIVFEPST  QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298. seq

```

1  ATGAAAACT  TTCCTTCCCT  TTTCTCCTCC  ATACTGATGT  CTGCCCTGAT
51  TGCCGTGTGG  TTCAGCCAAA  ACCCCATCAA  CGCCTACTGG  CAGCAGACCT
101 ACCACCGCAA  CAGCCCGCTC  GAACCGCTTG  CCGCTACGG  ATGGTGGCGG
151 AGCGGTGCGG  CGTTGCAAGA  AAACGCTAC  GCCCTTTCAG  ACGGCATCAA
201 AGCCTTCCTG  TCCGGCGAAA  CGCGCGGAC  GGCTCAAGAC  GCGGTTTCGG
251 CAGATATGCC  GTCTGAAGCC  GCCGCATCCG  AAGCCGTCCC  TCAAAACGGT
301 GAAACAGAAT  GGAACAAGA  CACCGAAGCC  GCCGCCGTCC  GCAGCGGCGA
351 CAAAGTCTTT  TTTGTGCGG  ACTCGCTGAT  GCAGGCGGTT  GCCCTTTCG
401 TGCAAAAAAG  CCTGAAACAG  CAATACGGCA  TCGAATCCGT  CAACCTCAGC
451 AAACAAAGCA  CGGGGCTGTC  CTACCTCTCA  TTCTTCGACT  GGCCGAAAAC
501 GATTGAAGAA  ACCCTGCAA  AACATCCCGA  AATCAGCGTA  CTCGCCGTCT
551 TCCTCGGACC  GAACGACCCG  TGGGATTTC  CCGTCGGCAA  ACTCTATCTC
601 AATTCGCTT  CCGACGAATG  GCGCAAGAA  TACCTGAAAC  GTGTCGACCG
651 CATCCTTGA  GCGCACACA  CGCACCGCGT  CCAAGTCGTC  TGGCTCGGCA
701 TCCCTACAT  GAAAAAGCC  AAGCTCGACG  GACAGATGCG  CTACCTAGAC
751 AAAGTCTTT  CGGAACATTT  GAAAGGCAAA  ATCATCCTGA  TTCCACCGAC
801 GCACACCTG  AGCGCGGGA  AAGACCGCTA  CACCGACTCC  GTCACGTC
851 ACGGCAAA  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901 GAAGACAAA  AACTGCTGGC  GGAATAATA  ATGAAAAAA  TCGTTTTGA
951 ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

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690

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```

1  MKNFLSLFSS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAPL SGETPPTAOD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201 KFASDEWAQE YLKRVDRILE AAHTRVQVV WLGIPLYMKA KLDGQMRYLD
251 KLLSEHLKGK IILIPTTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETENKQDTEAAAVRSGDKVF					
g298	ALSDGIKIFLSGETPPTAQDGGSDMPPEAAASEAAPFAGGTENKQTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIRSVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQQYGIBANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDPVGKLYLKFADEWAQYELKRVDRILEAAHTRVQVVWLGIPLYMKA					
g298	LAVFLGPNDPWFDPVGKRYLKFADEWAQYELKRVDRILEAAHTRVQVVWLGIPLYMKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGKIILIPTTHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
g298	KLDGQMRYLDKLLSEHLKGKIILIPTAQTLGGKGRYTDVNVNGKPVRYRSKDGIFHTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```

1  ATGAAAAACT TTCTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCTTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAAGTGGC
301 GAAACAGAAT GGAAACAAA CACCGAAGCC GCCCGCTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCG' CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAC
501 GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTCC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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751  AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCTGA TTCCACCGC
801  GCACACCTG AGCGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAA TCGTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1   MKNFLSLFAS IIMSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101 ETEWKQNTA AAVRTGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRIE AAHTHYVQVW WLGI PVMKKA KLDGQMYRLD
251 KLLSEYLGK IILIPHTAHL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWF	SQNPINAYWQQTYHRNSPL	EPLAAYGWWRSGAALQENAY			
a298	MKNFLSLFASILMSALIAVWF	SQNPINAYWQQTYHRNSPL	EPLAAYGWWRSGAALQENAY			
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQD	GGSADMPSEAAASEAVPQT	GETEWKQDTEAAAVRSGDKVF			
a298	ALSDGIKAFISGETPPTAQD	GGSADMPSEAAAPETAPQT	GETEWKQNTA AAVRTGDKVF			
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQ	QYGIESVNLSKQSTGLSYPS	FFDWPKTIEETLQKHPEISV			
a298	FAGDSLMOGVAPFVQKSLKQ	QYGIESVNLSKQSTGLSYPS	FFDWPKTIEETLKKHPEISV			
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWDFPVGKLYL	KFASDEWAQEYLKRVDRIE	AAHTHYVQVWVWLGI PVMKKA			
a298	LAVFLGPNDPWDFPVGKRYL	KFASDEWAQEYLKRVDRIE	AAHTHYVQVWVWLGI PVMKKA			
	250	260	270	280	290	300
m298.pep	KLDGQMYRLDKLLSEHLKGI	IILIPHTAHLSSGGKDRYTD	VNVNGKPVRYRSKDGIFHTA			
a298	KLDGQMYRLDKLLSEYLGKI	IILIPHTAHLSSGGKDRYTD	VNVNGKPVRYRSKDGIFHTA			
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPST	QPSSTQPX				
a298	EGQKLLAAKIMEKIVFEPST	QPSSTQPX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1   ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CGGCCACGCA
51  GGCAGAAGCC CTGCCCGTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCGCGCG CCTCGCCTTG GATGAAAAA CTCCGATCCG TCGCACAAGG
201 CAGCGGCGAG GCCTTCGCA TCCTGCAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACGCC CTGCGCAAC GCCTGCAAAA AACATGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCAAC AGCAGGAACA
401 ATACCGGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAAC CGGCAGCGGC
451 GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCTG ACCGTCAAACG
551 GCAACACCGT CTCGCCAAC GCGGCGGCT GGCAGTACT GGATACGGGC
601 GCGGCACTGC CCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGCGGCAT TACCGTTTC GCGATGGGCA
701 TCAACGGCGC ACAATTGACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCGGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCC TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAAT
851 GGTGGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACGCGCCCC GTCTCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
1001 CCGTTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
1051 ATATGCAGCA TGAATAACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGCGGAA ATGCTTGGCG
1151 ACAGCCTCGA AGAACTCGTC CGCGCGCGC CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
51 NAAASPMWKK LRSVAQSGSE AFRILQIGDS HTAGDFFTDA LRKRLQKTWG
101 DGGIGWYYP NVKGQRMMAV RHSGNWQSF SRNNTGDFPL GGILAQTGSG
151 GGMILTASDG KTGKQVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLAIQTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKWNWLNQ GWAADGVHVF SAQGYRRAAE MLADSLEELV RAAAIRQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

```

1 ATGAACCCCA AACACCTCAT CGCATTTCCTC GCCCTATTTCG CCGCCACGCA
51 GGCGAAGGCC CTACCTGTCTG CCTCCGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCTCCGC CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCAACAGG
201 CAGCGCGGAG ACCTTCCGTA TCCTGCAAAAT CGCGGACTCG CATACGCCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCGCGC AACGTCAAAG GGCAGCGCAT
351 GCGCGCGGTC CGGCACAACG GTAACCTGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCCGCTC GCGGCGATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTG ACCGTCAAACG
551 GCAACACCGT CTCGCCAAC GCGGCGGCT GGCAGTACT GGATACGGGC
601 GCGGCACTGC CCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGCGGCAT TACCGTTTC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTCG CCCAAACCGG CGCGGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAAT
851 GGTGGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
901 CTCATCATCG GCGCACCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
1001 CCGTTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC CATGGGCGGC
1051 ATATGCAGCA TGAATAACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGCGGAA ATGCTCGCGC
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51 NASASPMWKK LQSVQSGSE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101 DGGIGWYYP NVKGQRMMAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKWNWLNQ GWAADGVHVF SAKGYRRAAE MLADSLEELV RSAAIRQ*

```

m299/g299 95.5% identity in 397 aa overlap

```

10 20 30 40 50 60
m299.pep MNPKEHIAFSALFAATQAEALPVASVSLDTVTSPSAPYTDNGLLTDYGNASASPMWKK
||||:|||||

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g299	MNPKHFIAFSALFAATQAEALPVASVSPDVTVTSPSAPYTDNGLLTDYGNAAASFWMKK
	10 20 30 40 50 60
m299.pep	LQSV AQSGSETFRILQIGDSHTAGDPFTDSLRLKRLQKTWGDGGIGWVYPANVKGQRMMAV
	70 80 90 100 110 120
g299	LRSAVQSGSEAFRILQIGDSHTAGDPFTDALRLKRLQKTWGDGGIGWVYPANVKGQRMMAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFTRNNTGDFPLGGILAQTGSCCGMTLTASDGKTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAALPLAIQTTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGRFVRLTEVQQMORRRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNLTGVCGRFVLLTEVQQMORRRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAGYRRAAEMLADSLLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAGYRRAAEMLADSLLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

```

1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAAGCC CTACCTGTCTG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCCCGC
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCAGCGGTC CGGCACAAAC GTAACCTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGTC GCGGCGATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC CGCATGGGCA
701 TCAACGGCGC ACAATTAAAC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCCGGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTGCAGCA TGA AAAA ACTG GCTCAACCAC GGATGGGCGC CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```

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This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGQMAAV RHNGNWQSLT SRNNTGDFPL GGILAH TGSG
151  GSMTLTASDG IASKQVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIADIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQOMQ RRIARQGQTM FWSWQNAMGG
351  VCSMKNLNH  GWAAKDGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

	10	20	30	40	50	60
m299.pep	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTD	TNGLLTDYGNASASPWMKK				
a299	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTD	TNGLLTDYGNASASPWMKK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m299.pep	LQSV AQSGE TFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKGQMAAV					
a299	LQSV AQSGE TFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKGQMAAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAH TGSGGSMTLTASDGIASKQVSLFAKPLLAEQTL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAH TGSGGSMTLTASDGIASKQVSLFAKPLLAEQTL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m299.pep	TVNGNTVSANGGQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIADIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m299.pep	LIIGAPESLKNTLGVCGRPVRLTEVQOMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRPVRLTEVQOMQRRRIARQGQTMFWSWQNAMGGVCSMKNLNH					
	310	320	330	340	350	360
	370	380	390			
m299.pep	GWAAKDGVHFSAGYRRAAEMLADSLEELVRSAAIRQX					
a299	GWAAKDGVHFSAGYQSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGGGGCG AAAGGACGTG CC3ATGACGG TTTGATTACG GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GG3AACGGTG TTGTTTCTT TATTGGGCGT
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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCGGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACGCG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT AITGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTTC CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTTGTGT
1001 TTGCGCTGCC GGGCATTGTT TATGCGCCGA TAACCCGAAG TTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGCAATAT ATTGCCGTTA AAGGGCGCGT GTTCTTAAAA
1201 GAAGTCGGCT TGGCGGCAG TGTGTTGTTT ATCGGTTTTA TTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCGCAA TGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 CTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCGACGATA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATT GGGTATTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDRPVGK KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLGISALM RLLLTSPRK LTFMVFVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 TITDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIYPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPO
451 VIQAAYRIGD SVTNIIIPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIWIAL FCIWVFLGL PVGPGTPTFY PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTGTGGTGC AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTAGC TTTGTGATTG
701 CTTTGATTGG TTATTTTGT ACTGAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCAATCCAA
801 TGAATACACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTGCTCTT ATCCGCCCTA TTGGCTTGA GCATCGTCCC TGCCGACGGT
901 ATTTGCGTTC ATCCTGAAAC AGGATTGGTT TCCGGTTGCG CGTTTTTAAA
951 ATCGATTGTT GTTTTTATTT TCTGTTGTT TGCATGyCG GGCmTTGTTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

```



This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

```

1  MHSIYFFKEK QMSQTDQTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKM
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFPG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPELLACI THQAAVVGPE ANWFFGMWST FVIALIGYFV TEKIVPEQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXXIFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIGFILIC AFINIMGLISA SAQWAVTAPI FVPMLMLAGY APEVIQAAYR
451 ICDSTVNIIT PMMSYFGLIM ATWIKYKDA GVTGLISMML PYSAFFLIAW
501 IALFCIUVVF LGLPVGPGAP TFYPAP*

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Homology with a predicted ORF from *N. gonorrhoeae*

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	TQRDGRFLRTVEWLG	NMLPHPVTLFI	IFIVLLLIASAVGAY	FGL	
g302	MHSIYFFKEKQMSQTD	ARRSGRFLRTVEWLG	NMLPHPVTLFI	IFIVLLLIASAVGAY	FGL	
	10	20	30	40	50	60
m302.pep	70	80	90	100	110	120
	SVPDPRPVGAKGRADD	GLIYIVSLLNADGFI	KILTHTVKNFTGFAP	LPGTVLVSL	LLGVGIA	
g302	SVPDPRPVGAKGRADD	GLIHVVSLLDADGLI	KILTHTVKNFTGFAP	LPGTVLVSL	LLGVGIA	
	70	80	90	100	110	120
m302.pep	130	140	150	160	170	180
	EKSGGLISALMRLLLL	TKSPRKLTTFMVVFT	GILSNTASELGYVVL	IPLSAIIFHSLGRH	PL	
g302	EKSGGLISALMRLLLL	TKSPRKLTTFMVVFT	GILSNTASELGYVVL	IPLSAVIFHSLGRH	PL	
	130	140	150	160	170	180
m302.pep	190	200	210	220	230	
	AGLAAAFAGVSGGYSAN	LFISTIDPELLACITH	QAA-----	VVGPEANWFFMVAS	TFVI	
g302	AGLAAAFAGVSGGYSAN	LFISLTIDPELLAGIT	QAAQI	IHPDYVVGPEANWFF	MAASTFVI	
	190	200	210	220	230	240
m302.pep	240	250	260	270	280	290
	ALIGYFVTEKIVEPQL	GPYQSDLSQEEKDIR	HSNEITPLEYKGLI	WAGVVFV	ALSALLAW	
g302	ALIGYFVTEKIVEPQL	GPYQSDLSQEEKDIR	HSNEITPLEYKGLI	WAGVVFV	ALSALLAW	
	250	260	270	280	290	300
	300	310	320	330	340	350

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSI VVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SIVPADGILRHPETGLVAGSPFLKSI VVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLLXI FFAAQFVAFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SMSTLGLYLVII FFAAQFVAFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGFILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASQAQWAVTAPIFV PNLMLAGYAPEVIQAAYRIGDSVTNII TPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      NLMIGSASQAQWAVTAPIFV PNLMLAGYAPQVIQAAYRIGDSVTNII TPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGT LISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      IKYKKDAGVGT LISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGTPTFFYPVPX
          490      500      510      520      530

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTGATTACAC GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACCGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAAT CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 TGCCGCCATC ATCTTTCATT CCTCGGCCG CCATCCGCTT GCCGCTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGCGCGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGCGCCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACCTG TTTTATATGG
701 TAGCCAGTAC GTTGTGATT GCTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGT CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGCGC TGCGGTGGTG TTGTTGCCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCACGG TATTTTGGCT CATCTGAAA CAGGATTGGT
951 TTCGGTTTCG CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTGGTTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGCGGCAG CGTGTGTTT ATCGGTTTTA TTTAAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTGT
1551 TTGGGCGCTG CCGCTCGGTC CCGGCGGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQDTQRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVG KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLVGIA EKSGLISALM RLLLTSPRK LTTFMVVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMEA SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL FVGPGAPTFY PAP*

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m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	QRDGRFLRTVEW	LGNMPLPHPVTL	FIIFIVLLLLIAS	AVGAYFGL	
a302	MHSIYFFKEKQMSQTD	QRDGRFLRTVEW	LGNMPLPHPVTL	FIIFIVLLLLIAS	AAGAYFGL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLNADG	FIKILTHTVKNFT	GFAPLGTVLVSL	LGVGIA	
a302	SVPDPRPVGAKGRADD	GLIHVVSLDADG	LKILTHTVKNFT	GFAPLGTVLVSL	LGVGIA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLT	KSPRKLTTFMVV	FTGILSNTASELG	YVVLIPLSAI	IFHSLGRHPL	
a302	EKSGLISALMRLLLT	KSPRKLTTFMVV	FTGILSNTASELG	YVVLIPLSAI	IFHSLGRHPL	
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYS	ANLFLSTIDPELL	CITHQAA-----	VVGPEANWFFM	VASTFVI	
a302	AGLAAAFAGVSGGYS	ANLFLGTIDPELL	AGITQAAQIIHP	DYVVGPEANW	FFMVASTFVI	
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEP	QLGPYQSDLSQ	EEDIRHSNEIT	PLEYKGLIWAG	VVFVALSALL	AW
a302	ALIGYFVTEKIVEP	QLGPYQSDLSQ	EEDIRHSNEIT	PLEYKGLIWAG	VVFVALSALL	AW
	250	260	270	280	290	300
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPET	GLVSGSPFLKS	IVVFIFLLFAL	GXVYGRVTR	SLRGEQEVV	NAMEA
a302	SIVPADGILRHPET	GLVSGSPFLKS	IVVFIFLLFAL	PGIVYGRVTR	SLRGEQEVV	NAMEA
	310	320	330	340	350	360
	360	370	380	390	400	410
m302.pep	SMSTLXLXLIFFAA	QFVAFFNWTN	IGQYIAVKGAT	FLKEVGLGGS	VLFIGFILICA	FI
a302	SMSTLGLYLVIIFF	AAQFVAFFNWT	NIGQYIAVKGAT	FLKEVGLGGS	VLFIGFILICA	FI
	370	380	390	400	410	420
	420	430	440	450	460	470
m302.pep	NLMIGSASAQWAVT	APIFVPMMLAG	YAPEVIQAAYR	IGDSVTNIIT	PMMSYFGLIM	ATV
a302	NLMIGSASAQWAVT	APIFVPMMLAG	YAPEVIQAAYR	IGDSVTNIIT	PMMSYFGLIM	ATV
	430	440	450	460	470	480
	480	490	500	510	520	
m302.pep	IKYKKDAGVGTLS	MMLPYSAFFLIA	WIALFCIWVFL	GLPVGPGAPT	FYPAPX	
a302	IKYKKDAGVGTLS	MMLPYSAFFLIA	WIALFCIWVFL	GLPVGPGAPT	FYPAPX	
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

699

g305.seq  
 1 ATGGATTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG  
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG  
 101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC  
 151 CAGCTCGGTG CCGTTTTGGC GGTAGTGT TTGAATACCGGC AGCGTTTCAG  
 201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC  
 251 TCAATCTTGC CATTGCTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC  
 301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT  
 351 GCTGGTTTTG GCGCGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC  
 401 GAGCAGAGCC TAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC  
 451 TTGATGATCG GTGTTGCCCA AGTGTTCGCA CTGGTTCGG GTACGTCCCG  
 501 TTCGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA  
 551 CCGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTTCAGCA  
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT  
 651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCG GGTTCGTTAG  
 701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT  
 751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGTTGTTC  
 801 GGGCTGGATA AGTTGGGAAT GA

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep  
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI  
 51 QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLIAIF IPAAVMGLLF  
 101 LDKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA  
 151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMVAA  
 201 TAYDVLKHYR FFLHVDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF  
 251 AYYRIVFGIV IILLWLSGWI SWE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)  
 1 AtGGATTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG  
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG  
 101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC  
 151 CAGCTCGGTG CAGTTTTGGC GGTAGTGT TTGAATACCGGC AACGTTTCAG  
 201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC  
 251 TTAATCTTGC CATTGCTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC  
 301 GGCawacAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT  
 351 GCTGTTyTG GcCGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC  
 401 GAGCAGAGCC TAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC  
 451 TTGATGATCG GCGTTGCCCA AGTGTTCGCA CTGGTTCGG GTACGTCCCG  
 501 TTCGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA  
 551 TCGCGACAGA ATTCTCGTTT TTCTTGGCTG TGCCGATGAT GGTTCGCGCA  
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT  
 651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCG GGTTCGTTAG  
 701 CGGTAAAAGC GTTGCTGAGG TTGTTTCGG GTAC...

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)  
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI  
 51 QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLIAIF IPAAVMGLLF  
 101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA  
 151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMVAA  
 201 TAYDVLKHYR FFLHVDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60



701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRSRAEPKIADVVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMWGI					
a305	GGFFILWVEKRSRAEPKIVDVALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCAATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAAGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGCGGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCAGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAACCGTTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCGGAAC
551 AAATCCTCAA  CAGCCGAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGACAG  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAWCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAWGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGACGCG  ACAGGCAGTG  CGTAAGAAAG  CGTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTAAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGAACAA  ATCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCAAAGA  AGTCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG  
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA  
 701 GCGGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG  
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)  
 1 ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPNQXK  
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP  
 101 EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA  
 151 SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR  
 201 IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP  
 251 MR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX			
g306	MFMNKSQSGKGLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED			
g306	NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KORIICKWARMPTVRARKGSVPNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRIICKWARMPTNPGARKGSVPNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPRWSVIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq  
 1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT  
 51 CTTCGGTTTG ATACTGGCGA CGGTCATAT TGCCGGTATT TTGTTTTATC  
 101 TGAACCAGAG CGGTCAAAT SCGTTCAAAA TCCCGGTTC GTCGAAGCAG  
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAAGCCTA AGGAAGACAT  
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA  
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT  
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAAG GCGGACGAGC CGGAGCGGGA  
 351 AAAGTCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACG SAAGAGCGTG  
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA  
 451 AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA  
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGGAAC  
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

703

```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTTCGGTTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGEGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KGLSGFFFL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD QAVRKKALT EEREQTVGEK AQKKAETVK
151 KQAVKPSKET EKKASKEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

          10      20      30      40
m306.pep      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
               |:|||||||||||||||||||||||||:|||||||||
a306          MFMNKFSQSGKGLSGFFFLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
               10      20      30      40      50      60

          50      60      70      80      90      100
m306.pep      NOXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREPPD
               ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a306          NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
               70      80      90      100      110      120

          110     120     130     140     150     160
m306.pep      QAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
               ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a306          QAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAAKEKVAPKP
               130     140     150     160     170     180

          170     180     190     200     210     220
m306.pep      TPEQILNSGSIEKARSAAAEVQKMKTPTTRKQRIICKWARMPTVRARKGSVPNWQSWAY
               ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a306          TPEQILNSGSIEKARSAAAEVQKMKTPTTRKQRIICKWARMPTAGARKGSVPNWQSWAY
               190     200     210     220     230     240

          230     240     250
m306.pep      LPRWSVIRRDIKRFTGCKAAICLPMRX
               ||||||| ||||||| |||||||
a306          LPRWSVIRRDIKRFTGCKAAICLPMRX
               250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
51 cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccc
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gcccgaaatc gccattggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gaccggtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaaactc aaagacggca tcaatccgct gaccgatcc aaagccgaca
551 tcgcggaaaa cctgaaaaac atcaaaatcg tcyagcttga agccgcacaa
601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
651 cgccataaagc agcggcaga agctgaccga agccctgttc caagagccga

```



704

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc  
 751 caatggccta aagacgtaac cgaggcctat aactccgacg cgttcaaagc  
 801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg  
 851 aaggcgcagc caataaa

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

g307.pep

1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSADNG AAKKEIVFGT  
 51 TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFQ  
 101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLKSLEEV KDGSTVSAPN  
 151 DPSNFARALV MLNELGWIKL KDGINPLTAS KADIAENLKN IKIVELEAAQ  
 201 LPRSRADVDF AVVNGNYAIS SGMKLTEALF OEPSFAYVNW SAVKTADKDS  
 251 QWLKDVTEAY NSDAFKAYAH KRFEGYKYPA AWNEGAAX\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

m307.seq (partial)

1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC  
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG  
 101 AAGGCGCAGC CAAATAA

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

m307.pep (partial)

1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA AWNEGAAX\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

m307/g307

				10	20	30
m307.pep				QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA		
g307	SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKYPA					
	230	240	250	260	270	280

	39
m307.pep	AWNEGAAXX
g307	AWNEGAAXX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

a307.seq

1 ATGAAACCT TCTTCAAAAC CCTTTCGCC GCCGCACTCG CGCTCATCCT  
 51 CGCCGCTGCG GGCGGTCAAA AAGATAGCGC GCCCGCGCA TCCGCTTCTG  
 101 CCGCCGCCGA CAACGGCGCG GCGAAAAAG NAATCGTCTT CGGCACGACC  
 151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA  
 201 GAAAAAGGC TACACCGTCA AACTGGTCGA GTTTACCGAC TATGTGCGCC  
 251 CGAATCTGGC ATTGGCTGAG GCGAGTNGG ACATCAACGT CTTCACACAC  
 301 AAACCTATC TTGACGACTT CAAAAAGAA CACAATCTGG ACATCACCGA  
 351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCCG EGCAAGCTGA  
 401 AATCGCTGGA AGAAGTCAAA EACGGCAGCA CCGTATCCGC GCCCAACGAC  
 451 CGTCCCACT TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT  
 501 CAAACTCAAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG  
 551 CCGAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG  
 601 CCGCGTAGCC GCGCCGACGT GGATTGTGNC GTCGTCAACG GCAANTACGC  
 651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT  
 701 TTGCCTATGT CAACCTGCTT GCCGTCAAAA CCGCCGACAA AGACAGCCAA  
 751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA  
 801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG  
 851 GCGCAGCCAA ATAA

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

a307.pep

1 MKTFFKTLISA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT

705

```

51  VGDGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKNI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNW  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEQYKSPAA  WNEGAAX+

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                                OWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTDKDSQWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAXX
          |||||
a307      AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGCGGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACSCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1278; ORF 308.ng&gt;:

```

g308.pep
1  MLNRVYFIRL  GVADNLYPCL  SDFCFETIIA  GLPLQAVLWE  RMMVRLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLNVRETP  LAHLNLMKR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSI  AHTLSLFGID  TPDLAEQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGATCC  GATCGGCAAT  ATCGGGCGGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gcg...

```

This corresponds to the amino acid sequence &lt;SEQ ID 1280; ORF 308&gt;:

m308.pep (partial)

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  XTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHALSFLGID  TPDSAEWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
m308.pep	70	80	90	100	110	120
	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308.pep	130	140	150	160	170	180
	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
m308.pep	190	200	210	220	230	
	XTEMGGVVFPVPVAMYRKPOQTADDIVAHSAHLSFLGIDTPDSAEWQGM					
g308	VTEMGGVVFPVPVAMYRKPOQTADDIVAHSAHTLSFLGIDTPDLAEWQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTGTCGCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGCGC  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHALSFLGID  TPDSAEWQGM  AD*

```

707

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTI	IAGLPLQAVLWERRMMVRRLLI	IGISGASGFQY			
a308	MLNRIFYRILGVADNLYPYLSDFCFFTI	IAGLPLQAVLWERRMMVRRLLI	IGISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFHP	IGNIGACTIASGTF			
a308	GVKALXLLRAQDIETHLVVSKGAEMARASE	XYARDXVYALADXVHP	IGNIGACTIASGTF			
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTGMLVAPCSMRTLASVAHGFGDNLLTRA	ADVVLKERRRLVLMVRETPL	NLAHLDNMKR			
a308	KTGMLVAPCSMRTLASVHVGFGDNLLTRA	ADVVLKERRRLVLMVRETPL	NLAHLDNMKR			
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTENGGVVFPVPVAMYRKPQTADDIVAH	SVAHSLFGIDTPD	SAEWQGM			
a308	VTEMGVVFPVPVAMYRKPQTADDIVAH	SVAHSLFGIDTPD	SAEWQGMAD			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCTGTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGAACT
201 TTTGCCGCGG CAAGATGTCG AAACGCACCT TGTGATATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCCGA
401 CGCTTGCCCT TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGGC
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGGCGGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCT CGATGTACCG CAAAGCCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1284; ORF 308-1.ng&gt;:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVMVRETPL NLAHLDNMKR VTEMGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCTGTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGAACT
201 TTTGCCGCGG CAAGATGTCG AAACGCACCT TGTGATATCG AAAGGTCGGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCCGA
401 CGCTTGCCCT TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGGC
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGGCGGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCT CGATGTACCG CAAAGCCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1286; ORF 308-1&gt;:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI

```

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51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA  
 101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA  
 151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO  
 201 TADDIVAHSV AHALSFLGID TPDSAEWQGM AD\*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRVYFIRILGVADNLYPRLSDFCFFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
g308-1	MLNRVYFIRILGVADNLYPCLSDFCFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASEDYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRKQPTADDIVAHSAHLSFLGIDTPDSAEWQGMADX					
g308-1	VTEMGGVVFPVPAMYRKQPTADDIVAHSLHTLSFLGIDTPDLAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTGCGC ACAATTTGTA  
 51 TCCGTATTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTITGCCGT  
 101 TGCAGCGCGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC  
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGANCT  
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG  
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC  
 301 TTGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGCGCT GCATTGCCAG  
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCCGA  
 401 CGCTTGCTTC GGTCTGTCAC GGCTTCGGCG ACAACCTCTT GACCGGTGCG  
 451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTCTGA TGGTCCGCGA  
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA  
 551 TGGGCGGCGT GGTGTTTCCC CCGTTCCTG CGATGTACCG CAAACCGCAG  
 601 ACGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT  
 651 CGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTIIA GLPLOAVLWE RMMVRRLLI  
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA  
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLLTRA  
 151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO  
 201 TADDIVAHSV AHALSFLGID TPDSAEWQGM AD\*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCFFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
m308-1	MLNRVYFIRILGVADNLYPRLSDFCFFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVHGFNDLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					

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m308-1      KTDGMLVAPCSMRITLASVAHGFGDNLTRAADVVKERRRLVLMVRETPLNLALHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVFFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              |||||
m308-1      VTEMGGVFFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1  atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgctgcccg gcgcgctttg ggggtgtttgg
101 gtttggaaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaaacagtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgcccgttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctggt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgcaa acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg ccggtttccg tgccgaagcg gccggattcg
601 gaacggtttt tgetgttgga aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgcgc taccgcgatt
701 tgctgccttt gggcgcgag tgggcggaaa aggcggatgg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggtgccc gtcttcgcga caggctttgg
851 gcatacgcaa ccactaccgc caccgcgaag aacacgggtc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtaa cggttgacgc gctcaccgat gacggacatt
1001 atctcgggcg aacctcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggtt
1151 gcggctcgat aatgatgatg cacggccggt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcatgtcat cattaccggc ggcgcgcgcg cgaaagtcgc
1251 cgaagccctg ccgctcgcat ttttgcgga aaataccgtg gcgctggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1  MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILITV RAGGKTAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET L LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKAWVEN GTFATVGSAP YRDLSPLAGA WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFES RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNVAVSGMM DAVCGSIMMM HGRLKEKNGA
401 GKPDVVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAEGBG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1  ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGTG CCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCArATTAA TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG CCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CCGCGGGATT

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401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGACCC
701 GCTGGTTCAA CGCCTTGCGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTCGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTGCGT GTCATCATT CCGGCGGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTTC GCGGAAAATA CCGTGCGCGT
1101 GCGGGAACAAC CTCGTCAATT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
51 KLGILITV RTGGKTAVV GIGINFLPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSXK RRDSEFLLL DGGNSRLKWA
151 WVNGTFATV GSAPYRDLSP LGAEWAEKAD GNVRIVGCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTTGNAV ASGMMDAVCG SVMMHGRLK EKTGAGKPDV VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

          10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGILITV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETOIKWPNDLVVGRDKLGILITV
          10      20      30      40      50      60

          70      80      90     100     110
m311.pep RTGGKTAVVVGIGINFLPXEVENAASVQSLFQTASRRGNADAHAVLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVVVGIGINFLPKEVENAASVQSLFQTASRRGNADAHVLLLETLLAELGAVLEQ
          70      80      90     100     110     120

m311.pep -----XXXXXXXXX
          :
g311      YAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDRGVLHLETAEGEQTVVS
          130     140     150     160     170     180

          120     130     140     150     160     170
m311.pep XEISLRSDXRPVSXKRRDSEFLLLDGGNSRLKWAWVNGTFATVGSAPYRDLSPGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      GEISLRPDNRSVSPKRPDSEFLLEGGNSRLKWAWVNGTFATVGSAPYRDLSPGAE
          190     200     210     220     230     240

          180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLFSSAQALFGIRNHYRHPEEHGSDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLFSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYFPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKPVVDVIITGGGAAKVAEA					
g311	PAGKRYFPFPTTTGNAVASGMMDAVCGSIMMHGRLKEKNGAGKPVVDVIITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1  ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTT
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACGGTC AGGACGGGCG GCAAACCGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CCGCATCGCG GCGGGGAAAT
301 GCGGATGCCG CCGTGTTGCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA TATGCGCGGG ACGGATTTGC GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGAA ACGGCAGAGG GCAAACAGAC GGTCTGTCAG GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAAGCG GCGGGATTCT
601 GAACGTTTTC TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAAC GGCACGTTCT CAACCGTCGG TAGCGGCGCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCGCG
751 ATCGTCGGTT GCGCCGIGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGTCGCC CGAAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCAGT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCGGGGCG
1201 GGCAAGCCTG TCSATGTCAT CATTACCGGC GCGGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCG CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1  MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIETV RTGGKTAVAV GIGINEVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLHE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSPGLAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYPFPTT TGNASGMM DAVCGSVMMH HGRLKEKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap



712

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIIETV					
a311	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA AVLXXXXXXXX-----					
a311	RTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA AVLLETLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGQGVLLHLETAEGKQTVVS					
	130	140	150	160	170	180
m311.pep	-EISLRSDXRPVSVXKRRDSEFLLLDGGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE					
a311	GEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE					
	190	200	210	220	230	240
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR					
a311	WAEKV DGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR					
	250	260	270	280	290	
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLG GTIMPGFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLG GTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGN AVASGMMDAVCGSVMMHGR LKEKTGAGKPV DVIITGGGA AKVAEA					
a311	HAGKRYPFPTTTGN AVASGMMDAVCGSVMMHGR LKEKTGAGKPV DVIITGGGA AKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLN MIAAEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLN LIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGCGGCT
201 TTTGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTCAGAA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTCACT TTCGGCTGGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGGGCA CTGCGTGCC GCGCGGCTTT
501 GGGGTGTTTG GGTTCGAAA CGCAAATCAA GTGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAACAGT CAGGGCGGGC
601 GGTAAACCGG TTGCCGTGGT CCGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGAGTC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGTTTCG CGCCATTTTT

```

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801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGGACGG CGAAACCGTG TCGGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTTGA AACGCGAGaa ggcGAACAGa cggtcGtcag
951 cggcGaaaTC AGcctTGGGc CGGacaacag gtcggtttcc GTgcccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgtttg aagcggggaa cagccggctc
1051 aAGTGGGcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcGCC
1101 gtaCCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGCGCGATG
1151 GAAATGTCCG CATCGTCGGT TCGCGCTGT GCGGAGAATC CAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCGAGC GCCGCTTCA CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGCG GAACCATCAT GCCCGGCTC CACCTGATGA
1451 AAGAAATCGCT CGCCGTCCGA ACCGCCAAC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCA GCGGCATGAT
1551 GACCGCGGT TCGCGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCG GCGCGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1 MTVLKPSHWR VLAELADGLP QHVSQAREA DMKPQQLNGF WQMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLRLGERS GFQTKALHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLOSK GRGRGGRKWS HRLGECLMFS FGWAFDRPOY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIVTRAG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGA VLLLRDGETV CEGTVKGVDS
301 RGVHLLETAE GEQTVVSGEI SLRPNRSVS VPKRPDSERF LLEGGNSRL
351 KWAWYENTGF ATVGSAFYRD LSPLGAEWAE KADGNVIRVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQL GIRNHYRHE EHGSDRWENA LGSRRFSRNA
451 CVVVSCTGAV TVDALDDGH YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYFFFTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1 ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51 CGGTTTGGCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGGCGC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTTGGCGGT
201 TTTGATGCGC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCACACAAA ACCATATGCG TGACCCACCT
351 GCAAGTAGAG GGCAGGGGGC GGCAGGGGCG GAAAGTGGTC CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTTGACCG GCCGAGTAT
451 GAGTTGGGTT CGTGTGCGC TGTGCGGCA GTGGCGGTGC GCGCGGCTT
501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGTGGT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCA CCGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGACGCGCG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTTGA AACGCGAGAG GGAACACAGA CGGTCGTCAG
951 CGGCGAAATC AGCCTGCGGT CCGACGACAG CCGGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CCGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCTGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCA CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAAATCCT CGCCGTCCGA ACCGCCAAC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGG GGGCAAGCCT GTCGATGTCA TCATTACCG GCGCGCGCG
1651 GCAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1298; ORF 311-1&gt;:

m311-1.pep

```
1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GGRQGRKWS HRLGECLMFS FGWVFDROPY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVHLLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAWVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDFWNA LGSRRFSRRA
451 CVVSCGTAV TVDALDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLN MIAAEGREYE HI*
```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
m311-1.pep	GGRQGRKWSHRLGECLMFSFGWVFDROPYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
m311-1.pep	DLVVGRDKLGGILLETVRTGKTVAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRAGGKTVAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
m311-1.pep	QGVHLLETAEAGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLDGGNSRLKWAWVENGTF					
g311-1	RGVLHLETAEAGEQTVVSGEISLRPDNRSVSVFKRPDSERFLLLEGNSRLKWAWVENGTF					
	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
m311-1.pep	ATVGSAPYRDLSPGLGAWEAKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPGLGAWEAKADGNVRIVGCAVCGESKKAQVQEQLARKIEWLPSSAQAL					
	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
m311-1.pep	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
g311-1	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
m311-1.pep	HLMKESLAVRTANLNRHAGKRYFPFTTTGNASGMMDAVCGSVMHGRLEKKEKAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPFTTTGNASGMMDAVCGSVMHGRLEKKEKAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

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m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
             |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLNLI A AEGGESEHAX
             550      560      570      580      590

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCCATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTCAGCAG
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCMAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGTCTG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTCGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA GTGGCGTGCC GCGCGCCTT
501 GTCGCGTTTG GGTTTGAAAA CGCAAATCAA GTGCCAAAC GATTGGTCTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTCGAA AACCCCGCTT CCCTGCAATC GCTGTTTCAG ACGGCATCGC
701 GTCGCGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTG TGCACCTGGA AACGCGAGAG GGCAACAGA CGTTCGTCAG
951 CCGCGAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTT CTGCTGTTGG ACGCGGCGAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGA AAAA UGGCACGTTT GCAACCGTCG GTAGCCGCCG
1101 GTACCGCGAT TTGTCGCCCT TGGCGCGGGA GTGGCGGAA AAGGTGGATG
1151 GAAATGTCGG CATCGTCGGT TGCGCGGTGT GCGGAGAAAT CAAAAAGGCA
1201 CAAGTGCAAG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCTGTC TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGATACGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGSCAAT GCCGTCGCA CGGGCATGAT
1551 GGTGCGGTTT TGCGGCTCGG TTATGATGAT GCACGGCGGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTC TATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTLVKPSHWR VLAELADGLP QHVSQALMA DMKPOQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDFRPFQ
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGDRKLG GILLETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVILLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEFTVKGVDG
301 QGVHLLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAFYRD LSLPGAWEAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWFNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGCH YLGGTIMGPF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

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a311-1/m311-1 98.5% identity in 591 aa overlap

```

          10      20      30      40      50      60
a311-1.pep  MTLVKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGGLRQHDGYWR
             |||||
m311-1      MTLVKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGGLRQHDGYWR
          10      20      30      40      50      60

          70      80      90     100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
             |||||
m311-1      LVRPLAVFDAEGLRELTERS GFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
          70      80      90     100     110     120

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a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSFGWVDRPQYELGSLSPVAACRRALSRLGLKTQIKWPN					
m311-1	GRGRQGRKWSHRLGECIMFSFGWVDRPQYELGSLSPVAACRRALSRLGLDVQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTAVVVGIGINFLPKKEVENAASVQSLFQTASRRGNADA					
m311-1	DLVVGRDKLGGILIEVTRTGGKTAVVVGIGINFLPKKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHKGAVLLLRDGETVFEGTVKGVG					
m311-1	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHKGAVLLLRDGETVFEGTVKGVG					
a311-1.pep	310	320	330	340	350	360
	QGVLEHLETAEGKQTVVSGEISLRSDRPVSVPKRRDSERFLLLDGGNSRLKWAWEVNGTF					
m311-1	QGVLEHLETAEGKQTVVSGEISLRSDRPVSVPKRRDSERFLLLDGGNSRLKWAWEVNGTF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQRLARKIEWLPSSAQAL					
m311-1	ATVGSAPYRDLSPGAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQRLARKIEWLPSSAQAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGTTIMPGF					
m311-1	GIRNHYRHPEEHGSDRWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGTTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTGNVAVSGMMDAVCGSVMMHGRLEKKTGAGKP					
m311-1	HLMKESLAVRTANLNRHAGKRYFPPTTGNVAVSGMMDAVCGSVMMHGRLEKKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAGGEGSEHTX					
m311-1	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAGGEGSEHTX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggctcg gcaaagactT GGTGGCAacy Gcgaaacacc tTTccgcCAA
201 ATACGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt cgcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCTGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATCGGTGCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCCGCTGCG
551 CCAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTTC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTTCGGCGT
651 ATCCGGTCCA GCGGTGGTCA AAGCCGCGCT GGAAAAATCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTTGT CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CGGTACGCAC

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717

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCGG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGGTC TGCTCCGTTG GTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCGCGCA CACCATTTC GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRI SVT PIAQIAAATK ADSYVSV AQT
101 LDKA AKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNP FMA
201 GAFHSGEAD AVINVGVS GP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVC GTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKT VG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGCGCA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATCTT ACGTCAGCGT GCGCGAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTCGCCTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTG3CGGG
501 CGAAACCGTC AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAATTGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTwTGGCG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCT GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAAGTG CTTTCAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTCGCCGA CCCC GCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCat GATCAACAGC AAAACCACTG CCGTGCCCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGCGCA CAcGGTCGAG TTCGGCGGCT TGTGGgCTA
1251 CGCGCCTGTG ATGCCGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

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1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRI SVT PIAQIAAATH ADSYVSV AQT
101 LDKA AKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNP FXA
201 GAFHSGSDAV INVGVSGPGV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPV GDS VARILEEMGL SVC GTHGTTA
301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA BAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTA VRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

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